

Web site: <http://www-shgc.stanford.edu>  
 Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)  
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,  
 R. M.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IPAL Plate: 41 Row: g Column: 9  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: matched mRNA gi: 9994186  
 This clone has the following problem: frame shifted.

#### FEATURES

Location/Qualifiers  
 1..2826  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4614150"  
 /tissue\_type="kidney"  
 /clone\_lib="NIH MGC\_75"  
 /lab\_host="DH10B"  
 /note="vector: pDNR-LIB"

BASE COUNT 870 a 519 c 591 g 846 t

#### ORIGIN

Query Match 96.7%; Score 1484.8; DB 11; Length 2826;  
 Best Local Similarity 99.7%; Pred. No. 3.6e-286;  
 Matches 1497; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

```

QY 36 AACGAGTACAGATCCTCAGCATGAGAGAAATATTACTGTCTTACTTAATCGAATATT 95
DB 399 AAAGAGTACAGATCCTCAGCATGAGAGAAATATTACTGTCTTACTTAATCGAATATT 458
QY 96 CACGCCCAAGGTTTCTCATCTTATCCAGAAATACGGTCTTGGTATGGAGATTAGTA 155
DB 459 CACGCCCAAGGTTTCTCATCTTATCCAGAAATACGGTCTTGGTATGGAGATTAGTA 518
QY 156 GCAGTAGAGGAAATATGTATGATACAACTTACGTTTGTATGAAAGATTGGGCTTGAAGAC 215
DB 519 GCAGTAGAGGAAATATGTATGATACAACTTACGTTTGTATGAAAGATTGGGCTTGAAGAC 578
QY 216 CAGAGATGATATGCAAGTATGATTTGTAGAGTTTGGAAACCCAGTGTGAACCT 275
DB 579 CCAGAGATGATATGCAAGTATGATTTGTAGAGTTTGGAAACCCAGTGTGAACCT 638
QY 276 ATATTAGGCGCTGGTGTCTGCTGCTACTGTACAGAGAAACAGATTTCTAAAGAAAT 335
DB 639 ATATTAGGCGCTGGTGTCTGCTGCTACTGTACAGAGAAACAGATTTCTAAAGAAAT 698
QY 336 CAAATTAGGATAGATTTGTATCTGATGAATATTTCTTCTGAAACAGGGTTCTGCATC 395
DB 699 CAAATTAGGATAGATTTGTATCTGATGAATATTTCTTCTGAAACAGGGTTCTGCATC 758
QY 396 CACTACAACTTGTCTATGTCACAAATTCACAGAGCTGAGTCTTTCAGTGTACCCCT 455
DB 759 CACTACAACTTGTCTATGTCACAAATTCACAGAGCTGAGTCTTTCAGTGTACCCCT 818
QY 456 TCAGCTTTGCCACTGACCTGCTTTAATATGCTATTAATCTGCTTCTGAAACAGGGTTCTGAGAC 515
DB 819 TCAGCTTTGCCACTGACCTGCTTTAATATGCTATTAATCTGCTTCTGAAACAGGGTTCTGAGAC 878
QY 516 CTTATTTCGATATCTTGAACACAGAGATGCGAGTTGGACTTAGAAGATCTATATAGGCCA 575
DB 879 CTTATTTCGATATCTTGAACACAGAGATGCGAGTTGGACTTAGAAGATCTATATAGGCCA 938
QY 576 ACTTGGCACTTCTTGGCAAGGCTTTTGTATTTTGGAGAAATCCAGAGTGTGGATCTG 635
DB 939 ACTTGGCACTTCTTGGCAAGGCTTTTGTATTTTGGAGAAATCCAGAGTGTGGATCTG 998
QY 636 AACCTTCTACAGAGAGGTAAGATATACAGCTGCACACTCGTAACTTCTCAGTGTCC 695
DB 999 AACCTTCTACAGAGAGGTAAGATATACAGCTGCACACTCGTAACTTCTCAGTGTCC 1058
QY 696 ATAAGGGAAGAACTAAAGAGAAACGATACCAATTTTCTGGCCAGGTTGTCTCTCGTTAAA 755

```

```

DB 1059 ATAAGGGAAGAACTAAAGAGAAACCGATACCAATTTTGGCCAGGTTGTCCTCTGTTAAA 1118
QY 756 CGCTGTGTGGAACTGTGCCTGTGTCTCCACAAATTCGAATGAATGTCAATGTGCCA 815
DB 1119 CGCTGTGTGGAACTGTGCCTGTGTCTCCACAAATTCGAATGAATGTCAATGTGCCA 1178
QY 816 AGCAAGATTACTAAATAATACACAGAGTCTTCAAGTTGAGACCAAAACCGGTTCAGG 875
DB 1179 AGCAAGATTACTAAATAATACACAGAGTCTTCAAGTTGAGACCAAAACCGGTTCAGG 1238
QY 876 GGATTGCAAAATCACTACCGAGTGGCCCTGGAGCACCATGAGAGTGTCACTGTGTG 935
DB 1239 GGATTGCAAAATCACTACCGAGTGGCCCTGGAGCACCATGAGAGTGTCACTGTGTG 1298
QY 936 TGCAGAGGAGACACAGAGGAGTAGCCGCATCACCAACAGAGCTCTTGGCCAGAGCTGTG 995
DB 1299 TGCAGAGGAGACACAGAGGAGTAGCCGCATCACCAACAGAGCTCTTGGCCAGAGCTGTG 1358
QY 996 CAGTGCAGTGGCTGATTTCTATTAGAGAACGTTATGCGTTATCTCCATCTTAACTCAGTT 1055
DB 1359 CAGTGCAGTGGCTGATTTCTATTAGAGAACGTTATGCGTTATCTCCATCTTAACTCAGTT 1418
QY 1056 GTTTCCTTCAAGGACCTTTTCATCTTTCAGGATTTTACAGTGCATCTCTGAAAGAGAGACATC 1115
DB 1419 GTTTCCTTCAAGGACCTTTTCATCTTTCAGGATTTTACAGTGCATCTCTGAAAGAGAGACATC 1478
QY 1116 AAACAGAAATTAGAGAGTTGTGCAACAGCTCTTTTGGAGAGAGCGCTTAAAGGACAGGAGAAA 1175
DB 1479 AAACAGAAATTAGAGAGTTGTGCAACAGCTCTTTTGGAGAGAGCGCTTAAAGGACAGGAGAAA 1538
QY 1176 AGGTCTTCAATCGTGGAAAGAAAATTAATGTTGTATTAATAGATCACAGCTAGTTTC 1235
DB 1539 AGGTCTTCAATCGTGGAAAGAAAATTAATGTTGTATTAATAGATCACAGCTAGTTTC 1598
QY 1236 AGAGTTACCATGTAGCTATTCACCTAGCTGGGTCTCTGATTTTCAGTCTCTTTCGATACGGC 1295
DB 1599 AGAGTTACCATGTAGCTATTCACCTAGCTGGGTCTCTGATTTTCAGTCTCTTTCGATACGGC 1658
QY 1296 TTAGGTTAATGTCACTACAGGAAAAAACTGTGCAAGTGCAGCACCTGATTCCTGCTT 1355
DB 1659 TTAGGTTAATGTCACTACAGGAAAAAACTGTGCAAGTGCAGCACCTGATTCCTGCTT 1718
QY 1356 GCTTAACCTAAAGTCCATGCTCGGCGCTAAATTCGTATTAATCTGA-TTTTTTTT 1414
DB 1719 GCTTAACCTAAAGTCCATGCTCGGCGCTAAATTCGTATTAATCTGA-TTTTTTTT 1778
QY 1415 TTTTTCCTTTCCTCATATTCACATATGTAACCAAGAACATTCATGTACTACAAACCTGGT 1474
DB 1779 TTTTTCCTTTCCTCATATTCACATATGTAACCAAGAACATTCATGTACTACAAACCTGGT 1838
QY 1475 TTTTAAAAAGGAACCTATGTTGCTATGAATTTAAACTTGTGTCATGCTGATAGGACAGACTG 1534
DB 1839 TTTTAAAAAGGAACCTATGTTGCTATGAATTTAAACTTGTGTCATGCTGATAGGACAGACTG 1898
QY 1535 GA 1536
DB 1899 GA 1900

```

#### RESULT 2

BC051876  
 LOCUS 2655 bp mRNA linear HTC 05-MAY-2003  
 DEFINITION Homo sapiens cDNA clone IMAGE:6527736, containing frame-shift errors.  
 ACCESSION BC051876  
 VERSION BC051876.1 GI:30354290  
 KEYWORDS HTC.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 2655)

## AUTHORS

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Dietzenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Heiton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzyzinski, M.I., Skalska, U., Smalusz, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2 (bases 1 to 2655)

Strausberg, R.

Direct Submission

Submitted (01-MAY-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www.shgc.stanford.edu>

Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAP Plate: 110 Row: P Column: 4

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9994186

This clone has the following problem: frame shifted.

## FEATURES

Location/Qualifiers

1..2655

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6527736"

/tissue\_type="uterus, leiomyosarcoma"

/clone\_lib="NIH MGC\_71"

/lab\_host="DH10B"

/note="Vector: pCMV-SPORT6"

## BASE COUNT

822 a 479 c 551 g 803 t

## ORIGIN

Query Match 96.4%; Score 1481.4; DB 11; Length 2655;

Best Local Similarity 99.6%; Pred. No. 1.7e-285;

Matches 1495; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 36 AACGAGTACAGATCCTCAGCATGAGAGAATTATTACTGTCTACTTAATGGAATATT 95

DB 247 AAAGAGTACAGATCCTCAGCATGAGAGAATTATTACTGTCTACTTAATGGAATATT 306

QY 96 CACAGCCCAAGGTTTCTCATCTTATCCAGAAATACGGTCTTGGTATGGAGATTAGTA 155

DB 307 CACAGCCCAAGGTTTCTCATCTTATCCAGAAATACGGTCTTGGTATGGAGATTAGTA 366

QY 156 GCAGTAGAGGAAAAATGTTATGGATACAACTTACGTTTGTATGAAGAATTGGGCTTGAAGAC 215

DB 367 GCAGTAGAGGAAAAATGTTATGGATACAACTTACGTTTGTATGAAGAATTGGGCTTGAAGAC 426

QY 216 CCAGAGATGACATATGCAAGTATGATTTTGTAGAGTTTGAGAACCCAGTGTGGAATCT 275

DB 427 CCAGAGATGACATATGCAAGTATGATTTTGTAGAGTTTGAGAACCCAGTGTGGAATCT 486

QY 276 ATATTAGGGCGCTGGTGGTCTTCTGCTACTGTACCAGGAAAAACAGATTTCTAAAGAAAT 335

DB 487 ATATTAGGGCGCTGGTGGTCTTCTGCTACTGTACCAGGAAAAACAGATTTCTAAAGAAAT 546

QY 336 CAAATTAGGATAAGATTTTGTATCTGATGAATATTTTCTCTCTGAACCGAGGTTCTGCATC 395

DB 547 CAAATTAGGATAAGATTTTGTATCTGATGAATATTTTCTCTCTGAACCGAGGTTCTGCATC 606

QY 396 CACTACAACATTTGTCATGCCCAATTTACAGNAGCTGTGAGTCTTCACTGTACCCCT 455

DB 607 CACTACAACATTTGTCATGCCCAATTTACAGNAGCTGTGAGTCTTCACTGTACCCCT 666

QY 456 TCAGCTTTGCCACTGACCTGCTTAATTAATGCTATAAATGCTTCTAGTACCTTTGGAAGAC 515

DB 667 TCAGCTTTGCCACTGACCTGCTTAATTAATGCTATAAATGCTTCTAGTACCTTTGGAAGAC 726

QY 516 CTTATTTCGATATCTTTGAACCCAGAGAGATGGCAGTTGGACTTTAGAAGATCTATATAGGCCA 575

DB 727 CTTATTTCGATATCTTTGAACCCAGAGAGATGGCAGTTGGACTTTAGAAGATCTATATAGGCCA 786

QY 576 ACTTGGCAACTCTTCTGGCAGAGCTTTTGTATTTTGAAGAAATCCAGAGTGTGGATCTG 835

DB 787 ACTTGGCAACTCTTCTGGCAGAGCTTTTGTATTTTGAAGAAATCCAGAGTGTGGATCTG 846

QY 636 AACCTTCTAAACAGAGAGAGTAAAGATTATACAGCTCCACACCTCGTAACTTCTCAGTGTCC 695

DB 847 AACCTTCTAAACAGAGAGAGTAAAGATTATACAGCTCCACACCTCGTAACTTCTCAGTGTCC 906

QY 696 ATAAGGGAAGAACTAAAGAGAACCGATACCAATTTTCTGGCCAGGTTGTCTCTCTGGTAAA 755

DB 907 ATAAGGGAAGAACTAAAGAGAACCGATACCAATTTTCTGGCCAGGTTGTCTCTCTGGTAAA 966

QY 756 CGCTGTGGTGGAACTGTGCTGCTCTCCCAATTTGCAATTTGCAATTTGCTGCTGCTGCTG 815

DB 967 CGCTGTGGTGGAACTGTGCTGCTCTCCCAATTTGCAATTTGCAATTTGCTGCTGCTGCTG 1026

QY 816 AGCAAGTTACTTAAAAATACCAAGAGTCTTCACTGAGTGGAGACCAACCCGCTGTGAG 875

DB 1027 AGCAAGTTACTTAAAAATACCAAGAGTCTTCACTGAGTGGAGACCAACCCGCTGTGAG 1086

QY 876 GGATTGCAAAATCACTCACCAGCGTGGCCCTGGAGCAACCATGAGGAGTGTGACTGTGTG 935

DB 1087 GGATTGCAAAATCACTCACCAGCGTGGCCCTGGAGCAACCATGAGGAGTGTGACTGTGTG 1146

QY 936 TGCAGAGGAGCAGAGGAGTAGCCGATACACCCAGCAGCTCTTGGCCAGAGCTGTG 995

DB 1147 TGCAGAGGAGCAGAGGAGTAGCCGATACACCCAGCAGCTCTTGGCCAGAGCTGTG 1206

QY 996 CAGTGCAGTGGCTGATTTCTATTAGAGAACGTATGCTTATCTCCATCTTAAATCTCAGTT 1055

DB 1207 CAGTGCAGTGGCTGATTTCTATTAGAGAACGTATGCTTATCTCCATCTTAAATCTCAGTT 1266

QY 1056 GTTCTCTTCAAGGACCTTTTCATCTTTCAAGTATTACAGTGCATTTGAAAGAGGAGACATC 1115

DB 1267 GTTCTCTTCAAGGACCTTTTCATCTTTCAAGTATTACAGTGCATTTGAAAGAGGAGACATC 1326

QY 1116 AAACAGAAATTAGAGTTGTGCAAGCTCTTTTGAAGAGGAGGCTTAAAGAGCAGGAGAA 1175

DB 1327 AAACAGAAATTAGAGTTGTGCAAGCTCTTTTGAAGAGGAGGCTTAAAGAGCAGGAGAA 1386

QY 1176 AGGTCTTCAATCGTGGAAAGAAAAATTAATGTTGTTAAATAGATCACCAGCTAGTTTC 1235

DB 1387 AGGTCTTCAATCGTGGAAAGAAAAATTAATGTTGTTAAATAGATCACCAGCTAGTTTC 1446

Qy	1236	AGAGTTTACCAATGTAAGTATTC	CGATTCGTA	CTAGCTGGGTTCTGTA	TTTCCAGTTCCTTTCGATACGGC	12395
Db	1447	AGAGTTTACCAATGTAAGTATTC	CGATTCGTA	CTAGCTGGGTTCTGTA	TTTCCAGTTCCTTTCGATACGGC	1506
Qy	1296	TTAGGGTAAATGTCAGTACAG	AAAAAAACCTG	TGCAAGTGAGCACCTGAT	TCCGGTTGCCTT	1355
Db	1507	TTAGGGTAAATGTCAGTACAG	AAAAAAACCTG	TGCAAGTGAGCACCTGAT	TCCGGTTGCCTT	1566
Qy	1356	GCTTAACCTCTAAAGCTCCATG	CTCTGGGCTAAATCGTATA	AAATCTGGAATTTT	TTTTTT	1415
Db	1567	GCTTAACCTCTAAAGCTCCATG	CTCTGGGCTAAATCGTATA	AAATCTGGAATTTT	TTTTTT	1623
Qy	1416	TTTTTTTTTGCTCATATTCACAT	ATGTAAC	CAGAACATTCATGTACT	CAAAACCTGGTT	1475
Db	1624	TTTTTTTTTGCTCATATTCACAT	ATGTAAC	CAGAACATTCATGTACT	CAAAACCTGGTT	1683
Qy	1476	TTTTAAAAAGGAACATGTTGCT	ATGTAATTAACCTTG	TGTCATCTGATAGCAGACTGG		1535
Db	1684	TTTTAAAAAGGAACATGTTGCT	ATGTAATTAACCTTG	TGTCATCTGATAGCAGACTGG		1743
Qy	1536	A	1536			
Db	1744	A	1744			

```

RESULT 3
BQ068266
LOCUS
DEFINITION
BQ068266          999 bp          mRNA          linear          EST 02-APR-2002
AGENCOURT_6794408 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5770510
5', mRNA sequence.

```

ACCESSION	BQ068266
VERSION	BQ068266.1
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE  
1 (bases 1 to 999)  
AUTHORS NTH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
mammalia; eutheria; primates; catarrhini; hominidae; homo.

BASE COUNT	290 a	213 c	235 g	261 t
ORIGIN	THIS IS A NINTEC LIBRARY.			

Query Match	51.3%;	Score 787.2;	DB 13;	Length 999;
Best Local Similarity	98.8%;	Pred. No. 6.9e-147;		
Matches 826;	Conservative 0;	Mismatches 8;	Indels 4;	Gaps 3;
QY	4	GTAAATTCAGTTTTCCAGCAACAGGAAACAGAAACGGAGTACAAAGATTCCTCAGCATGAGA	63	
DB	51	GTAAATTCAGTTTTCCAGCAACAGGAAACAGAAACGGAGTACAAAGATTCCTCAGCATGAGA	110	
QY	64	GAATTAATACGTGCTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCATCTATTATC	123	
DB	111	GAATTAATACGTGCTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCATCTATTATC	170	
QY	124	CAGAAATACGGTCTTGGTATCGAGATTAGTAGCAGTAGAGGAAATGATATGATACAAC	183	
DB	171	CAGAAATACGGTCTTGGTATCGAGATTAGTAGCAGTAGAGGAAATGATATGATACAAC	230	
QY	184	TTACGTTTGAATGAAGATTTGGCTTTGAAGACCCAGAAATGACATATGCAAGTATGATT	243	
DB	231	TTACGTTTGAATGAAGATTTGGCTTTGAAGACCCAGAAATGACATATGCAAGTATGATT	290	
QY	244	TTGTAGAAGTTGAGGAACCCAGTGATGGAACCTATATTAGGCGCGTGGTGGTTCGGTA	303	
DB	291	TTGTAGAAGTTGAGGAACCCAGTGATGGAACCTATATTAGGCGCGTGGTGGTTCGGTA	350	
QY	304	CTGTACAGAGAAACAGATTTCTAAAGGAAATCAAAATTAGGATAAAGATTGTATCTGATG	363	
DB	351	CTGTACAGAGAAACAGATTTCTAAAGGAAATCAAAATTAGGATAAAGATTGTATCTGATG	410	
QY	364	AATATTTTCCTTCGAAACGAGGTTCTGCATCCACTACAAATGTGCATGCCACAATCA	423	
DB	411	AATATTTTCCTTCGAAACGAGGTTCTGCATCCACTACAAATGTGCATGCCACAATCA	470	
QY	424	CAGAGCTGTAGTCCCTTCAGTGTACTACCCCTTCAGCTTTGCCACTGGACCTGCTTAATA	483	
DB	471	CAGAGCTGTAGTCCCTTCAGTGTACTACCCCTTCAGCTTTGCCACTGGACCTGCTTAATA	530	
QY	484	ATGCTATAACTGCGCTTTAGTACCTTGGAAACCTTATTCGATATCTTTGAAACAGAGAT	543	
DB	531	ATGCTATAACTGCGCTTTAGTACCTTGGAAACCTTATTCGATATCTTTGAAACAGAGAT	590	
QY	544	GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACCTCTTTGGCAAGCTTTTG	603	
DB	591	GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACCTCTTTGGCAAGCTTTTG	650	
QY	604	TTTTTTGGAAGAAATCCAGAGTGGTGGATCTGAAACCTTCTTAAACAGAGGAGTAAATAT	663	
DB	651	TTTTTTGGAAGAAATCCAGAGTGGTGGATCTGAAACCTTCTTAAACAGAGGAGTAAATAT	710	
QY	664	ACAGCTGCACACCTCGTAACTTCTCAGTGTCC--ATAAGGGAAGAACTAAAGAGAACCGA	721	
DB	711	ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGGAAGAACTAAAGAGAACCGA	770	
QY	722	TACCA-TTTTCTGGCCAGGTGTCTCCTGTGTAAACGCTGTGTGGGAACTGTGCTGTT	780	
DB	771	TACCATTTTTCTGGCCAGTGTGTCTCCTGTGTAAACGCTGTGTGGGAACTGTGCTGTT	830	
QY	781	GTCTCCACAATTCGAATGAATGTCAAT-GTGTCCCAAGCAAGTTACTAAAAATACC	837	
DB	831	GTCTCCACAATTCGAATGAATGTCCATGTGTGCCAAGCAAGTTCTAAAAAATAAC	888	
RESULT 4				
LOCUS	BG677432			
DEFINITION	602652559P1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4750095 5',	969 bp	mRNA	linear
VERSION	BG677432			
KEYWORDS	BG677432.1 GI:13908829			
	EST.			

REFERENCE  
AUTHORS 1 (bases 1 to 969)  
TITLE NIH-MGC <http://mgc.nci.nih.gov/>.  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished  
Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: James Cleaver, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLAM10604 row: f column: 16  
High quality sequence stop: 764.

```

FEATURES
  source      1. .969
  Location/Qualifiers
    high quality sequence stop:

```

```

1. 369
   organism="Homo sapiens"
   mol_type="rRNA"
   db_xref="taxon:9606"
   /clone=IMAGE:4750095
   /tissue type="squamous cell
   /lab host="DH10B (T1 phage-
   /clone lib="NCI CGAP skn"
   /note="Organ: skin; Vector:
   Site 2: SalI; Cloned undir.
   Average insert size 1.5kb.
   Technologies. Note: this is
   223 c 221 g 268 t
   a

```

BASE COUNT  
ORIGIN

Query Match	50.8%	Score 779.6;	DB 10;	Length 969;
Best Local Similarity	91.8%	Pred. No. 2.3e-145;		
Matches 845; Conservative	1;	Mismatches 70;	Indels 4;	Gaps 2;

Qy	621	AGAGTGGTGAGTCTGCAACCTTCTTAACAGAGGAGGTAAAGTTATATACAGTGCACACCTCGT	680
Db	1	ATAGTGGTGAGTCTGCAACCTTCTTAACAGAGGAGGTAAAGTTATATACAGTGCACACCTCGT	60
Qy	681	AACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCAATTTTCTGGCCACGGT	740
Db	61	AACTTCTCAGGTCCATAAGGGAAGAACTAAAGAGAACCGATACCAATTTTCTGGCCAGGT	120
Qy	741	TGTCCTCTGGTTAAACGCTGTGGTGGGAACHTGTGCCTGTGTCTCCACAATTCGAATGAA	800
Db	121	TGTCCTCTGGTTAAACGCTGTGGTGGGAACHTGTGCCTGTGTCTCCACAATTCGAATGAA	180
Qy	801	TGTCAAATGTGTCCCAAGCAAAAGTTACTAAAAAAATACCACGAGGTCCCTTCAGTTCAGACCA	860
Db	181	TGTCAAATGTGTCCCAAGCAAAAGTTACTAAAAAAATACCACGAGGTCCCTTCAGTTCAGACCA	240
Qy	861	AASACCGGTGTACGGGATTCGCAAAATACCTACACGACGTGGCCCTGGAGCACCATGAG	920
Db	241	AAGACCGGTGTACGGGATTCGCAAAATACCTACACGACGTGGCCCTGGAGCACCATGAG	300
Qy	921	GAGTGTCACTGTGTGCAGAGGAGCACAGGAGGATAGCCGATACCCACACGACGCTC	980
Db	301	GAGTGTCACTGTGTGCAGAGGAGCACAGGAGGATAGCCGATACCCACACGACGCTC	360
Qy	981	TTGCCACAGAGCTGTGCAGTGGCTGATTCCTATTAGAGAACGTATGCGTTATCTCCA	1040
Db	361	TTGCCACAGAGCTGTGCAGTGGCTGATTCCTATTAGAGAACGTATGCGTTATCTCCA	420
Qy	1041	TCCTTAATCTCAGTTGTGTTCCTTCAAGGACCTTTTCATCTTCAGAGATTTACAGTGCATCT	1100
Db	421	TCCTTAATCTCAGTTGTGTTCCTTCAAGGACCTTTTCATCTTCAGAGATTTACAGTGCATCT	480
Qy	1101	GAAGAGGAGACATCAAAACAAATTAGAGTGTGCAACACGCTCTTTTGTAGAGAGGCGCT	1160
Db	481	GAAGAGGAGACATCAAAACAAATTAGAGTGTGCAACACGCTCTTTTGTAGAGAGGCGCT	540
Qy	1161	AAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAATTA---AATGTTGTATTAAT	1217

Db	541	AAAGGCAGGAGAAAGGCTCTTCAATCGTGGAAAGAAATTACCCACTGTTGTATTACAT	600
Qy	1218	AGATCACCACTAGTATTCAGAGTTACCATGTACGTATTCACCTAGCTGGGCTCTGTATTT	1277
Db	601	AGATCACCACTAGTATTCAGAGTTACCATGTACGTATTCACCTAGCTGGGCTCTGTATTT	660
Qy	1278	CAGTCTCTTCGATACCGCTTAGGTAAATGTCACGACAGGAAAAAACTGTCGAAGTGAGC	1337
Db	661	CAGTCTCTTCGATACCGCTTAGCGTAATGTCAGTACAGGAAAAAACTGTCGAAGTGAGC	720
Qy	1338	ACCTGATTCCGTTGCCCTTGCTTAACTC-TAAAGCTCCATGCTCCTGGGCCCTAAAAATCGTAT	1396
Db	721	ACCTGATTCCGTTGCCCTTGCTTAACTCTTAAAGCTCCATGCTCCTGGGCCCTAAAAATCGTAT	780
Qy	1397	AAATCTGGATATTTTTTTTTTTTTTTTTTTTGGTCAATATTCACATATGTAAACAGAACATTCT	1456
Db	781	AAGATCTGGATTTCACTACGGTTCTCGGGGCACATTTCCCTTTTTTAAACACAGAACTTTC	840
Qy	1457	ATGTACTACAAACCTGTTTAAAAAGGAACATATGTTGCTATGAATTAACCTTGTCACA	1516
Db	841	TTGTTCTTACAACCTGGTTTTTCCACACGGGCACATATGTCGCTTTGAATTAACCTTGTCAC	900
Qy	1517	TGCTGATPAGACAGACTGGA	1536
Db	901	GGGCCATAGGACCCACGGGA	920

RESULT 5

BG185961

LOCUS

DEFINITION RST4916 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.

BG185961

811 bp

mRNA

linear

EST 21-APR-2001

RESULT 5  
BG185961

Accession	Length	Source	Library	EST
BG185961	811 bp	mRNA	linear	EST 21-APR-2001
RST4916	Athersvs	RAGE Library	Homo sapiens	CDNA, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS

Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McGilligott, K., Booser, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cochran, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.

**TITLE**

Nat. Biotechnol. 19 (5), 440-445 (2001)

MEDLINE	PUBMED	COMMENT
---------	--------	---------

Athersys, Inc.  
3201 Carnegie Ave, Cleveland, OH 44115, USA  
Tel: 216 431 9900  
Fax: 216 361 9596  
Email: [scain@atersys.com](mailto:scain@atersys.com)  
High quality sequence stop: 495.

**FEATURES**

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though, the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
172 c 195 q 216 t 3 others
a

```

BASE COUNT	ORIGIN
1	1
2	2
3	3
4	4
5	5
6	6
7	7
8	8
9	9
10	10
11	11
12	12
13	13
14	14
15	15
16	16
17	17
18	18
19	19
20	20
21	21
22	22
23	23
24	24
25	25
26	26
27	27
28	28
29	29
30	30
31	31
32	32
33	33
34	34
35	35
36	36
37	37
38	38
39	39
40	40
41	41
42	42
43	43
44	44
45	45
46	46
47	47
48	48
49	49
50	50
51	51
52	52
53	53
54	54
55	55
56	56
57	57
58	58
59	59
60	60
61	61
62	62
63	63
64	64
65	65
66	66
67	67
68	68
69	69
70	70
71	71
72	72
73	73
74	74
75	75
76	76
77	77
78	78
79	79
80	80
81	81
82	82
83	83
84	84
85	85
86	86
87	87
88	88
89	89
90	90
91	91
92	92
93	93
94	94
95	95
96	96
97	97
98	98
99	99
100	100

Query Match





```

QY 1017 TAGAGAACGATGCGTTATCTCCATCTTAATCTCAGTTGTGTTTGTCTTCAAGGACCTTTCA 1076
Db 643 TAGAGAACGATGCGTTATCTCCATCTTAATCTCAGTTG-TTGCTTCAAGGACCTTTCA 701

QY 1077 TCTTCAGGATTTACAGTCATTTCTGAAAGAGGAGACATCAACAGAAATTAGGAGTTGTGC 1136
Db 702 TCTTCAGGATTTACAGTCATTTCTGAAAGAGGAGACATCAACAGAAATTAGGAGTTGTGC 761

QY 1137 AACAGCTCTTTTGAAGAGGAGGCTTAAAGGACAGAGAAAGGCTTTC-AATCGTGAAG 1195
Db 762 AACAGCTCTTTGAGAGGAGGCTTAAAGGACAGAGAAAGGCTTTC-CAATCTGGAAG 821

QY 1196 AAAATTAAATGTTGTTAATTAATAGATACCAGCTAGTTTTCAGAGTTTACCATGTACGTATT 1255
Db 822 AAAATTAAATGTTGTTAATTAATAGATACCAGGATAGTTTCAGAGGTTTACCATGTACGTAA 881

RESULT 7
BI870535 802 bp mRNA linear EST 11-OCT-2001
LOCUS 603394005F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5404105 5',
DEFINITION mRNA sequence.
ACCESSION BI870535
VERSION BI870535.1 GI:16044208
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 802)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M12030 row: i column: 02
High quality sequence stop: 791.
Location/Qualifiers
1..802
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5404105"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 90"
/note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 Kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC library."
BASE COUNT 227 a 169 c 198 g 208 t
ORIGIN
Query Match 47.7%; Score 733; DB 12; Length 802;
Best Local Similarity 97.6%; Pred. No. 4.7e-136;
Matches 786; Conservative 1; Mismatches 11; Indels 7; Gaps 4;

QY 550 TGGACTTAGAAGATCTATATAGGCAACTTGGCACTTCTTGGCAGGCTTTGTTTGG 609
Db 3 TGGACTTAGAAGATCTAT-TAGGCAACTTGGCACTTCTG---CAGGCTTTGTTTGG 57

QY 610 GAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTGAAGATTATACAGCT 669
Db 58 GAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTGAAGATTATACAGCT 117

```

```

QY 670 GCACACCTCGTAACCTTCTCAGTGTCCATTAAGGGAAGAACTAAAGAGAACCGATACCACTTT 729
Db 118 GCACACCTCGTAACCTTCTCAGTGTCCATTAAGGGAAGAACTAAAGAGAACCGATACCACTTT 177

QY 730 TCTGGCCAGGTTGTCTCTCTGGTTAAACGCTGTGTGGGAACTGTGTGCTGTGTGTCTCCACA 789
Db 178 TCTGGCCAGGTTGTCTCTCTGGTTAAACGCTGTGTGGGAACTGTGTGCTGTGTGTCTCCACA 237

QY 790 ATTGCAATCAATGTCAATGTGTCCCAAGCAAAAGTTACTTAAATAATACCAGAGGTCCTTC 849
Db 238 ATTGCAATCAATGTCAATGTGTCCCAAGCAAAAGTTACTTAAATAATACCAGAGGTCCTTC 297

QY 850 AGTTGAGACCAAAACCGGCTGTCCAGGGGATTGACAAATCACTCACCGAGTGGCCCTGG 909
Db 298 AGTTGAGACCAAAACCGGCTGTCCAGGGGATTGACAAATCACTCACCGAGTGGCCCTGG 357

QY 910 AGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGCAAGAGGATAGCCGCATCACC 969
Db 358 AGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGCAAGAGGATAGCCGCATCACC 417

QY 970 ACCAGCAGCTCTTGCCAGAGCTGTGACGTGACGTGAGTGGCTGATTTCTATTAGAGAACGTATG 1029
Db 418 ACCAGCAGCTCTTGCCAGAGCTGTGACGTGACGTGAGTGGCTGATTTCTATTAGAGAACGTATG 477

QY 1030 CGTTATCTCCATCTTAATCTCAGTTGTTTGTCTTCAAGGACCTTTCATCTTCAAGGATTTA 1089
Db 478 CGTTATCTCCATCTTAATCTCAGTTGTTTGTCTTCAAGGACCTTTCATCTTCAAGGATTTA 537

QY 1090 CAGTGTATTTCTGAAGAGGAGACATCAAAACAGAAATTAGAGTTGTGCAACAGCTCTTTTG 1149
Db 538 CAGTGTATTTCTGAAGAGGAGACATCAAAACAGAAATTAGAGTTGTGCAACAGCTCTTTTG 597

QY 1150 AGAGGAGGCTTAAAGACAGGAGAAAGCTTCTCAATCTGTGGAAGAAATTTAAATGTC 1208
Db 598 AGAGGAGGCTTAAAGACAGGAGAAAGCTTCTCAATCTGTGGAAGAAATTTAAATGTC 657

QY 1209 GTATTAAATAGATCACACCTAGTTTTCAGAGTTTACCATGTACGTATTTCACCTAGCTGGGT 1268
Db 658 GTATTAAATAGATCACACCTAGTTTTCAGAGTTTACCATGTACGTATTTCACCTAGCTGGGT 717

QY 1269 TCTGTATTTTCAAGTCTTTTCGATACGCTTAAAGTAAATGTCAGTACAGGAAAAAACTGTG 1328
Db 718 TCTGTATTTTCAAGTCTTTTCGATACGCTTAA-GTATATGTCGATACGAAAAAACTGTG 776

QY 1329 CAAAGTACGACCTGATTCGTTGCC 1353
Db 777 CAAAGTACGACCTGATTCGTTGCC 801

RESULT 8
AK052947 2765 bp mRNA linear HTC 05-DEC-2002
LOCUS Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched
DEFINITION C poly-peptide, full insert sequence.
ACCESSION AK052947
VERSION AK052947.1 GI:26343118
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLES High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Komoto, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLES Normalization and subtraction of cap-trapper-selected cDNAs to

```

prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
2049374  
11042159

# REFERENCE

## AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Harada, E., Watanabe, M., Yoneeda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

# TITLE

Genome Res. 10 (11), 1757-1771 (2000)

# JOURNAL

## MEDLINE

## PUBMED

## REFERENCE

## AUTHORS

Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bona, M., F. Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schombach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whitaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohetsuki, S., and Hayashizaki, Y.

# TITLE

Functional annotation of a full-length mouse cDNA collection  
Nature 409 (6821), 685-690 (2001)

# JOURNAL

## MEDLINE

## PUBMED

## REFERENCE

## AUTHORS

Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

# TITLE

Nature 420, 563-573 (2002)

# JOURNAL

## MEDLINE

## PUBMED

## REFERENCE

## AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Inotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.

# TITLE

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

# COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.  
URL: http://genome.gsc.riken.go.jp/  
URL: http://fantom.gsc.riken.go.jp/.

# FEATURES

## source

## Location/Qualifiers

## 1. .2765

## /organism="Mus musculus"

## /mol\_type="mRNA"

## /strain="C57BL/6J"

## /db\_xref="FANTOM\_DB:D930001M08"

## /db\_xref="taxon:10090"

## /clone="D930001M08"

## /tissue type="head"

## /clone\_lib="RIKEN full-length enriched mouse cDNA library"

## /dev\_stage="15 days embryo"

## 274. .1311

## /notes="unnamed protein product; platelet-derived growth factor, C polypeptide (MGD|G1:1859631, GB|NM\_019971, evidence: BLASTN, 99%, match=2691)"

## putative"

## /codon\_start=1

## /protein\_id="BAC35216.1"

## /db\_xref="GI:26343119"

## /translation="MLLLGLLLTSLAQRTGTRAESNLSSKLQSLSDKQGVDPDRHVVVITSGNSIGSPKPHYPRNNVLRVAVDENVRVQLTDFEFGLEDPEDDICKYDFVEEPEPSDGLKRGVCGSPKQSKGNHIRIRFVSDVFRSEPGCFIHYSTIIPQVETTSVSLPPSSLSLDLNNVATFASTLEELIRVLEPRWQVLDLSLYPWTQLQKALYKSKVNLNKLKRVKLYSCTPRNFSVRIEELKRTDITFPFGCLLVKRCGNCACLLHNCNECCVPRKVKYKHYEVLQRLPKTGKGLKSLTDLVALEHHEE

## CDVCRGNAGG"

## polyA\_signal

## 2738. .2743

## /notes="putative"

## polyA\_site

## 2765

## /notes="putative"

## BASE COUNT

## 766 a 593 c 635 g 771 t

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## 817; Conservative

## 0; Mismatches

## 160; Indels

## 0; Gaps

## 0;

## QY

## 4

## GTAATTCAGTTTCCAGCAACAGAAACAGAACGGAGTACAGATCTCTCAGCATGAGA

## 63

## Db

## 356

## GCAAGTTGAGCTCTCCAGCGACAGAAACAGAACGGAGTACAGATCTCTCAGCATGAGA

## 415

## QY

## 64

## GAATTAATCTGCTCTACTAATGAAAGTATTACAGCCCAAGGTTTCTCTCATCTTATC

## 123

## Db

## 416

## GAGTTGCTACTATCTGTAATGGAGCATCCACAGCCCGAAGTTTCTCTCATCATATACC

## 475

## QY

## 124

## CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGATATCAAC

## 183

## Db

## 476

## CAAGAAATATGGTCTGCTGGTGGAGATTAGTTCAGTAGATGAATGTCGGATCCAGC

## 535

## QY

## 184

## TTACGTTTGAAGAAAGTTTGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT

## 243

## Db

## 536

## TGACATTTGATGAGAGATTGGGCTGGAAGATCCAGAGACGATATATGCAAGTATGATT

## 595

## QY

## 244

## TTGTAGAAGTTGAGGAGCCAGTGTAGGAACTATATTAGGCGCTGGTGGTCTTGSTA

## 303

## Db

## 596

## TTGTAGAAGTTGAGGAGCCAGTGTAGGAACTATATTAGGCGCTGGTGGTCTTGSTA

## 655

## QY

## 304

## CTGTACCAAGAAACAGATTTCTTAAGGAAATCAATATTAGGATAAGATTGTATCTGATG

## 363

## Db

## 656

## CTGTGCGAGAAAGCAGATTTCTTAAGGAAATCAATATTAGGATAAGATTGTATCTGATG

## 715

## QY

## 364

## AATATTTTCTTCTGAACAGAGGTTTCTGATCCATCAACATTTGTCTGATGCCACAATTC

## 423

## Db

## 716

## AGTATTTTCCATCTGAACCCGATTTCTGATCCATCAAGTATTTATCATGCCACAAGTCA

## 775

## QY

## 424

## CAGAGCTGTGAGTCTTTCAGTGTCTACCCCTTACCTTTCAGCTTGCACCTGGACCTGCTTA

## 483

## Db

## 776

## CAGAAACCAACAGAGTCTTTCAGTGTCTTTCAGTGTCTTTCAGTGTCTTTCAGTGTCTT

## 835

## QY

## 484

## ATGCTATAACTGCCTTTAGTACCTTGAAGACCTTATTTCGATATCTTGAACACAGAGAT

## 543

[illegible]

CDS	/dev_stage="adult"									
	751..1788									
	/note="unnamed protein product; platelet-derived growth factor, C polypeptide (MGD G1:1859631, GB NM_019971, evidence: BLASTN, 99%, match=2691) putative"									
	/codon_start=1									
	/protein_id="BAC28455.1"									
	/db_xref="GI:26329433"									
	/translation="MLLLGLLLTSLAGQRTGTRAEENLSKQLQSSDKQNGVQDP RHERVVTISGNGSIHSPKFPHTYPRMVLVAVDENRVIQLTFDRFGLDEPDD ICKDFVEBPSDSGLRWGSGTVFKQTSKGNHRIREFVDEYFPSEFCHYK STIMQVETTPSPVLPSSSLDLNNAVTAFTSLLEIRYLEPDRWQVLDLSIKP TWOLGKAPFLCKSKVNLNLLKEVKLYSCTPRNFVSIREELKRYDTTIPWPCLL VKRCGNCACCLHNCNEQCVRKVTKKYHEVLQLRPKTVGKGLKSLTDVALEHHE CDCVCRGNAGG"									
	3216..3221									
	/note="putative"									
	3244									
polyA_signal	/note="putative"									
	BASE COUNT 821 a 810 C 763 G 850 T									
ORIGIN										
Query Match 46.9%; Score 721; DB 11; Length 3244;										
Best Local Similarity 83.6%; Pred. No. 9.4e-134;										
Matches 817; Conservative 0; Mismatches 160; Indels 0; Gaps 0;										
QY	4	GTAAATTCAGTTTCCAGCAACAGGAACAGAGTCAAGATCTCTCAGCATGAGA	63							
Db	833	GCAAGTTGAGCTCTCCAGCGACAGGAACAGAGCGAGTACCCCGCATGAGA	892							
QY	64	GAAATATTACTGTCTACTAATGAAGTATTACAGCCCAAGGTTTCTCTACTATT	123							
Db	893	GAGTTGTCACTATCTGTGTAATGGAGCATCACAGCCCGGAAGTTTCTCTATAC	952							
QY	124	CAAGAAATACGTTCTGTTATGGAGATTAGTAGCAGTAGAGAAATGTTATGAT	183							
Db	953	CAAGAAATATGTTGTTGTTGGAGATTAGTTGCAGTAGATGAAATGTGCGGAT	1012							
QY	184	TTACGTTTGTATCAAGATTGGGCTTGAAGACCCAGAGATGACATATGCAAGT	243							
Db	1013	TGACATTTGATGAGATTGGCTTGAAGATCCAGAGCATATATGCAAGTATG	1072							
QY	244	TGTGAGAGTTGAGAACCCAGTATGGAACATATATTAGGCGCTGGTGGTTCT	303							
Db	1073	TGTGAGAGTTGAGAGCCAGTATGGAAGTGTTTAGGCGCTGGTGGTTCTGG	363							
QY	304	CTGTACCCAGGAAACAGATTTCTAAGGAAATCAAAATAGGATAAGATTG	363							
Db	1133	CTGTGCCAGGAAAGCAGCTTCTAAGGAAATCATATCAGGATAAGATTG	1192							
QY	364	AATATTTTCTCTCTGAACACAGGTTCTGCATCCACTACAAATTTGTCAC	423							
Db	1193	AGTATTTTCCATCTGAACCCGATCTGCATCCACTACAGTATTATCATGCC	1252							
QY	424	CAGAAGCTGTGAGTCCCTCAGTGTACCCCTTCAGCTTTGCGACTGGAC	483							
Db	1253	CAGAAACACAGAGTCCCTCGGTGTGTGCCCTTCATCTTTGTATTGGAC	1312							
QY	484	ATGCTTAACTCCCTTTAGTACCTTGAAGACCTTATTCGATATCTTTGA	543							
Db	1313	ATGCTGTGACTGCTTCAGTACCTTGAAGAGCTGATTCGGTACCTAGAG	1372							
QY	544	GCCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTCTTCT	603							
Db	1373	GGCAGTTGGACTTGGACAGCCTCTCAAGCCCAACATGGCAGCTTTTGG	1432							
QY	604	TTTTTGGAGAAATCCAGAGTGGTGGATCTGAACCTTCTTAAACAGAG	663							
Db	1433	TGTATGGGAAAAAAGCAAGTGGTGAATCTGAATCTCTCTCAAGGAAG	1492							
QY	664	ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATATAGGGAAGAACT	723							

Db	1493	ACAGCTGCACACCCCGGAACCTTCTCAGTGTCCATACGGGAGAGCTAAAGAGACAGATA	1552							
QY	724	CCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAAGTGTGCTGTGTC	783							
Db	1553	CCATATTCTGGCCAGGTTGTCTCCTGGTCAAGCGCTGTGGAGGAATTTGTGCTGTGTC	1612							
QY	784	TCCACAAATTGCAATGAATGTCAATGTGTCCCAAGCAAAAGTTACTAAAAAATACCAGAGG	843							
Db	1613	TCCATAATTGCAATGAATGTCAATGTGTCCCAAGTAAAGTTACAAAAAGTACCATGAGG	1672							
QY	844	TCCTTCAGTTGAGACCAAAASACCGGTGTACAGGGATTGCACAAATCACTCACCGAGCTGG	903							
Db	1673	TCCTTCAGTTGAGACAAAACTGGAGTCAAGGGATTGCATAAGTCACTCACTGATGTGG	1732							
QY	904	CCCTGGAGACCATGAGGAGTGTGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	963							
Db	1733	CTCTGTGAACACCAAGGGAATGTGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1792							
QY	964	ATCACCACCAAGCAGCTC	980							
Db	1793	AGCCTTCGTAGCAGCAC	1809							
RESULT 10										
AK042767										
LOCUS										
DEFINITION										
Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730022g11 product:platelet-derived growth factor, C polypeptide, full insert sequence.										
ACCESSION										
AK042767.1 GI:26335314										
VERSION										
HTC; CAP trapper.										
KEYWORDS										
SOURCE										
ORGANISM										
Mus musculus										
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.										
1										
REFERENCE										
AUTHORS										
TITLE										
High-efficiency full-length cDNA cloning										
Meth. Enzymol. 303, 19-44 (1999)										
JOURNAL										
MEDLINE										
PUBMED										
10349636										
2										
REFERENCE										
AUTHORS										
TITLE										
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes										
Genome Res. 10 (10), 1617-1630 (2000)										
JOURNAL										
MEDLINE										
PUBMED										
20499374										
11042159										
3										
REFERENCE										
AUTHORS										
TITLE										
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer										
Genome Res. 10 (11), 1757-1771 (2000)										
JOURNAL										
MEDLINE										
PUBMED										
20530913										
11076861										
4										
REFERENCE										
AUTHORS										
TITLE										
Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yananaka, I., Saito, T., Okazaki, Y., Goshobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Giusti, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Konno, H.,										

Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Macchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.

**TITLE**  
Functional annotation of a full-length mouse cDNA collection  
**JOURNAL**  
Nature 409 (5821), 685-690 (2001)  
**MEDLINE**  
21085660  
**PUBMED**  
11217851

**REFERENCE**  
5  
**AUTHORS**  
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
**TITLE**  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
**JOURNAL**  
Nature 420, 563-573 (2002)  
**REFERENCE**  
6 (bases 1 to 3405)

**AUTHORS**  
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Saito, K., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, Y., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

**TITLE**  
Direct Submission  
**JOURNAL**  
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@sc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]

**COMMENT**  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.go.jp/  
URL: http://fantom.gsc.riken.go.jp/.

**FEATURES**  
source

1. 3405  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="FANTOM,DB:A730022G11"  
/db\_xref="taxon:10090"  
/clone="A730022G11"  
/tissue="cerebellum"  
/clone\_lib="RIKEN full-length enriched mouse cDNA library"  
/dev\_stage="7 days neonate"  
769..1806  
/notes="unnamed protein product; platelet-derived growth factor, C polypeptide (MGDI|GI:1859631, GB|NM\_019971, evidence: BLASTN, 99%, match=2691)  
putative"

**CDS**

/codon\_start=1  
/protein\_id="BAC13158.1"  
/db\_xref="GI:26335315"  
/translation="MLLGLGLLTSALAGQRTGTRABSNLSKLQSSDKRQGVQDP RHEVTVISNGSHSPKFPHTYPRNVLVYRVAVDENVRIQLTFDERFLEDPDD ICKYDFVEEPDSGLVGEWCGSTVPQSGKGNHRRFVPEPFGFCHY SIIMQVTEFTSPVLPSSLSLDLNNAVTASTLEELRYLEPRWQVLDLSLYKP TWQLLGKFLYKGSKVNLLKKEVKLYSCTPRNFVSIRBELKRTDIFWPGCLL

VRCGNCACCLHNCNEQCQVPRKVTYKHYVLQRLRPKTVKGLHLSLTDVALEHHEE  
CDCVCRGNAGG"

BASE COUNT 854 a 830 c 819 g 902 t  
ORIGIN

Query Match 46.9%; Score 721; DB 11; Length 3405;  
Best Local Similarity 83.6%; Pred. No. 9.3e-134;  
Matches 817; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

QY 4 GTAAATTCACAGTTTCCAGCAACAGGACAGACGAGTACAGATCCTCAGCATGAGA 63  
Db 851 GCAAGTTGCAAGCTCTCCAGCGACAGGACAGGAGTCAAGATCCCGCGCATGAGA 910  
QY 64 GAATTTATTACTGTGTCTACTAATGGAAGTATTACAGCCCAAGGTTTCTCTATCTATATC 123  
Db 911 GAGTTGTCACATATCTCGTAAATGGAGCATCCACAGCCCGAAGTTTCTCTATATATACC 970  
QY 124 CAAGAAATACCGTCTTGGTATGGAGATTAGTAGCAGTAGAGAGAAATGTATGATGATACAA 183  
Db 971 CAAGAAATATGGTGTGGTGTGGAGATTAGTTGCAAGTAGATCAAAATGTGCGGATCCAGC 1030  
QY 184 TTACGTTTGTAGTAAAGATTTTCGGCTTGAAGACCCAGAGAGATGACATATGCAAGTATGATT 243  
Db 1031 TGACATTTGTAGAGAGATTTCGGCTTGAAGATCCAGAGACGATATATGCAAGTATGATT 1090  
QY 244 TTGTAGAAGTTGAGGAAACCCAGTGTGAACTATATTAGGCGCTGGTGTGGTCTCTGTTA 303  
Db 1091 TTGTAGAAGTTGAGGAGCCAGTGTGAACTGTATTAGGAGCGTGGTGTGGTCTCTGGA 1150  
QY 304 CTGTACACGAGAAACAGATTTCTAAAGAAATCAAAATTTAGGATAGATTTGTATCTGATG 363  
Db 1151 CTGTGCCAGGAAAGCAGATTTCTAAAGAAATCATATCAGGATAAGATTTGTATCTGATG 1210  
QY 364 AATATTTTCTTCTGAAACAGGTTCTGCATCCCACTACAACATGTGCATGCCACATTC 423  
Db 1211 AGTATTTTCCATCTGAACCCGAGTTCTGCATCCCACTACAGTATTATCATGCCACAAGTCA 1270  
QY 424 CAGAAGCTGTGAGTCTTTCAGTGTGTACCCCCCTTCAGCTTTTCCCACTGCACCTGCTTAATA 483  
Db 1271 CAGAAACCCAGAGTCTTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT 1330  
QY 484 ATGCTATACTGCTTCTTCTGAGTGTGTACCTTGAAGACCTTTATTCGATATCTTGAACAGAGAT 543  
Db 1331 ATGCTGTGACTGCTTCTGAGTGTGTACCTTGAAGAGTGTATTCGATATCTTGAAGACAGAT 1390  
QY 544 GGCAAGTTGGACTTAGAGATCTATATAGGCCAATCTGGCACTTCTTGGCAAGGCTTTTG 603  
Db 1391 GGCAAGTTGGACTTAGAGATCTTCAAGGCCAATCTGGCACTTCTTGGCAAGGCTTTTCC 1450  
QY 604 TTTTGGAGAGAAATCCAGAGTGTGTGATCTGAACCTTCTAAGAGAGAGGTTAAGATTAT 663  
Db 1451 TGTATGGAGAGAGAGAGAGAGAGTGTGATCTGATATCTCTCAAGAGAGAGGTTAAGACTCT 1510  
QY 664 ACAGTGCACACCTCGTAACTTCTCAGTGTCCATAAGGAGAGAACTAAGAGAGACCGATA 723  
Db 1511 ACAGTGCACACCCCGGAACTTCTCAGTGTCCATAAGGAGAGAGCTAAGAGAGAGAGATA 1570  
QY 724 CCATTTTCTGCCAGGTTGCTCTCTGCTTAAACGCTGTGGTGGAACTGTGCTGCTGTTGTC 783  
Db 1571 CCATTTTCTGCCAGGTTGCTCTCTGCTTAAACGCTGTGGGAGAAATTTGCTGCTGTTGTC 1630  
QY 784 TCCCAATTTCAATGATGATGTCATGTCTCCCAAGCAAGTTTACTTAAATAATPACCACGAGG 843  
Db 1631 TCCCAATTTCAATGATGATGTCATGTCTCCCAAGCAAGTTTCAATAAGTATCAATCATGAGG 1690  
QY 844 TCCTTCAGTTGAGACCAAAACACCGTGTTCAGGGGATGTCACAAATCACTACCCAGCCTGG 903  
Db 1691 TCCTTCAGTTGAGACCAAAACACCGTGTTCAGGGGATGTCACAAATCACTACCTACTGATGG 1750  
QY 904 CCCTGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGAGGACGACAGGAGGATAGCCG 963  
Db 1751 CTCTGAAACACCCAGGAGATGTGACTGTGTGTAGAGGAAACGCCAGGAGGGGTAACTGC 1810

```

QY 964 ATCACCACGAGCAGCTC 980      769 bp      mRNA      linear      EST 04-MAR-2003
Db 1811 AGCCTTCGTAGCAGCAC 1827

RESULT 11
CB309471
LOCUS
DEFINITION AGENCOURT_11834776_NICHD_Rh_Ov1_Macaca_mulatta_cdna_clone
IMAGE:6893055 5', mRNA sequence.
ACCESSION CB309471
VERSION CB309471.1 GI:28832181
KEYWORDS EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Macaca.
1 (bases 1 to 769)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Eliot Spindel
cDNA Library Preparation: CLONTECH
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM3156 row: 1 column: 14
High quality sequence stop: 590.
FEATURES
source
1..769
/organism="Macaca mulatta"
/mol_type="mRNA"
/db_xref="taxon:9544"
/clone="IMAGE:6893055"
/tissue_type="Ovary"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHD Rh Ov1"
/note="Organ: ovary; Vector: pDNR-LIB; Site 1: Sfi I;
Site 2: Sfi I; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.0-4.0 kb. Tissue pooled from
pre-pubertal, post pubertal and menopausal monkeys.
Constructed by Clontech. Note: this is a NICHD Library."
BASE COUNT 220 a 158 c 188 g 202 t 1 others
ORIGIN
Query Match 45.4%; Score 696.8; DB 14; Length 769;
Best Local Similarity 95.9%; Pred. No. 7.9e-129;
Matches 724; Conservative 1; Mismatches 29; Indels 1; Gaps 1;

QY 494 TGCCTTAGTACCTTGAAGACCTTATTCGATATCTTGAACACGAGAGATGGCAGTTGGA 553
Db 3 TGCCTTAGTACCTTGAAGACCTTATTCGATATCTTGAACACGAGAGATGGCAGTTGGA 62

QY 554 CTTAGAGAGCTATATAGGCCAATCTTGCACCTTCTTGGCAAGCTTTGTTTGTGGAAG 613
Db 63 CTTAGAGAGCTATATAGGCCAATCTTGCACCTTCTTGGCAAGCTTTGTTTGTGGAAG 122

QY 614 AAAATCCAGAGTGGTGGATCTGAACCTTCTTAACAGAGAGAGGTAAGATTATACGCTGCAC 673
Db 123 AAAATCCAGAGTGGTGGATCTGAACCTTCTTAACAGAGAGGTAAGATTATACGCTGCAC 182

QY 674 ACCTCGTAACCTTCTAGTGTCCATAGGAAGAACTAAAGAGAACCGATACCAATTTCTG 733
Db 183 ACCTCGTAACCTTCTAGTGTCCATAGGAAGAACTAAAGAGAACCGATACCAATTTCTG 242

QY 734 GCCAGGTGTCTCTGTTAAACGCTGTGGTGGCACTGTGCTGCTTCCCAATTTG 793

```

```

Db 243 GCCAGGTGTCTCTGTTAAACGCTGTGGAGGAACTGTGCTGTTGTCTCCCAATTTG 302
QY 794 CAATGAATGTCAATGTCTCCCAAGCAAGTACTAAAAAATACCACGAGGTCTTTCAGTT 853
Db 303 CAATGAATGTCAATGTCTCCCAAGCAAGTACTAAAAAATACCACGAGGTCTTTCAGTT 362
QY 854 GAGACCAAAACGCTGTCTCAGGGGATTGCACAAATCACTCAACCGACGTGGCCCTGGAGCA 913
Db 363 GAGACCAAAAGACTGGTGTCTCAGAGGATTGCATAAATCACTCACTGATGTGGCCCTTAGAGCA 422
QY 914 CCATGAGAGTGTGACTGTGTGTCAGAGGAGGACACAGGAGGATAGCGGATCACCACCA 973
Db 423 CCATGAGAGTGTGACTGTGTGTCAGAGGAGGACACAGGAGGATAGCGGATCACCACCA 482
QY 974 GCAGCTCTGCCACAGACTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACTATGCGTT 1033
Db 483 GCAGCTCTGCCACAGACTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACTATGCGTT 542
QY 1034 ATCTCCATCTCTTAATCTCAGTGTGTTGCTTCAAGGACCTTTTCATCTTCAGGATTTACAGT 1093
Db 543 ATCTCCATCTCTTAATCTCAGTGTGTTGCTTCAAGGACCTTTTCATCTTCAGGATTTACAGT 602
QY 1094 GCATTTCTGAAAGAGGAGACATCAAAAGAAATTAGAGTGTGCAACAGCTCTTTTGAGAG 1153
Db 603 GCCTTCTGAAAGAGGAGACATCAAAAGAAATTAGAGTGTGCAACAGCTCTTTTGAGAG 662
QY 1154 GAGGCCCTTAAAGGACAGGAGAAAGCTCTCAATCGTGGAAAGAAAATTTAAATGTTGTAAT 1213
Db 663 GAGGCCCTTAAAGGACAGGAGAAAGCTCTTCAATCGTGGAAAGAAAATTTAAATGTTGTAAT 722
QY 1214 AAATAGATCAACGACTAGTTT-CAGAGTTACCATG 1247
Db 723 AAATAGATCAACGACTAGTTT-CAGAGTTACCATG 757

RESULT 12
BC029099
LOCUS
DEFINITION BC029099 2893 bp mRNA linear HTC 20-SEP-2002
Mus musculus, Similar to platelet-derived growth factor, C
polypeptide, clone IMAGE:3660797, mRNA.
ACCESSION BC029099
VERSION BC029099.1 GI:20809397
KEYWORDS HTC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2893)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (01-MAY-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunsaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 35 Row: p Column: 20
This clone was selected for full length sequencing because it

```



passed the following selection criteria: matched mRNA gi: 10242384  
This clone has the following problem: frame shifted.

```
FEATURES
  source
    1. .2893
      /organism="Mus musculus"
      /mol_type="mRNA"
      /strain="CZECH II"
      /db_xref="taxon:10090"
      /clone="IMAGE:3660797"
      /tissue_types="Mammary tumor metastasized to lung.
      MMTV-LTR/Wnt1 model. Expression driven by an MMTV-LTR
      enhancer."
      /clone_lib="NCI CGAP Ju30"
      /lab_host="DH10B"
      /note="Vector: pCMV-SPORT6"
BASE COUNT      868 a 597 c 650 g 778 t
ORIGIN
Query Match      45.2%; Score 693.8; DB 11; Length 2893;
Best Local Similarity 83.4%; Pred. No. 2.6e-128;
Matches 788; Conservative 0; Mismatches 157; Indels 0; Gaps 0;
QY 36 AACGGAGTACAGATCCTCAGCATGAGAGAAATTATTACTGTCTCTACTAATGGAGTATT 95
   |||
Db 439 AAAGGAGTGAAGATCCCGGCATGAGAGAGTTGTCTACTATATCTGTAATGGAGCATC 498
   |||
QY 96 CACAGCCCAAGTTTCTCTACTATTATCCAGAAATACGGTCTTTGGTATGAGATTAGTA 155
   |||
Db 499 CACAGCCCAAGTTTCTCTACTATACATACCAAGAAATATGGTCTGGTGTGAGATTAGTT 558
   |||
QY 156 GCAGTAGAGGAAATGTATGGATACAACTTACGTTTGTATGAAGATTGGCTTTGAAGAC 215
   |||
Db 559 GCAGTAGATGAAATGTGCGGATCCAGTGCATTTGTATGAGAGATTGGGCTGGAAGAT 618
   |||
QY 216 CCAGAAGATCACATATCAAGTATGATTTGTAGAGTTGAGGAACCCAGTATGGAAC 275
   |||
Db 619 CCAGAAGACATCTATCAAGTATGATTTGTAGAGTTGAGGAGCCAGTATGGAAGT 678
   |||
QY 276 ATATTAGGGCGTGGTGTGGTCTGTACTGTACACAGGAAACAGATTTCTTAAAGGAAAT 335
   |||
Db 679 GTTTTAGGACGCTGGTGTGGTCTGTGGGACTGTGCCAGGAAGCAGACTTCTTAAAGGAAAT 738
   |||
QY 336 CAAATTAGGATAGATTTGATCTGATGAATATTTTCTTCTGAAACAGGTTCTGCATC 395
   |||
Db 739 CATATCAGGATAGATTTGATCTGATGAGTATTTTCCATCTGAAACCGGATTTCTGCATC 798
   |||
QY 396 CACTACAACTTTGTCATGCCCAACTTACAGAACTGTGAGTCTCTTCAAGTCTACCCCT 455
   |||
Db 799 CACTACAGTATTATCATGCCACAGTACAGAAACCCAGAGTCCTTGGTGTGCCCT 858
   |||
QY 456 TCAGCTTTGCCACCTGGACCTGTTAATATGCTATAACTGCTTTAGTACCTTGGAGAC 515
   |||
Db 859 TCATCTTTGTCAATGGACCTGCTCAACAACTGTGACTGCTTCAAGTACCTTGGAGAG 918
   |||
QY 516 CTATTTCGATATCTTGACAGAGAGATGGCAGTTGGACTTAGAGATCTATATAGGCCA 575
   |||
Db 919 CTGATTCGGTACCTAGAGCCAGATTCGATGGCAGGTGACCTTGGACAGCTCTCAAGCCA 978
   |||
QY 576 ACTTGGCAACTTCTTGGCAAGGCTTTTGTGTTTGGAGAGAAATCCAGAGTGGTGGATCTG 635
   |||
Db 979 ACATGGCAGCTTTTGGGCAAGGCTTCTCTGTATGGGAAAGAAAGCAAGTGGTGAATCTG 1038
   |||
QY 636 AACCTTCTACAGAGGAGTGAATTTATACAGCTGCACTCTCTAATCTCTCAGTGTCC 695
   |||
Db 1039 AATCTCTAAAGGAGAGGTAAAACTCTACAGCTGCACACCCCGGAACTTCTCAGTGTCC 1098
   |||
QY 696 ATAGGGAAGAACTAAAGAGAACCGATACCAATTTCTGGCCAGGTTGCTCCTGTTAAA 755
   |||
Db 1099 ATACGGGAAGAGCTAAAGAGAGACAGATACCATATTTCTGGCCAGGTTGCTCCTGGTCAAG 1158
   |||
QY 756 CGCTGTGTGGGAAGTGTGCTGTGTGCTCCACAAATTCGAATGAATGCAATGTGTCCCA 815
   |||
Db 1159 CGCTGTGGAGAAATTTGGCTGTGTGCTCCATTAATTTGCAATGAATGTCAGTGTGTCCCA 1218
   |||
```

```
QY 816 AGCAAGTTTACTAAAAATATACACGAGGTCTTTCAGTTGAGACCAAAACCGGTGTGAG 875
   |||
Db 1219 CGTAAAGTTTACAAAAAGTATACCATGAGTCTCTTTCAGTTGAGACCAAAACCGGTGTGAG 1278
   |||
QY 876 GGATTGCACAAATCACTACCGAGTGGCCCTGAGCACCACCATGAGGATGTGACTGTGTG 935
   |||
Db 1279 GGATTGCATAAGTCACTCATTTGATGTGGCTCTGGAACACCAACGAGGAATGTGACTGTGTG 1338
   |||
QY 936 TGCAAGGGAGACAGCAGGAGGATAGCCGCATCACACACGACGACGCTC 980
   |||
Db 1339 TGTAGAGAAACGCGAGGAGGTAAGTCTGAGGCTTCGTAGCAGCAC 1383
   |||
```

```
RESULT 13
LOCUS      BQ015321/c
DEFINITION UI-H-ED1-axw-j-04-0-UI.sl NCI CGAP_ED1 Homo sapiens CDNA clone
IMAGE:5834595 3', mRNA sequence.
ACCESSION  BQ015321
VERSION     BQ015321.1
KEYWORDS    GI:19740222
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 686)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE        National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL      Unpublished
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgapsb-re@mail.nih.gov
              Tissue Procurement: Dr. Jose Mercuende
              CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
              CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
              DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
              Clone Distribution: Clone distribution information can be found
              through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
              Seq primer: M13 FORWARD
POLYA-Yes
```

```
FEATURES
  source
    1. .686
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:5834595"
      /tissue_type="Chondrosarcoma"
      /dev_stage="Adult"
      /lab_host="DH10B (Life Technologies)"
      /clone_lib="NCI CGAP ED1"
      /note="Organ: Left Pubic Bone; Vector: pT73-Pac
      (Pharmacia) with a modified polylinker; Site 1: EcoR I;
      Site 2: Not I; NCI CGAP_ED1 is a normalized CDNA library
      containing the following tissue(s): Chondrosarcoma cell
      line C85. The library was constructed according to Bonaldo
      , Lennon and Soares, Genome Research, 6:791-806, 1996.
      First strand cDNA synthesis was primed with an oligo-dT
      primer containing a Not I site. Double stranded cDNA was
      ligated to an EcoR I adaptor, digested with Not I, and
      cloned directionally into pT73-Pac vector. The
      oligonucleotide used to prime the synthesis of
      first-strand cDNA contains a library tag sequence that is
      located between the Not I site and the (dT)18 tail. The
      sequence tag for this library is GCTCAAGGCT.
      TAG_LIB=UI-H-ED1
      TAG_TISSUE=chondrosarcoma
      TAG_SEQ=CGTCAAGGCT"
BASE COUNT      197 a 152 c 130 g 207 t
ORIGIN
```

Query Match 41.7%; Score 640; DB 12; Length 686;  
Best Local Similarity 98.7%; Pred. No. 1.7e-117;



prepare mouse tissues.

Please visit our web site for further details.

URL: <http://genome.gsc.riken.go.jp/>

URL: <http://fantom.gsc.riken.go.jp/>

## FEATURES

source

Location/Qualifiers

1..2502  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="FANTOM DB:C130008P20"  
/db\_xref="taxon:10090"  
/clone="C130008P20"  
/tissue\_type="head"  
/clone\_lib="RIKEN full-length enriched mouse cDNA library"  
/dev\_stage="16 days embryo"

misc\_feature

1..2502

/note="platelet-derived growth factor, C polypeptide  
(MGD|MG:1859631, GB|NM\_019971, evidence: BLASTN, 99%,  
match=2691)"

BASE COUNT

711 a 529 c 523 g 739 t

ORIGIN

Query Match 39.3%; Score 604.2; DB 11; Length 2502;

Best Local Similarity 84.2%; Pred. No. 2e-110;

Matches 681; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

Qy 36 AACGAGTACAGATCCTCAGCATGAGAGATTTACTGTCTACTAATGCAAGTATT 95

Db 188 AAAGAGTGAAGATCCCGCATGAGAGTTGTCACTATATCTGGTAATGGAGCATC 247

Qy 96 CACAGCCCAAGTTTCCTCATCTATCTATCCAGAAATACGGTCTTGGTATGGAGATTAGTA 155

Db 248 CACAGCCCAAGTTTCCTCATCATACATACCAAGAAATATGGTCTGGTGTGGAGATTAGTT 307

Qy 156 CGAGTAGAGGAAATGTATGATACCACTAGCTTTGATGAAGATTGGGCTTCAAGAC 215

Db 308 CGAGTAGATGAATGTCCGATCCAGCTGACATTTGATGAGAGATTGGGCTGGAAGAT 367

Qy 216 CCAGAGATGACATATGCAAGTATGATTTGTAGAAGTTTGAGAACCCAGTGTGGAAT 275

Db 368 CCAGAGACGATATATGCAAGTATGATTTGTAGAAGTTTGAGAGCCAGTGTGGAAT 427

Qy 276 ATATTAGGCGCTGTGTGGTCTGGTACTGTACAGAGAAACAGATTTCAAGGAAT 335

Db 428 GTTTTAGACGCTGTGTGGTCTGGGACTGTGCCAGGAAGACAGACTTTCAAGGAAT 487

Qy 336 CAATTAGATAAGATTTGTATCTGATCAATATTTTCTCTGACACAGGTTCTGCATC 395

Db 488 CATATCAGGATAGATTTGTATCTGATGAGTATTTTCCATCTGAACCCGGATCTGCATC 547

Qy 396 CACTACAACTGTGATGCCCAATTCACAGAGCTGTGAGTCTTCAAGTGTACCCCT 455

Db 548 CACTACAGTATATCATGCCCAAGTCCACAGAAACACAGAGTCTTCCGTTGCCCCCT 607

Qy 456 TCAGCTTGCCACTGGACCTCTTAATATGCTATATCTGCTTACCTTTAGTACCTTGAAGAC 515

Db 608 TCATCTTTGTCATTTGGACCTGCTCAACAATGCTGACTGCTTCCAGTACCTTGAAGAG 667

Qy 516 CTTATTCGATATCTTGAACACAGAGATGGCAGTTGGACTTAGAGATCTATATAGGCCA 575

Db 668 CTGATTCGTTACCTAGACAGATCGATGGCAGGTGGACTTGGACAGCTCTACAGCCA 727

Qy 576 ACTTGGCACTTTTGGCAAGCTTTTCTGTTTGGAGAAATCCAGAGTGGTGGATCTG 635

Db 728 ACATGGCAGCTTTTGGGCAAGCTTTCTCTGTATGGGAAAAAAGCAAGTGGTGAATCTG 787

Qy 636 AACCTTCTAACAGAGGAGTAAATATACAGCTGCACACCTCTGTAATCTCTAGTGTCC 695

Db 788 AATCTCTCTCAAGGAGAGTAAACTCTACAGCTGCACACCCCGGAATCTCTAGTGTCC 847

Qy 696 ATAAGGGAAGAACTAAAGAGAACGATACCAATTTTCTGGCCAGGTTGCTCTCTGTTAAA 755

Db 848 ATACGGGAGAGCTAAAGAGACAGATACCATATTTCTGGCCAGGTTGCTCTCTGTCAGG 907

Qy 756 CGCTGTGGTGGCACTGTGTCCTGTGTCTCCACAATTGCAATGAATGTCATGTCCTCA 815  
Db 908 CGCTGTGGAGGAATTTGGCTTGTCTCCATAATTGCAATGAATGTCATGTCCTCA 967  
Qy 816 AGCAAAAGTTTACTAAAAATACACGAGGT 844  
Db 968 CGTAAAGTTTACAAAAAAGTACCATGAGGT 996

RESULT 15

Bi911795

LOCUS

DEFINITION

603065222F1 NIH\_MGC\_118 Homo sapiens cDNA clone IMAGE:5214461 5',

mRNA sequence.

ACCESSION

Bi911795

VERSION

Bi911795.1

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 789)

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished

COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs@mail.nih.gov](mailto:cgapbs@mail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: L14M11538 row: k column: 06  
High quality sequence start: 26  
High quality sequence stop: 762.

FEATURES

source

Location/Qualifiers

1..789

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5214461"

/tissue\_type="leukocyte"

/lab\_host="DH10B"

/clone\_lib="NIH\_MGC\_118"

/note="Vector: pCMV-SPORT6; Site1: NotI; Site2: EcoRV  
(destroyed); RNA source leukocytes from anonymous pool of  
non-activated adult donors. Library is oligo-dT primed  
and directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.7 kb, insert size range  
1.2-3.3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 027. Note:  
this is a NIH MGC Library."

237 a 158 c 186 g 208 t

BASE COUNT

ORIGIN

Query Match 37.3%; Score 572.4; DB 12; Length 789;

Best Local Similarity 99.0%; Pred. No. 5.3e-104;

Matches 576; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 36 AACGAGTACAGATCCTCAGCATGAGAGATTATTACTGTCTACTAATGGAAGTATT 95

Db 201 AAAGAGTACAGATCCTCAGCATGAGAGATTATTACTGTCTACTAATGGAAGTATT 260

Qy 96 CACAGCCCAAGTTTCCTCATCTACTATCCAGAAATACGGTCTTGGTATGGAGATTAGTA 155

Db 261 CACAGCCCAAGTTTCCTCATCTACTATCCAGAAATACGGTCTTGGTATGGAGATTAGTA 320

Qy 156 GCATGAGGGAATGTATGGATACAACTTACGTTTGTATGAAGATTGGGCTTGAAGAC 215

```
Db 321 GCAGTAGAGGAAATGATGATACAACTTACGTTTGTATGAAGATTGGGCTTGAAGAC 380
Qy 216 CCAGAGATGACATATGCAAGTATGATTTTGTAGAAGTTGAGGAACCCAGTGTGGAAC 275
Db 381 CCAGAGATGACATATGCAAGTATGATTTTGTAGAAGTTGAGGAACCCAGTGTGGAAC 440
Qy 276 ATATTAGGCGCTGGTGTGGTTCTGGTACTGTACAGGAAACAGATTTCCTAAAGGAAAT 335
Db 441 ATATTAGGCGCTGGTGTGGTTCTGGTACTGTACAGGAAACAGATTTCCTAAAGGAAAT 500
Qy 336 CAAATTAGGATAGATTGTATCTGATGAATATTTTCTCTGAAACCAAGGTTCTGCATC 395
Db 501 CAAATTAGGATAGATTGTATCTGATGAATATTTTCTCTGAAACCAAGGTTCTGCATC 560
Qy 396 CACTACAACTTGTCTATGCGCAATTCACAGAACTGTGAGTCTTCACTGCTACCCCT 455
Db 561 CACTACAACTTGTCTATGCGCAATTCACAGAACTGTGAGTCTTCACTGCTACCCCT 620
Qy 456 TCAGCTTTGCCACTGGACCTGCTTAATAATGCTATACTGCTTTAGTACCTTGGAGAC 515
Db 621 TCAGCTTTGCCACTGGACCTGCTTAATAATGCTATACTGCTTTAGTACCTTGGAGAC 680
Qy 516 CTTATTCGATATCTTGAACCAAGAGATGGCAGTTGGACTTAGAAGATCTATAGGCCA 575
Db 681 CTTATTCGATATCTTGAACCAAGAGATGGCAGTTGGACTTAGAAGATCTATAGGCCA 740
Qy 576 ACTTGGCAACTTCTTGGCAAGGCTTTTCTTTTGGAGAAA 617
Db 741 ACTTGGCAACTTCTTGGCAAGGCTTCCGTTTGGAGCAAAA 782
```

Search completed: November 26, 2003, 05:47:49  
Job time : 2245.94 secs



```

PR 21-MAY-1999; 99US-0135426.
PR 15-JUL-1999; 99US-0144022.
XX (LUDM-) LUDWIG INST CANCER RES.
PA (UTHE-) UNIV HELSINKI LICENSING LTD.
XX
PI Erikson U, Aase K, Lee X, Ponten A, Dutela M, Alitalo K;
PI Oestman A, Heidin C, Betscholz C;
XX
DR WPI: 2000-292954/25.
DR N-PSDB; AAA12524.
XX
PT Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation,
PT differentiation, growth and motility of cells expressing the PDGF-C
PT receptor -
XX
PS Disclosure; Fig 4; 135pp; English.
XX
CC The present sequence represents a human platelet-derived growth factor C
CC (PDGF-C) (formally designated VEGF-F) fragment. PDGF-C polypeptides have
CC the ability to stimulate and enhance proliferation or differentiation,
CC and/or growth or motility of cells expressing a PDGF-C receptor.
CC PDGF-C polypeptides can be used in pharmaceuticals for promoting cell
CC proliferation, preferably in combination with one other growth factor
CC and heparin. Pharmaceuticals comprising PDGF-C polypeptides can also
CC be used for stimulating connective tissue or wound healing. The
CC PDGF-C polypeptide can be enzymatically processed to generate the active
CC truncated form of PDGF-C and used to regulate the receptor-binding
CC specificity of PDGF-C. PDGF-C can also be used to promote fibroblast
CC mitogenesis in a mammal and to induce PDGF alpha receptor activation.
CC PDGF-C antagonists can be used to inhibit tumour growth of a tumour
CC expressing PDGF-C in a mammal. Specific types of human tumours, e.g.
CC choroidcarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma
CC and erythroleukemia, can be identified by testing for expression of
CC PDGF-C. PDGF-C antagonists can also be used to inhibit tissue
CC remodelling during invasion of tumour cells into a normal population of
CC cells. Antagonists can also be used to treat fibrotic conditions,
CC especially found in the lung, kidney or liver.
XX
SQ Sequence 318 AA;
Query Match 100.0%; Score 1734; DB 21; Length 318;
Best Local Similarity 100.0%; Pred. No. 7.6e-167;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GKQFSSNKQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVWIQ 60
Db 1 GKQFSSNKQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVWIQ 60
QY 61 LTDERFGLDPEDDICKYDFVEEPESDGTILGRWCGSGTVPGKQISKGNQIRFVSD 120
Db 61 LTDERFGLDPEDDICKYDFVEEPESDGTILGRWCGSGTVPGKQISKGNQIRFVSD 120
QY 121 EYFSPGFCIHYNVMPQTEAVSPVLPPSLPLDLLNNAITAFSTLEDLIRYLEPER 180
Db 121 EYFSPGFCIHYNVMPQTEAVSPVLPPSLPLDLLNNAITAFSTLEDLIRYLEPER 180
QY 181 WQLDLEDLYRPTWLLGKAFVFGKSRVDNLNLTTEVRVLYSCTPRNFVSIREELKRTD 240
Db 181 WQLDLEDLYRPTWLLGKAFVFGKSRVDNLNLTTEVRVLYSCTPRNFVSIREELKRTD 240
QY 241 TIFWPGCLLYKRCGNCACCLHNCNCCQVPSKVTKKYHEVLQIRPKTGVRLHKSITDV 300
Db 241 TIFWPGCLLYKRCGNCACCLHNCNCCQVPSKVTKKYHEVLQIRPKTGVRLHKSITDV 300
QY 301 ALEHHEECDCVCRGSTGG 318
Db 301 ALEHHEECDCVCRGSTGG 318
RESULT 2
AA333679
ID AAY33679 standard; Protein; 345 AA.

```

```

XX AAY33679;
XX
DT 11-JAN-2000 (first entry)
XX
DE Human VEGF-E protein.
XX
KW VEGF-E; human; vascular endothelial cell growth factor; wound repair;
KW treatment; cardiovascular disorder; endothelial disorder; therapy;
KW tissue generation; regeneration; cardiac hypertrophy; cancer; detection;
KW angiogenic disorder; age-related macular degeneration; vascular disease;
KW neovascularization; tumor; gene mapping.
XX
OS Homo sapiens.
XX
PN WO9947677-A2.
XX
PD 23-SEP-1999.
XX
PF 10-MAR-1999; 99WO-US05190.
XX
PR 17-MAR-1998; 98US-0040220.
XX
PR 02-NOV-1998; 98US-0184216.
XX
PA (GETH ) GENENTECH INC.
XX
PI Ferrara N, Kuo SS;
XX
DR WPI: 1999-580306/49.
DR N-PSDB; AAZ23691.
XX
PT New growth factor polypeptide useful for treating cardiovascular or
PT endothelial disorders, e.g. cardiac hypertrophy -
XX
PS Claim 1; Fig 2; 122pp; English.
XX
CC This invention describes the isolation of a novel human vascular
CC endothelial cell growth factor-E (VEGF-E) polypeptide which has
CC tranquilizer, vulnery and cardiant activity. VEGF-E can be administered
CC therapeutically, especially by expressing encoding polynucleotides, to
CC treat cardiovascular or endothelial disorders in mammals, especially
CC humans. It is useful in wound repair and tissue generation and
CC regeneration, and may especially be used to treat cardiac hypertrophy
CC It can be combined with a carrier in pharmaceutical compositions, which
CC can be administered to treat disorders as above. VEGF-E can be used to
CC screen for antagonists and agonists, and the antagonists administered to
CC treat angiogenic disorders in mammals (especially humans) e.g. cancer or
CC age-related macular degeneration. It can be used to generate antibodies,
CC useful therapeutically as antagonists, as above. The antibodies are also
CC useful to detect VEGF-E polypeptide, especially to diagnose
CC cardiovascular, endothelial or angiogenic disorders in mammals (e.g.
CC vascular disease, or neovascularization associated with tumor formation),
CC by contacting the antibody with a tissue sample and detecting formation
CC of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding
CC VEGF-E can be used to diagnose cardiovascular and endothelial disorders
CC in mammals, by detecting abnormally high or low VEGF-E gene expression in
CC tissue samples. They can also be used to diagnose a disease or
CC susceptibility to a disease related to a mutated form of VEGF-E (e.g. a
CC cardiovascular, endothelial or angiogenic disorder such as a tumor), by
CC detecting a mutation in the VEGF-E encoding sequence isolated from a
CC sample. They may also be used to produce probes useful to detect related
CC sequences or for gene mapping. This sequence represents the human VEGF-E
CC protein described in the method of the invention.
XX
SQ Sequence 345 AA;
Query Match 99.7%; Score 1728; DB 20; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.4e-166;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 KFOFSSNKQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVWIQ 61
Db 29 KFOFSSNKQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVWIQ 88

```

QY	62	TFDERFGLDPEDDICKYDFVEVEEPPSDGTTILGRWCGSGTVPGKQISKGNQIRIRFVSDE	121
Db	89	TFDERFGLDPEDDICKYDFVEVEEPPSDGTTILGRWCGSGTVPGKQISKGNQIRIRFVSDE	148
QY	122	YFSEPGFCIHYNIVMQFTAVSPSVLPSPALPLDLLNNAITAFSTLEDLIRYLEPERW	181
Db	149	YFSEPGFCIHYNIVMQFTAVSPSVLPSPALPLDLLNNAITAFSTLEDLIRYLEPERW	208
QY	182	QLDLEDLYRPTWQLLKAFVFGRKSRVVDLMLLTFEEVRLYSCTPRNFVSISREELKRTDT	241
Db	209	QLDLEDLYRPTWQLLKAFVFGRKSRVVDLMLLTFEEVRLYSCTPRNFVSISREELKRTDT	268
QY	242	IFWPGCLLVKRCGNCACCLHNCQCQVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDVA	301
Db	269	IFWPGCLLVKRCGNCACCLHNCQCQVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDVA	328
QY	302	LEHHECDCVCRGSTGG	318
Db	329	LEHHECDCVCRGSTGG	345
RESULT 3			
AAAY41766			
ID	AAAY41766 standard; Protein; 345 AA.		
XX	XX		
AC	AAAY41766;		
XX	XX		
DT	07-DEC-1999 (first entry)		
XX	XX		
DE	Human PRO200 protein sequence.		
XX	XX		
KW	Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;		
KW	probe; blood coagulation disorder; cancer; cellular adhesion disorder;		
KW	secreted protein; transmembrane protein.		
XX	XX		
OS	Homo sapiens.		
XX	XX		
PN	WO9946281-A2.		
XX	XX		
PD	16-SEP-1999.		
XX	XX		
PF	08-MAR-1999; 99WO-US05028.		
XX	XX		
PR	10-MAR-1998; 98US-0077450.		
PR	11-MAR-1998; 98US-0077632.		
PR	11-MAR-1998; 98US-0077641.		
PR	11-MAR-1998; 98US-0077649.		
PR	12-MAR-1998; 98US-0077791.		
PR	13-MAR-1998; 98US-0078004.		
PR	17-MAR-1998; 98US-0040220.		
PR	20-MAR-1998; 98US-0078886.		
PR	20-MAR-1998; 98US-0078910.		
PR	20-MAR-1998; 98US-0078936.		
PR	20-MAR-1998; 98US-0078939.		
PR	25-MAR-1998; 98US-0079294.		
PR	26-MAR-1998; 98US-0079456.		
PR	27-MAR-1998; 98US-0079663.		
PR	27-MAR-1998; 98US-0079664.		
PR	27-MAR-1998; 98US-0079689.		
PR	27-MAR-1998; 98US-0079728.		
PR	30-MAR-1998; 98US-0079786.		
PR	30-MAR-1998; 98US-0079920.		
PR	31-MAR-1998; 98US-0079923.		
PR	31-MAR-1998; 98US-0080105.		
PR	31-MAR-1998; 98US-0080107.		
PR	31-MAR-1998; 98US-0080165.		
PR	31-MAR-1998; 98US-0080194.		
PR	01-APR-1998; 98US-0080327.		
PR	01-APR-1998; 98US-0080328.		
PR	01-APR-1998; 98US-0080333.		
PR	01-APR-1998; 98US-0080334.		
PR	08-APR-1998; 98US-0081049.		

PR	08-APR-1998;	98US-0081070.
PR	08-APR-1998;	98US-0081071.
PR	09-APR-1998;	98US-0081195.
PR	09-APR-1998;	98US-0081203.
PR	09-APR-1998;	98US-0081239.
PR	15-APR-1998;	98US-0081817.
PR	15-APR-1998;	98US-0081838.
PR	15-APR-1998;	98US-0081952.
PR	15-APR-1998;	98US-0081955.
PR	21-APR-1998;	98US-0082568.
PR	21-APR-1998;	98US-0082569.
PR	22-APR-1998;	98US-0082700.
PR	22-APR-1998;	98US-0082704.
PR	22-APR-1998;	98US-0082804.
PR	23-APR-1998;	98US-0082767.
PR	23-APR-1998;	98US-0082796.
PR	27-APR-1998;	98US-0083336.
PR	28-APR-1998;	98US-0083322.
PR	29-APR-1998;	98US-0083392.
PR	29-APR-1998;	98US-0083495.
PR	29-APR-1998;	98US-0083496.
PR	29-APR-1998;	98US-0083499.
PR	29-APR-1998;	98US-0083500.
PR	29-APR-1998;	98US-0083545.
PR	29-APR-1998;	98US-0083554.
PR	29-APR-1998;	98US-0083558.
PR	30-APR-1998;	98US-0083559.
PR	05-MAY-1998;	98US-0083742.
PR	06-MAY-1998;	98US-0084366.
PR	06-MAY-1998;	98US-0084414.
PR	07-MAY-1998;	98US-0084441.
PR	07-MAY-1998;	98US-0084598.
PR	07-MAY-1998;	98US-0084600.
PR	07-MAY-1998;	98US-0084627.
PR	07-MAY-1998;	98US-0084637.
PR	07-MAY-1998;	98US-0084639.
PR	07-MAY-1998;	98US-0084640.
PR	13-MAY-1998;	98US-0084643.
PR	13-MAY-1998;	98US-0085323.
PR	13-MAY-1998;	98US-0085338.
PR	15-MAY-1998;	98US-0085339.
PR	15-MAY-1998;	98US-0085573.
PR	15-MAY-1998;	98US-0085579.
PR	15-MAY-1998;	98US-0085580.
PR	15-MAY-1998;	98US-0085582.
PR	15-MAY-1998;	98US-0085689.
PR	15-MAY-1998;	98US-0085697.
PR	15-MAY-1998;	98US-0085700.
PR	18-MAY-1998;	98US-0085704.
PR	22-MAY-1998;	98US-0086023.
PR	22-MAY-1998;	98US-0086392.
PR	22-MAY-1998;	98US-0086414.
PR	22-MAY-1998;	98US-0086430.
PR	28-MAY-1998;	98US-0086486.
PR	28-MAY-1998;	98US-0087098.
PR	28-MAY-1998;	98US-0087106.
PR	30-JUL-1998;	98US-0087208.
PR	11-SEP-1998;	98US-0094651.
XX		98US-0100038.
PA	(GETH ) GENENTECH INC.	
XX	Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;	
PI	WPI; 1999-551358/46.	
XX	N-PSDB; AAZ34296.	
DR	New secreted and transmembrane polypeptides and their polynucleotides,	
XX	useful for treating blood coagulation disorders, cancers and cellular	
PT	adhesion disorders -	
XX	Claim 12; Fig 207; 530pp; English.	
PS		
XX		





XX 03-MAY-2000; 2000WO-US40047.  
 XX PF  
 XX 03-MAY-1999; 99US-0304216.  
 XX PR  
 XX 10-NOV-1999; 99US-0164463.  
 XX PR  
 XX 04-FEB-2000; 2000US-0180169.  
 XX PR  
 XX (ZYMO) ZYMOGENETICS INC.  
 XX PA  
 XX Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;  
 XX PI  
 XX WPI; 2000-687541/67.  
 XX DR  
 XX N-PSDB; AAC81582.  
 XX Growth factor homologs and the nucleic acids that encode them, useful  
 XX e.g. for treating liver damage, ischemia, multiple sclerosis and  
 XX Alzheimer's disease -  
 XX PT  
 XX Claim 48; Page 125-126; 143pp; English.  
 XX PS  
 XX The invention relates to the human growth factor homologue zvegfg4  
 XX (AAB48653), and nucleic acids encoding it (AAC81555). Zvegfg4 is a member  
 XX of the PDGF (platelet-derived growth factor)/VSGF (vascular endothelial  
 XX growth factor) family. Zvegfg4 has a growth factor domain (AAB48654)  
 XX characterised by a PDGF cysteine knot structure, and a CUB domain  
 XX (AAB48655) which has a beta barrel structure. Zvegfg4 has PDGF-like  
 XX activity, having mitogenic activity on fibroblasts, vascular smooth  
 XX muscle cells and pericytes, and has also been shown to stimulate bone  
 XX growth. The invention also relates to fusion proteins comprising human  
 XX zvegfg4 or fragments thereof, particularly human zvegfg4/human zvegfg3  
 XX fusions; expression constructs and host cells comprising human zvegfg4  
 XX nucleic acids; the recombinant expression of human zvegfg4; an antibody  
 XX which binds to human zvegfg4 or a fragment thereof; a method of activating  
 XX a cell-surface PDGF receptor using a zvegfg4-derived polypeptide; a  
 XX method of modulating the proliferation, differentiation, migration or  
 XX metabolism of bone cells, comprising exposing bone cells to  
 XX zvegfg4-derived polypeptides; and a method of detecting a genetic  
 XX abnormality in the zvegfg4 gene of a patient. Zvegfg4 proteins and derived  
 XX fragments may be used to stimulate tissue development or repair, or  
 XX cellular differentiation or proliferation. They are particularly used for  
 XX the treatment or repair of liver damage, and may also be used to  
 XX modulate neurite growth (e.g., in the treatment of Alzheimer's disease or  
 XX multiple sclerosis). Due to their osteogenic activity, they may be used  
 XX in the treatment of periodontal disease and fractures. They may also be  
 XX used to enhance expansion and mobilisation of haematopoietic stem cells  
 XX and endothelial precursor stem cells, which may be useful in the  
 XX treatment of ischaemia, in wound healing, and in the modulation of the  
 XX immune system. The present sequence represents human zvegfg3.  
 XX  
 XX SQ Sequence 345 AA;  
 XX Query Match 99.7%; Score 1728; DB 21; Length 345;  
 XX Best Local Similarity 100.0%; Pred. No. 3.4e-166;  
 XX Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX 2 KQFSSNKEQGVDPQHERITVTSTNGSIHSPFPHTYPRNTVLVWELVAEENVVQL 61  
 XX 29 KQFSSNKEQGVDPQHERITVTSTNGSIHSPFPHTYPRNTVLVWELVAEENVVQL 88  
 XX  
 XX 62 TDFRFGLEDDEDDICKYDFVEVEPSPDGTILGRWCGSGTVPKGQISKGNQIRIRFVSD 121  
 XX 89 TDFRFGLEDDEDDICKYDFVEVEPSPDGTILGRWCGSGTVPKGQISKGNQIRIRFVSD 148  
 XX  
 XX 122 YFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181  
 XX 149 YFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208  
 XX  
 XX 182 QLDLEDLYRPTWQLLGKAFVGRKSRVVDLNLTEEVRLYSTPNTFNVSIREELKRTDT 241  
 XX 209 QLDLEDLYRPTWQLLGKAFVGRKSRVVDLNLTEEVRLYSTPNTFNVSIREELKRTDT 268  
 XX  
 XX 242 IFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYTHEVLQLRPKTVGRGLHKLSTDA 301  
 XX 149 YFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208

DB 269 IFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYTHEVLQLRPKTVGRGLHKLSTDA 328  
 QY 302 LEHHEECDCVCRGSGTG 318  
 DB 329 LEHHEECDCVCRGSGTG 345  
 RESULT 6  
 AAB24250  
 ID AAB24250 standard; Protein; 345 AA.  
 XX AC AAB24250;  
 XX DT 08-FEB-2001 (first entry)  
 XX DE Human platelet-derived growth factor related protein LP8.  
 XX KW Human; platelet derived growth factor related protein; LP8; VEGFh;  
 XX KW vascular endothelial growth factor h; tissue regeneration; vulnerary;  
 XX KW atherosclerosis; PDGF-related protein; antiarteriosclerotic.  
 XX OS Homo sapiens.  
 XX PN WO200059940-A2.  
 XX PD 12-OCT-2000.  
 XX PF 24-MAR-2000; 2000WO-US06427.  
 XX PR 06-APR-1999; 99US-0127913.  
 XX (ELTL) LILLY & CO ELLI.  
 XX PI Hammond LJ, Na S;  
 XX WPI; 2000-664991/64.  
 XX N-PSDB; AAC64426.  
 XX Enhancing tissue growth and promoting wound healing by administering  
 XX platelet-derived growth factor related protein, LP8 or its analog and  
 XX treating atherosclerosis by administering LP8 antagonist -  
 XX Claim 4; Page 63-64; 64pp; English.  
 XX The present invention describes a method for enhancing tissue growth,  
 XX promoting wound healing or stimulating smooth muscle growth by administering  
 XX a platelet-derived growth factor (PDGF) related protein,  
 XX designated LP8 or its analogue. Also described is a method of slowing  
 XX the progress of atherosclerosis or treating atherosclerosis comprising  
 XX the administration of an LP8 antagonist. The method is useful for  
 XX enhancing tissue growth, promoting wound healing and stimulating smooth  
 XX muscle growth. Antagonists of LP8 are useful for treating  
 XX atherosclerosis. The present sequence represents human LP8, which is  
 XX also called VEGFh.  
 XX SQ Sequence 345 AA;  
 XX Query Match 99.7%; Score 1728; DB 21; Length 345;  
 XX Best Local Similarity 100.0%; Pred. No. 3.4e-166;  
 XX Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX 2 KQFSSNKEQGVDPQHERITVTSTNGSIHSPFPHTYPRNTVLVWELVAEENVVQL 61  
 XX 29 KQFSSNKEQGVDPQHERITVTSTNGSIHSPFPHTYPRNTVLVWELVAEENVVQL 88  
 XX  
 XX 62 TDFRFGLEDDEDDICKYDFVEVEPSPDGTILGRWCGSGTVPKGQISKGNQIRIRFVSD 121  
 XX 89 TDFRFGLEDDEDDICKYDFVEVEPSPDGTILGRWCGSGTVPKGQISKGNQIRIRFVSD 148  
 XX  
 XX 122 YFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181  
 XX 149 YFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208





Db 329 LEHHECDCVCRGSTGG 345

RESULT 10

AA10644

ID AAB10644 standard; Protein; 345 AA.

XX

AC AAB10644;

XX

DT 19-JAN-2001 (first entry)

XX

DE Human VEGF-X protein #4.

XX

XX VEGF-X; vascular endothelial growth factor; human; vulnary; cytostatic;

KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;

KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;

KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;

KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;

KW venous sore; diabetic ulcer; burns; skin graft growth.

XX

OS Homo sapiens.

XX

PN W0200037641-A2.

XX

PD 29-JUN-2000.

XX

PF 21-DEC-1999; 99WO-US30503.

XX

PR 22-DEC-1998; 98GB-0028377.

PR 18-MAR-1999; 99US-0124967.

PR 08-NOV-1999; 99US-0164131.

XX

XX (JANC ) JANSEN PHARM NV.

XX

XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JH, Gosiewska A;

PI Dhanaraj SN, Xu J;

XX

DR WPI; 2000-442669/38.

DR N-PSDB; AAA71990.

XX

XX New vascular endothelial growth factor protein, useful for treating or

PT preventing diseases associated with inappropriate angiogenesis activity

PT such as cancer, rheumatoid arthritis, psoriasis and wounds -

XX

PS Disclosure; Fig 30B; 127pp; English.

XX

XX This invention describes a novel vascular endothelial growth factor-X

CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has

CC vulnary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and

CC antidiabetic activity and acts as an angiogenesis and vascularization

CC regulator. An antisense molecule of the invention is useful for treating

CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic

CC retinopathy by inhibiting angiogenic activity or inappropriate

CC vascularization including formation and proliferation of new blood

CC vessels, growth and development of tissues, tissue regeneration and organ

CC for preparing medicaments for treating wounds such as dermal ulcers,

CC pressure sores, venous sores, diabetic ulcers and burns and to promote

CC skin graft growth, tissue repair, proliferation of new blood vessels,

CC tissue regeneration and organ repair by promoting angiogenic activity or

CC vascularization. This sequence represents a human VEGF-X protein

CC described in the method of the invention.

XX

SQ Sequence 345 AA;

Query Match 99.7%; Score 1728; DB 21; Length 345;

Best Local Similarity 100.0%; Pred. No. 3.4e-166;

Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KFOFSSNKEQGVDPQHERITVSTNGSIHSPFPHYPTNTVLVRLVAVERNWIQL 61

DB 29 KFOFSSNKEQGVDPQHERITVSTNGSIHSPFPHYPTNTVLVRLVAVERNWIQL 88

Qy 62 TFDERFGLDEPDDICKYDFEVEEPEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE 121

Db 89 TFDERFGLDEPDDICKYDFEVEEPEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE 148

Qy 122 YFPSEPGFCIHYNIWMPQFTTEAVSPSVLPSPALPLDLNNNAITAFSTLEDLIRVLEPERW 181

Db 149 YFPSEPGFCIHYNIWMPQFTTEAVSPSVLPSPALPLDLNNNAITAFSTLEDLIRVLEPERW 208

Qy 182 QLDLEDLYRPTWLLGKAFVGRKSRVVDNLLLTETEEVRLYSCCTPRNFSVSIREELKRTDT 241

Db 209 QLDLEDLYRPTWLLGKAFVGRKSRVVDNLLLTETEEVRLYSCCTPRNFSVSIREELKRTDT 268

Qy 242 IFWPGCLLVKRCGNCACCLHNCNECQCVPSKVTKYHEVLQLRPKTGVRGLHSLTDVA 301

Db 269 IFWPGCLLVKRCGNCACCLHNCNECQCVPSKVTKYHEVLQLRPKTGVRGLHSLTDVA 328

Qy 302 LEHHECDCVCRGSTGG 318

Db 329 LEHHECDCVCRGSTGG 345

RESULT 11

AA10650

ID AAB10650 standard; Protein; 345 AA.

XX

AC AAB10650;

XX

DT 19-JAN-2001 (first entry)

XX

DE Human 990126vegX protein.

XX

XX VEGF-X; vascular endothelial growth factor; human; vulnary; cytostatic;

KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;

KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;

KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;

KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;

KW venous sore; diabetic ulcer; burns; skin graft growth.

XX

OS Homo sapiens.

XX

PN W0200037641-A2.

XX

PD 29-JUN-2000.

XX

PF 21-DEC-1999; 99WO-US30503.

XX

PR 22-DEC-1998; 98GB-0028377.

PR 18-MAR-1999; 99US-0124967.

PR 08-NOV-1999; 99US-0164131.

XX

XX (JANC ) JANSEN PHARM NV.

XX

XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JH, Gosiewska A;

PI Dhanaraj SN, Xu J;

XX

DR WPI; 2000-442669/38.

DR N-PSDB; AAA71990.

XX

XX New vascular endothelial growth factor protein, useful for treating or

PT preventing diseases associated with inappropriate angiogenesis activity

PT such as cancer, rheumatoid arthritis, psoriasis and wounds -

XX

PS Disclosure; Fig 30B; 127pp; English.

XX

XX This invention describes a novel vascular endothelial growth factor-X

CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has

CC vulnary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and

CC antidiabetic activity and acts as an angiogenesis and vascularization

CC regulator. An antisense molecule of the invention is useful for treating

CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic

CC retinopathy by inhibiting angiogenic activity or inappropriate

CC vascularization including formation and proliferation of new blood

CC vessels, growth and development of tissues, tissue regeneration and organ

CC for preparing medicaments for treating wounds such as dermal ulcers,

CC pressure sores, venous sores, diabetic ulcers and burns and to promote

CC skin graft growth, tissue repair, proliferation of new blood vessels,

CC tissue regeneration and organ repair by promoting angiogenic activity or

CC vascularization. This sequence represents a human VEGF-X protein

CC described in the method of the invention.

XX

SQ Sequence 345 AA;

Query Match 99.7%; Score 1728; DB 21; Length 345;

Best Local Similarity 100.0%; Pred. No. 3.4e-166;

Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KFOFSSNKEQGVDPQHERITVSTNGSIHSPFPHYPTNTVLVRLVAVERNWIQL 61

DB 29 KFOFSSNKEQGVDPQHERITVSTNGSIHSPFPHYPTNTVLVRLVAVERNWIQL 88

CC for preparing medicaments for treating wounds such as dermal ulcers,  
 CC pressure sores, venous sores, diabetic ulcers and burns and to promote  
 CC skin graft growth, tissue repair, proliferation of new blood vessels,  
 CC tissue regeneration and organ repair by promoting angiogenic activity or  
 CC vascularization. This sequence represents the human 990126vegX protein  
 CC used to illustrate the method of the invention.

XX  
 SQ Sequence 345 AA;

Query Match 99.7%; Score 1728; DB 21; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-166;  
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTLVWRLVAEENVMQL 61  
 Db 29 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTLVWRLVAEENVMQL 88  
 Qy 62 TFDERFGLDEDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE 121  
 Db 89 TFDERFGLDEDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE 148  
 Qy 122 YFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181  
 Db 149 YFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208  
 Qy 182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLTEEVRLYSCTPRNFSVIREELKRTDT 241  
 Db 209 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLTEEVRLYSCTPRNFSVIREELKRTDT 268  
 Qy 242 IFWPGCLLVKRCGNCACCLHNCNECCQVPSKVTKYKHEVLQRLPKTGVRGLHKS LTDVA 301  
 Db 269 IFWPGCLLVKRCGNCACCLHNCNECCQVPSKVTKYKHEVLQRLPKTGVRGLHKS LTDVA 328  
 Qy 302 LEHHEECDCVCRGSGTG 318  
 Db 329 LEHHEECDCVCRGSGTG 345

## RESULT 12

AAB10651  
 ID AAB10651 standard; Protein; 345 AA.

AC AAB10651;

XX 19-JAN-2001 (first entry)

XX Human VEGF-X protein #3.

XX VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;  
 KW antiarthritis; antipsoaritic; antidiabetic; treatment;  
 KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;  
 KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;  
 KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;  
 KW venous sore; diabetic ulcer; burns; skin graft growth.

XX Homo sapiens.

XX WO200037641-A2.

XX 29-JUN-2000.

XX 21-DEC-1999; 99WO-US30503.

XX 22-DEC-1998; 98GB-00283377.

XX 18-MAR-1999; 99US-0124967.

XX 08-NOV-1999; 99US-0164131.

XX (JANC ) JANSSEN PHARM NV.

XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JH, Gosiowska A;

XX Dhanaraj SN, Xu J;

XX WPI; 2000-442669/38.

XX New vascular endothelial growth factor protein, useful for treating or  
 PT preventing diseases associated with inappropriate angiogenesis activity  
 PT such as cancer, rheumatoid arthritis, psoriasis and wounds -  
 XX Claim 72; Fig 12; 127pp; English.

CC This invention describes a novel vascular endothelial growth factor-X  
 CC (VEGF-X) protein (Ia) and its encoding polynucleotide (Iia) which has  
 CC vulnery, cytostatic, antirheumatic, antiarthritis, antipsoaritic and  
 CC antidiabetic activity and acts as an angiogenesis and vascularization  
 CC regulator. An antisense molecule of the invention is useful for treating  
 CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic  
 CC retinopathy by inhibiting angiogenic activity or inappropriate  
 CC vascularization including formation and proliferation of new blood  
 CC vessels, growth and development of tissues, tissue regeneration and organ  
 CC and tissue repair in a subject. The products of the invention are useful  
 CC for preparing medicaments for treating wounds such as dermal ulcers,  
 CC pressure sores, venous sores, diabetic ulcers and burns and to promote  
 CC skin graft growth, tissue repair, proliferation of new blood vessels,  
 CC tissue regeneration and organ repair by promoting angiogenic activity or  
 CC vascularization. This sequence represents the human VEGF-X protein  
 CC described in the method of the invention.

XX Sequence 345 AA;

Query Match 99.7%; Score 1728; DB 21; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-166;  
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTLVWRLVAEENVMQL 61

Db 29 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTLVWRLVAEENVMQL 88

Qy 62 TFDERFGLDEDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE 121

Db 89 TFDERFGLDEDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE 148

Qy 122 YFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181

Db 149 YFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208

Qy 182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLTEEVRLYSCTPRNFSVIREELKRTDT 241

Db 209 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLTEEVRLYSCTPRNFSVIREELKRTDT 268

Qy 242 IFWPGCLLVKRCGNCACCLHNCNECCQVPSKVTKYKHEVLQRLPKTGVRGLHKS LTDVA 301

Db 269 IFWPGCLLVKRCGNCACCLHNCNECCQVPSKVTKYKHEVLQRLPKTGVRGLHKS LTDVA 328

## RESULT 13

AAB19578  
 ID AAB19578 standard; Protein; 345 AA.

XX AAB19578;

XX 22-JAN-2001 (first entry)

XX Human PRO200 (vascular endothelial growth factor B).

XX PRO200; vascular epithelial growth factor B; VEGF-B; human;  
 KW ocular disease; retinopathy; maculopathy; therapy;  
 KW retinitis pigmentosa; macular degeneration; retinal detachment;  
 KW retinal tear; macular hole; myopia; traumatic chorioretinopathy;  
 KW acute retinal necrosis syndrome; contusion; edema;  
 KW retinal vision occlusion; vascular disease; retinal vasculitis;  
 KW thrombocytopenic purpura; uveitis; retinal occlusion.

OS Homo sapiens.

XX Key Location/Qualifiers

PH 1..14

FT /label= Signal\_peptide

FT Protein 15..345

FT /label= Mature\_Pro200 25..29

FT Modified-site /note= "Asn is N-glycosylated"

FT Modified-site 55..59

FT /note= "Asn is N-glycosylated"

FT Modified-site 254..258

FT /note= "Asn is N-glycosylated"

FT Modified-site 15..21

FT /note= "N-myristoylation"

FT Modified-site 117..123

FT /note= "N-myristoylation"

FT Modified-site 127..133

FT /note= "N-myristoylation"

FT Modified-site 281..287

FT /note= "N-myristoylation"

FT Modified-site 282..288

FT /note= "N-myristoylation"

FT Modified-site 319..325

FT /note= "Amidation"

XX WO200053760-A2.

XX PD 14-SEP-2000.

XX PF 10-MAR-2000; 2000WO-US06319.

XX PR 12-MAR-1999; 99US-0123957.

XX PA (GETH ) GENENTECH INC.

XX PI Ferrara N, Goddard A, Gurney AL, Hebert C, Henzel WJ, Kabakoff RC,

PI Klein RD, Kljavin IU, Kuo SS, La Fleur M, Wood WI;

DR WPI: 2000-587437/55.

DR N-PSDB; AAA88515.

XX Novel PRO polypeptides useful for preventing or rescuing retinal cells

PT from injury caused by ocular diseases such as retinitis pigmentosa,

PT retinopathy, retinal degenerative diseases, degenerative myopia,

PT uveitis -

XX Claim 2; Fig 2; 140pp; English.

XX The present sequence is that of human PRO200 or vascular

CC endothelial growth factor E (VEGF-E), as predicted from a cDNA

CC clone (see AAA88515) that was isolated from a glioma cell line G61

CC library using probes (see AAA8523-26) based on an expressed sequence

CC tag (see AAA8522) that showed homology to VEGF. PRO200 has a

CC predicted mol wt. of 39.029 and a pI of about 6.06. A method for

CC producing PRO polypeptides, including PRO200, using a host cell

CC transformed with a vector comprising a PRO nucleic acid is claimed.

CC The invention relates to the use of PRO polypeptides to delay,

CC prevent or rescue retinal cells such as retinal neurons selected from

CC photoreceptors, retinal ganglion cells, displaced retinal ganglion

CC cells, amacrine cells, displaced amacrine cells, horizontal and

CC bipolar neurons, and supportive cells (including Muller cells and

CC pigment epithelial cells) from injury and degradation. The retinal

CC cells are preferably photoreceptors and photoreceptor cell injury or

CC death is caused by retinal injury, light or environmental trauma or

CC by an ocular disease selected from retinitis pigmentosa, macular

CC degeneration, including age-related, retinal detachment, retinal

CC tears, retinopathy, retinal degenerative diseases, macular holes,

CC degenerative myopia, acute retinal necrosis syndrome, traumatic

CC chorioretinopathies or contusion such as Furttscher's retinopathy,

CC edema, ischemic conditions such as central or branch retinal vision

CC occlusion, collagen vascular diseases, thrombocytopenic purpura,

CC uveitis, retinal vasculitis and occlusion associated with Eales

CC disease and systemic lupus erythematosus (claimed).

XX SQ Sequence 345 AA;

Query Match 99.7%; Score 1728; DB 21; Length 345;

Best Local Similarity 100.0%; Pred. No. 3.4e-166; Indels 0; Gaps 0;

Matches 317; Conservative 0; Mismatches 0;

QY 2 KQFSSNKEQGVQDPQHERIITVTNGSIHSPRPHTYPRNTVLVRLVAVENVMIQI 61

DB 29 KQFSSNKEQGVQDPQHERIITVTNGSIHSPRPHTYPRNTVLVRLVAVENVMIQI 88

QY 62 TFDERFGLDEDDICKYDFVEVEBPSSDGTILGRWCGSGTVPKQISKGNQIRIRFVSDE 121

DB 89 TFDERFGLDEDDICKYDFVEVEBPSSDGTILGRWCGSGTVPKQISKGNQIRIRFVSDE 148

QY 122 YPSPGFCIHYNIVMPOFTEAVSPVLPPSPALPDLNLNNAITAFSTLEDLIRYLEPERW 181

DB 149 YPSPGFCIHYNIVMPOFTEAVSPVLPPSPALPDLNLNNAITAFSTLEDLIRYLEPERW 208

QY 182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLITBEVRLYCTPRNFSVSIREELKRTDT 241

DB 209 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLITBEVRLYCTPRNFSVSIREELKRTDT 268

QY 242 IFWPGCLLVKRCGNCACCLHNCNCCQVPSKVTKYHVEVLQIRPKTVGRGLHKSITDVA 301

DB 269 IFWPGCLLVKRCGNCACCLHNCNCCQVPSKVTKYHVEVLQIRPKTVGRGLHKSITDVA 328

QY 302 LEHHEECDCVCRGSGTG 318

DB 329 LEHHEECDCVCRGSGTG 345

RESULT 14

AAAB33414

ID AAB33414 standard; Protein; 345 AA.

XX AC AAB33414;

XX DT 29-JAN-2001 (first entry)

XX DE Human PRO200 protein UNQ174 SEQ ID NO:2.

XX KW Human; immune related disease; diagnosis; antiinflammatory; cardiant;

KW dermatological; antiarthritic; antirheumatic; immunosuppressive;

KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;

KW antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;

KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;

KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;

KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;

KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;

KW autoimmune thrombocytopenia; immune-mediated renal disease;

KW demyelinating disease; hepatobiliary disease; Whipple's disease;

KW inflammatory bowel disease; gluten-sensitive enteropathy;

KW autoimmune disease; immune-mediated skin disease; allergic disease;

KW immunological disease; transplantation associated disease;

KW graft rejection; graft-versus-host-disease.

XX OS Homo sapiens.

XX WO200053758-A2.

XX PD 14-SEP-2000.

XX PF 02-MAR-2000; 2000WO-US05841.

XX PR 08-MAR-1999; 99WO-US05028.

PR 10-MAR-1999; 99US-0123618.

PR 12-MAR-1999; 99US-0123957.

PR 23-MAR-1999; 99US-0125775.

PR 12-APR-1999; 99US-0128849.

PR 20-APR-1999; 99WO-US08615.

PR 28-APR-1999; 99US-0131445.



PR 04-MAY-1999; 99US-0132371.  
 PR 14-MAY-1999; 99US-0134287.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 28-JUL-1999; 99US-0146222.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.  
 PR 13-SEP-1999; 99WO-US20944.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 05-OCT-1999; 99WO-US23089.  
 PR 29-OCT-1999; 99US-0162506.  
 PR 29-NOV-1999; 99WO-US28214.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 30-NOV-1999; 99WO-US28409.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 02-DEC-1999; 99WO-US28551.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 16-DEC-1999; 99WO-US30999.  
 PR 30-DEC-1999; 99WO-US31374.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;  
 PI Kabatoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;  
 PI Stewart TA, Tamas D, Watanabe CK, Wood WI, Yan W;  
 DR WPI; 2000-572271/53.  
 DR N-PSDB; AAC58579.  
 XX  
 PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of  
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid  
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -  
 XX  
 XX Claim 33; Fig 2; 309pp; English.  
 XX  
 CC The present invention describes sixty four human PRO proteins which can  
 CC be used in the treatment of immune related diseases. The human PRO  
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for  
 CC treating and diagnosing immune related disorders. The disorders are  
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
 CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central  
 CC and peripheral nervous systems, hepatobiliary diseases, inflammatory  
 CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,  
 CC autoimmune or immune-mediated skin diseases, allergic diseases,  
 CC immunological diseases of the lung, and transplantation associated  
 CC diseases including graft rejection and graft-versus-host-disease.  
 CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used  
 CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and  
 CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.  
 XX  
 XX Sequence 345 AA;  
 XX  
 XX Query Match 99.7%; Score 1728; DB 21; Length 345;  
 XX Best Local Similarity 100.0%; Pred. No. 3.4e-166;  
 XX Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KQFSSNKEQGVQDPQHERIITVSTNGSIHSPFPHTYPRNTVLVWRLVAEENVVQL 61  
 DB 29 KQFSSNKEQGVQDPQHERIITVSTNGSIHSPFPHTYPRNTVLVWRLVAEENVVQL 88  
 QY 62 TFDERFGLDEPDDICKYDFVEVEEPPSDGTILGWCGSGVTPGKQISKGNQIRIRFVSDE 121  
 DB 89 TFDERFGLDEPDDICKYDFVEVEEPPSDGTILGWCGSGVTPGKQISKGNQIRIRFVSDE 148  
 QY 122 YFPSEPGFCIHYNVMPQFTEAVSPSVLPSPALPLDLLNNAITAFSTLEDLIRVLEPERW 181  
 DB 149 YFPSEPGFCIHYNVMPQFTEAVSPSVLPSPALPLDLLNNAITAFSTLEDLIRVLEPERW 208  
 QY 182 QLDLEDLYRPTWQLGKAFVGRKSRVVDLNLLEEVRLYSCTPRNFVSIREELKRTDT 241  
 DB 209 QLDLEDLYRPTWQLGKAFVGRKSRVVDLNLLEEVRLYSCTPRNFVSIREELKRTDT 268  
 QY 242 IFWPGCLLVRCGCGNACCLHNCNQCQVPSKTKKTHEVLQLPKTGVRGLHSLTDVA 301  
 DB 269 IFWPGCLLVRCGCGNACCLHNCNQCQVPSKTKKTHEVLQLPKTGVRGLHSLTDVA 328  
 QY 302 LEHHECDCVCRGSTGG 318  
 DB 329 LEHHECDCVCRGSTGG 345  
 RESULT 15  
 AAB24412  
 ID AAB24412 standard; Protein; 345 AA.  
 XX  
 AC AAB24412;  
 XX  
 DT 07-NOV-2000 (first entry)  
 XX  
 DE Human PRO713 protein sequence SEQ ID NO:137.  
 XX  
 KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;  
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;  
 KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;  
 KW cyostatic; gene therapy; vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200032221-A2.  
 XX  
 XX 08-JUN-2000.  
 XX  
 XX 30-NOV-1999; 99WO-US28313.  
 XX  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 16-DEC-1998; 98US-0112850.  
 PR 12-JAN-1999; 99US-0115554.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 28-APR-1999; 99US-0131445.  
 PR 14-MAY-1999; 99US-0134287.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.  
 PR 13-SEP-1999; 99WO-US20944.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 05-OCT-1999; 99WO-US23089.  
 PR 29-OCT-1999; 99US-0162506.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A;  
 XX Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;  
 XX Watanabe CK, Williams PM, Wood WI;

XX WPI; 2000-412154/35.  
DR N-PSDB; AAA77621.  
XX  
PT Nucleic acids encoding PRO polypeptides useful for preventing,  
PT diagnosing and treating disorders in mammals -  
XX angiotensin disorders in mammals -  
XX  
PS Claim 72; Fig 50; 315pp; English.  
XX  
CC The present invention describes nucleic acids encoding PRO polypeptides  
CC useful for preventing, diagnosing and treating disorders in mammals by  
CC cardiovascular, endothelial or angiotensin disorder in mammals by  
CC modulating cell proliferation, angiogenesis and cardiovascularisation,  
CC and for identifying agonists and antagonists of these processes. The  
CC nucleic acids and the proteins they encode may be used in the  
CC prevention, treatment and diagnosis of diseases associated with  
CC inappropriate PRO expression such as cardiovascular, endothelial or  
CC angiotensin disorders in mammals (e.g. atherosclerosis, cancers and  
CC cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors  
CC containing them and the PRO polypeptide may be used to treat disorders  
CC associated with decreased PRO expression. AAA77510 to AAA77721 and  
CC AAB24388 to AAB24435 represent nucleotide and protein sequences used in  
CC the exemplification of the present invention.  
XX  
SQ Sequence 345 AA;  
Query Match 99.7%; Score 1728; DB 21; Length 345;  
Best Local Similarity 100.0%; Pred. No. 3.4e-166;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENWVQL 61  
DB 29 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENWVQL 88  
QY 62 TFDERFGLDPEDDICKYDFVEVEEPSDGTILGRWCGSTVPGKQISKGNQIRIRFVSDE 121  
DB 89 TFDERFGLDPEDDICKYDFVEVEEPSDGTILGRWCGSTVPGKQISKGNQIRIRFVSDE 148  
QY 122 YFPSEPGFCIHYNIVMPQTEAVSPSVLPFSAFLDLNNAITAFSTLEDLIRYLEPERW 181  
DB 149 YFPSEPGFCIHYNIVMPQTEAVSPSVLPFSAFLDLNNAITAFSTLEDLIRYLEPERW 208  
QY 182 QLDLEDLYRPTWQLLKGAFVFGKRSRVVDNLNLTVEVRLYSCTPRNFSVSIRELKETDT 241  
DB 209 QLDLEDLYRPTWQLLKGAFVFGKRSRVVDNLNLTVEVRLYSCTPRNFSVSIRELKETDT 268  
QY 242 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTKYHEVLQLRPKTVGRGLHKS LTDVA 301  
DB 269 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTKYHEVLQLRPKTVGRGLHKS LTDVA 328  
QY 302 LEHHECDVCVCGSTGG 318  
DB 329 LEHHECDVCVCGSTGG 345

Search completed: November 25, 2003, 21:02:14  
Job time : 34.125 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1728	99.7	345	4	US-09-040-220D-2	Sequence 2, Appli
2	1728	99.7	345	4	US-09-457-066-2	Sequence 2, Appli
3	1728	99.7	345	4	US-09-265-686-2	Sequence 2, Appli
4	1728	99.7	345	4	US-09-540-224-5	Sequence 5, Appli
5	1728	99.7	345	4	US-09-564-595D-33	Sequence 33, Appli
6	1728	99.7	345	4	US-09-706-968-2	Sequence 2, Appli
7	1559	89.9	345	4	US-09-457-066-43	Sequence 43, Appli
8	1559	89.9	345	4	US-09-564-595D-35	Sequence 35, Appli
9	1559	89.9	345	4	US-09-706-968-43	Sequence 43, Appli
10	1335	76.4	302	4	US-09-564-595D-54	Sequence 54, Appli
11	1266.5	73.0	303	4	US-09-564-595D-57	Sequence 57, Appli
12	1098	63.3	316	4	US-09-564-595D-55	Sequence 55, Appli
13	1051.5	60.6	317	4	US-09-564-595D-56	Sequence 56, Appli
14	741	42.7	370	4	US-09-457-066-37	Sequence 37, Appli
15	741	42.7	370	4	US-09-540-224-2	Sequence 2, Appli
16	741	42.7	370	4	US-09-564-595D-2	Sequence 2, Appli
17	741	42.7	370	4	US-09-706-968-37	Sequence 37, Appli
18	736	42.4	370	4	US-09-540-224-4	Sequence 4, Appli
19	736	42.4	370	4	US-09-564-595D-53	Sequence 53, Appli
20	172.5	9.9	730	3	US-08-872-757-2	Sequence 2, Appli
21	172.5	9.9	730	4	US-09-850-048A-2	Sequence 2, Appli
22	172	9.9	1012	4	US-09-285-385C-4	Sequence 4, Appli
23	171	9.9	1015	4	US-09-285-385C-2	Sequence 2, Appli
24	169	9.7	788	1	US-09-285-385C-2	Sequence 2, Appli
25	169	9.7	986	4	US-08-572-225-1	Sequence 1, Appli
26	165	9.5	3623	4	US-09-285-385C-19	Sequence 19, Appli
27	163.5	9.4	909	3	US-09-341-461-2	Sequence 2, Appli
					US-08-936-135-18	Sequence 18, Appli

```
RESULT 2
US-09-457-066-2
; Sequence 2, Application US/09457066
; Patent No. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457.066
; NUMBER FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-457-066-2

Query Match      99.7%; Score 1728; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 2.1e-179;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 KQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVWVQL 61
Db  29 KQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVWVQL 88
Qy  62 TFDERFGLDPEDDICKYDFVEVEEPSDGTILGRWCSGTVPGKQISKGNQIRIRFVSDE 121
Db  89 TFDERFGLDPEDDICKYDFVEVEEPSDGTILGRWCSGTVPGKQISKGNQIRIRFVSDE 148
Qy  122 YFSEPGFCIHYNIVMPQFTEAVSPVLPPSALPLDLNNAITAFSTLEDLIRYLEPERW 181
Db  149 YFSEPGFCIHYNIVMPQFTEAVSPVLPPSALPLDLNNAITAFSTLEDLIRYLEPERW 208
Qy  182 QLDLEDLYRPTWQLLKGAFVGRKSRVVDLNLTEEVRLYSCTPRNFVSISREELKRTDT 241
Db  209 QLDLEDLYRPTWQLLKGAFVGRKSRVVDLNLTEEVRLYSCTPRNFVSISREELKRTDT 268
Qy  242 IFWPGCLLVKRCGNCACCLHNCNECCVPSKVTKKYHEVLQRLPKTGVRGLHKS LTDVA 301
Db  269 IFWPGCLLVKRCGNCACCLHNCNECCVPSKVTKKYHEVLQRLPKTGVRGLHKS LTDVA 328
Qy  302 LEHHECDCVCRGSTGG 318
Db  329 LEHHECDCVCRGSTGG 345

RESULT 4
US-09-540-224-5
; Sequence 5, Application US/09540224
; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540.224
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 345
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-540-224-5

Query Match      99.7%; Score 1728; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 2.1e-179;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 KQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVWVQL 61
Db  29 KQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVWVQL 88
Qy  62 TFDERFGLDPEDDICKYDFVEVEEPSDGTILGRWCSGTVPGKQISKGNQIRIRFVSDE 121
Db  89 TFDERFGLDPEDDICKYDFVEVEEPSDGTILGRWCSGTVPGKQISKGNQIRIRFVSDE 148
Qy  122 YFSEPGFCIHYNIVMPQFTEAVSPVLPPSALPLDLNNAITAFSTLEDLIRYLEPERW 181
Db  149 YFSEPGFCIHYNIVMPQFTEAVSPVLPPSALPLDLNNAITAFSTLEDLIRYLEPERW 208
Qy  182 QLDLEDLYRPTWQLLKGAFVGRKSRVVDLNLTEEVRLYSCTPRNFVSISREELKRTDT 241
Db  209 QLDLEDLYRPTWQLLKGAFVGRKSRVVDLNLTEEVRLYSCTPRNFVSISREELKRTDT 268

RESULT 3
US-09-265-686-2
; Sequence 2, Application US/09265686
; Patent No. 6455283
; GENERAL INFORMATION:
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Kuo, Sophia S.
; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1
; FILE REFERENCE: F1122P2
; CURRENT APPLICATION NUMBER: US/09/265.686
; CURRENT FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: US 09/040,220
; PRIOR FILING DATE: 1998-03-17
; PRIOR APPLICATION NUMBER: US 09/184,216
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PR1
; ORGANISM: Human
```

```
US-09-265-686-2

Query Match      99.7%; Score 1728; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 2.1e-179;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 KQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVWVQL 61
Db  29 KQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVWVQL 88
Qy  62 TFDERFGLDPEDDICKYDFVEVEEPSDGTILGRWCSGTVPGKQISKGNQIRIRFVSDE 121
Db  89 TFDERFGLDPEDDICKYDFVEVEEPSDGTILGRWCSGTVPGKQISKGNQIRIRFVSDE 148
Qy  122 YFSEPGFCIHYNIVMPQFTEAVSPVLPPSALPLDLNNAITAFSTLEDLIRYLEPERW 181
Db  149 YFSEPGFCIHYNIVMPQFTEAVSPVLPPSALPLDLNNAITAFSTLEDLIRYLEPERW 208
Qy  182 QLDLEDLYRPTWQLLKGAFVGRKSRVVDLNLTEEVRLYSCTPRNFVSISREELKRTDT 241
Db  209 QLDLEDLYRPTWQLLKGAFVGRKSRVVDLNLTEEVRLYSCTPRNFVSISREELKRTDT 268
Qy  242 IFWPGCLLVKRCGNCACCLHNCNECCVPSKVTKKYHEVLQRLPKTGVRGLHKS LTDVA 301
Db  269 IFWPGCLLVKRCGNCACCLHNCNECCVPSKVTKKYHEVLQRLPKTGVRGLHKS LTDVA 328
Qy  302 LEHHECDCVCRGSTGG 318
Db  329 LEHHECDCVCRGSTGG 345

RESULT 4
US-09-540-224-5
; Sequence 5, Application US/09540224
; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540.224
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 345
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-540-224-5

Query Match      99.7%; Score 1728; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 2.1e-179;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 KQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVWVQL 61
Db  29 KQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVWVQL 88
Qy  62 TFDERFGLDPEDDICKYDFVEVEEPSDGTILGRWCSGTVPGKQISKGNQIRIRFVSDE 121
Db  89 TFDERFGLDPEDDICKYDFVEVEEPSDGTILGRWCSGTVPGKQISKGNQIRIRFVSDE 148
Qy  122 YFSEPGFCIHYNIVMPQFTEAVSPVLPPSALPLDLNNAITAFSTLEDLIRYLEPERW 181
Db  149 YFSEPGFCIHYNIVMPQFTEAVSPVLPPSALPLDLNNAITAFSTLEDLIRYLEPERW 208
Qy  182 QLDLEDLYRPTWQLLKGAFVGRKSRVVDLNLTEEVRLYSCTPRNFVSISREELKRTDT 241
Db  209 QLDLEDLYRPTWQLLKGAFVGRKSRVVDLNLTEEVRLYSCTPRNFVSISREELKRTDT 268
```

QY 242 IFWPGCLLVKRCGNCACCLHNCNECQCVPKVKYKHYEVLQRLPKTGVRLHKSLLTDA 301  
Db 269 IFWPGCLLVKRCGNCACCLHNCNECQCVPKVKYKHYEVLQRLPKTGVRLHKSLLTDA 328  
QY 302 LEHHECDCVCRGSTG 318  
Db 329 LEHHECDCVCRGSTG 345

## RESULT 5

US-09-564-595D-33  
; Sequence 33, Application US/09564595D  
; Patent No. 6495668  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4  
; FILE REFERENCE: 99-19  
; CURRENT APPLICATION NUMBER: US/09/564,595D  
; CURRENT FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: US 09/304,216  
; PRIOR FILING DATE: 1999-05-03  
; PRIOR APPLICATION NUMBER: US 60/164,463  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: US 60/180,169  
; PRIOR FILING DATE: 2000-02-04  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 33  
; LENGTH: 345  
; TYPE: PR1  
; ORGANISM: Homo sapiens  
US-09-564-595D-33

Query Match 99.7%; Score 1728; DB 4; Length 345;  
Best Local Similarity 100.0%; Pred. No. 2.1e-179;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENWVQL 61  
Db 29 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENWVQL 88  
QY 62 TFDERFGLDPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPKQISKGNQIRIRFVSDE 121  
Db 89 TFDERFGLDPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPKQISKGNQIRIRFVSDE 148  
QY 122 YFPSEFGFCHYNIWMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181  
Db 149 YFPSEFGFCHYNIWMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208  
QY 182 QLDLEDLYRPTWOLLGKAFVGRKSRVVDNLNLTTEEVRLYSCTPRNFVSIRBELKRTDT 241  
Db 209 QLDLEDLYRPTWOLLGKAFVGRKSRVVDNLNLTTEEVRLYSCTPRNFVSIRBELKRTDT 268  
QY 242 IFWPGCLLVKRCGNCACCLHNCNECQCVPKVKYKHYEVLQRLPKTGVRLHKSLLTDA 301  
Db 269 IFWPGCLLVKRCGNCACCLHNCNECQCVPKVKYKHYEVLQRLPKTGVRLHKSLLTDA 328  
QY 302 LEHHECDCVCRGSTG 318  
Db 329 LEHHECDCVCRGSTG 345

## RESULT 6

US-09-706-968-2  
; Sequence 2, Application US/09706968  
; Patent No. 6528050  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.

; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60C1  
; CURRENT APPLICATION NUMBER: US/09/706,968  
; CURRENT FILING DATE: 2000-11-06  
; PRIOR APPLICATION NUMBER: US/09/541,752  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 345  
; TYPE: PR1  
; ORGANISM: Homo sapiens  
US-09-706-968-2

Query Match 99.7%; Score 1728; DB 4; Length 345;  
Best Local Similarity 100.0%; Pred. No. 2.1e-179;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENWVQL 61  
Db 29 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENWVQL 88  
QY 62 TFDERFGLDPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPKQISKGNQIRIRFVSDE 121  
Db 89 TFDERFGLDPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPKQISKGNQIRIRFVSDE 148  
QY 122 YFPSEFGFCHYNIWMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181  
Db 149 YFPSEFGFCHYNIWMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208  
QY 182 QLDLEDLYRPTWOLLGKAFVGRKSRVVDNLNLTTEEVRLYSCTPRNFVSIRBELKRTDT 241  
Db 209 QLDLEDLYRPTWOLLGKAFVGRKSRVVDNLNLTTEEVRLYSCTPRNFVSIRBELKRTDT 268  
QY 242 IFWPGCLLVKRCGNCACCLHNCNECQCVPKVKYKHYEVLQRLPKTGVRLHKSLLTDA 301  
Db 269 IFWPGCLLVKRCGNCACCLHNCNECQCVPKVKYKHYEVLQRLPKTGVRLHKSLLTDA 328  
QY 302 LEHHECDCVCRGSTG 318  
Db 329 LEHHECDCVCRGSTG 345

## RESULT 7

US-09-457-066-43  
; Sequence 43, Application US/09457066  
; Patent No. 6432673  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60  
; CURRENT APPLICATION NUMBER: US/09/457,066  
; CURRENT FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 43  
; LENGTH: 345  
; TYPE: PR1  
; ORGANISM: Mus musculus  
US-09-457-066-43

Query Match 89.9%; Score 1559; DB 4; Length 345;  
Best Local Similarity 87.1%; Pred. No. 4.9e-161;  
Matches 276; Conservative 26; Mismatches 15; Indels 0; Gaps 0;

Qy 2 KQFSSNKEQNGVQDPOHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVWQL 61  
Db 29 KLQSSDKEQNGVQDPRHVRVITSGNHSIHPKFTYPRNVLVWRLVAEENVWQL 88  
Qy 62 TFDERFGLDPEDDICKYDFVEVEEPPSDGTILGWCSGTVPKGQISGNQIRIRFVSDE 121  
Db 89 TFDERFGLDPEDDICKYDFVEVEEPPSDGTILGWCSGTVPKGQISGNHIRIRFVSDE 148  
Qy 122 YFPSEPGFCHYNIWMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181  
Db 149 YFPSEPGFCHYSIIMPQVTTETTSVLPSPSSLDLNNAVTAFSTLEELIRYLEPDRW 208  
Qy 182 QLDLEDLYRPTWQLLKGAFVGRKSRVVDNLNLTTEEVRVLYSCTPRNFSVSIREELKRTDT 241  
Db 209 QVLDLSLYKPTWQLLKGAFVGRKSKVNVNLLKEEVKLYSCTPRNFSVSIREELKRTDT 268  
Qy 242 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTKKYHEVLQRLPKTGVRLGHLKSLTDVA 301  
Db 269 IFWPGCLLVKRCGNCACCLHNCNECQVPRKVTKYHEVLQRLPKTGVRLGHLKSLTDVA 328  
Qy 302 LEHHEECDCVCRGSTGG 318  
Db 329 LEHHEECDCVCRGNAGG 345

## RESULT 8

US-09-564-595D-35  
; Sequence 35, Application US/09564595D  
; Patent No. 6495668  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4  
; FILE REFERENCE: 99-19  
; CURRENT APPLICATION NUMBER: US/09/564,595D  
; PRIOR FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: US 09/304,216  
; PRIOR FILING DATE: 1999-05-03  
; PRIOR APPLICATION NUMBER: US 60/164,463  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: US 60/180,169  
; PRIOR FILING DATE: 2000-02-04  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 35  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-564-595D-35

Query Match 89.9%; Score 1559; DB 4; Length 345;  
Best Local Similarity 87.1%; Pred. No. 4.9e-161;  
Matches 276; Conservative 26; Mismatches 15; Indels 0; Gaps 0;  
Qy 2 KQFSSNKEQNGVQDPOHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVWQL 61  
Db 29 KLQSSDKEQNGVQDPRHVRVITSGNHSIHPKFTYPRNVLVWRLVAEENVWQL 88  
Qy 62 TFDERFGLDPEDDICKYDFVEVEEPPSDGTILGWCSGTVPKGQISGNQIRIRFVSDE 121  
Db 89 TFDERFGLDPEDDICKYDFVEVEEPPSDGTILGWCSGTVPKGQISGNHIRIRFVSDE 148  
Qy 122 YFPSEPGFCHYNIWMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181  
Db 149 YFPSEPGFCHYSIIMPQVTTETTSVLPSPSSLDLNNAVTAFSTLEELIRYLEPDRW 208  
Qy 182 QLDLEDLYRPTWQLLKGAFVGRKSRVVDNLNLTTEEVRVLYSCTPRNFSVSIREELKRTDT 241  
Db 209 QVLDLSLYKPTWQLLKGAFVGRKSKVNVNLLKEEVKLYSCTPRNFSVSIREELKRTDT 268  
Qy 242 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTKKYHEVLQRLPKTGVRLGHLKSLTDVA 301  
Db 269 IFWPGCLLVKRCGNCACCLHNCNECQVPRKVTKYHEVLQRLPKTGVRLGHLKSLTDVA 328  
Qy 302 LEHHEECDCVCRGSTGG 318  
Db 329 LEHHEECDCVCRGNAGG 345

Db 269 IFWPGCLLVKRCGNCACCLHNCNECQVPRKVTKYHEVLQRLPKTGVRLGHLKSLTDVA 328  
Qy 302 LEHHEECDCVCRGSTGG 318  
Db 329 LEHHEECDCVCRGNAGG 345  
RESULT 9  
US-09-706-968-43  
; Sequence 43, Application US/09706968  
; Patent No. 6528050  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60C1  
; CURRENT APPLICATION NUMBER: US/09/706,968  
; CURRENT FILING DATE: 2000-11-06  
; PRIOR APPLICATION NUMBER: US/09/541,752  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 43  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-706-968-43

Query Match 89.9%; Score 1559; DB 4; Length 345;  
Best Local Similarity 87.1%; Pred. No. 4.9e-161;  
Matches 276; Conservative 26; Mismatches 15; Indels 0; Gaps 0;  
Qy 2 KQFSSNKEQNGVQDPOHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVWQL 61  
Db 29 KLQSSDKEQNGVQDPRHVRVITSGNHSIHPKFTYPRNVLVWRLVAEENVWQL 88  
Qy 62 TFDERFGLDPEDDICKYDFVEVEEPPSDGTILGWCSGTVPKGQISGNQIRIRFVSDE 121  
Db 89 TFDERFGLDPEDDICKYDFVEVEEPPSDGTILGWCSGTVPKGQISGNHIRIRFVSDE 148  
Qy 122 YFPSEPGFCHYNIWMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181  
Db 149 YFPSEPGFCHYSIIMPQVTTETTSVLPSPSSLDLNNAVTAFSTLEELIRYLEPDRW 208  
Qy 182 QLDLEDLYRPTWQLLKGAFVGRKSRVVDNLNLTTEEVRVLYSCTPRNFSVSIREELKRTDT 241  
Db 209 QVLDLSLYKPTWQLLKGAFVGRKSKVNVNLLKEEVKLYSCTPRNFSVSIREELKRTDT 268  
Qy 242 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTKKYHEVLQRLPKTGVRLGHLKSLTDVA 301  
Db 269 IFWPGCLLVKRCGNCACCLHNCNECQVPRKVTKYHEVLQRLPKTGVRLGHLKSLTDVA 328  
Qy 302 LEHHEECDCVCRGSTGG 318  
Db 329 LEHHEECDCVCRGNAGG 345  
RESULT 10  
US-09-564-595D-54  
; Sequence 54, Application US/09564595D  
; Patent No. 6495668  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4  
; FILE REFERENCE: 99-19

Query Match 73.0%; Score 1266.5; DB 4; Length 303;  
Best Local Similarity 78.9%; Pred. No. 2.6e-129;



```
Db 180 EDLENMYLTPRYGRSY-HDRKSK-VDLRLNDKAKRYSCTPRNYSVNIREEKLNAVY 237
Qy 243 FWPGLLVKRCGNCACCLHNCNCCVPSKVKYHEVLQLRP---KTGVRGLHKS LTD 299
Db 238 FFPFCLLVKRCGNCAGGTNNWRSCTNSKTKYKHYHEVLQFEPGHKRRGRKTAVALVD 297
Qy 300 VALEHHEECDCVC 312
Db 298 IQLDHERCDDIC 310

RESULT 13
US-09-564-595D-56
; Sequence 56, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-56

Query Match 60.6%; Score 1051.5; DB 4; Length 317;
Best Local Similarity 63.8%; Pred. No. 6.5e-106;
Matches 204; Conservative 36; Mismatches 55; Indels 25; Gaps 6;

Qy 20 ERITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVIQLTFDERFGLDEPDIDCKY 79
Db 2 DETIQKGVNGYVQSPRPNSYPRNLLTWRLHS-QENTRIQLVFDNQFGLAEANDICRY 60
Qy 80 DFVEVEEPSDGT--ILGRWCGSGTVPGKQISKGNQIRIRFVSDYFSEPGCIHYNIVM 137
Db 61 DFVEVEDISSTIIRGRWCGHKEVPPRIKSRNQIKITFRSDDYFVAKPGFKIYVSL-L 119
Qy 138 PQTEAV-----SPSVLPSPSALPLDLNNAITAFSTLEDLIRYLEP 178
Db 120 EDFQPAASSETNWESVTSISGVSYNPSVTDPT-LIADALDKKIAEFDVEDLLKYFNP 178
Qy 179 ERQWLDLEDYRPTWQLLGAFFGRKSRVDNLNLTVEEVLVYSCTPRNSVSIRESLKR 238
Db 179 ESWQEDLENMYLTPRYGRSY-HDRKSKVVDNLNLTVEEVLVYSCTPRNSVSIRESLKR 237
Qy 239 TDIFWPGLLVKRCGNCACCLHNCNCCVPSKVKYHEVLQLRPKTVGRGLHKS LTD 298
Db 238 TDIFWPGLLVKRCGNCACCLHNCNCCVPSKVKYHEVLQLRPKTVGRGLHKS LTD 297
Qy 299 DVALEHHEECDCVCRGSGTG 318
Db 298 DVALEHHEECDCVCRGSGTG 317

RESULT 14
US-09-457-066-37
; Sequence 37, Application US/09457066
; Patent No. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-457-066-37

Query Match 42.7%; Score 741; DB 4; Length 370;
Best Local Similarity 46.6%; Pred. No. 4.7e-72;
Matches 153; Conservative 52; Mismatches 93; Indels 30; Gaps 9;
```

```
Qy 10 EQNGVQD-POHERIIVSTNGSIHSPRPHTYPRNTVLVRLVAEENVIQLTFDERFG 68
Db 42 ESNHLDLYRDETIOVKGNGYVQSPRPNSYPRNLLTWRLHS-QENTRIQLVFDNQFG 100
Qy 69 LEDPEDDICKYDFVEVEEPSDGT--ILGRWCGSGTVPGKQISKGNQIRIRFVSDYFSE 126
Db 101 LEEAENDICRYDFVEVEDISSTIIRGRWCGHKEVPPRIKSRNQIKITFRSDDYFVAK 160
Qy 127 PGFCIHYNIVMQPQTEAV-----SPSVLPSPSALPLDLNNAITAFS 167
Db 161 PGFKIYVSL-LEDQFPAASSETNWESVTSISGVSYNPSVTDPT-LIADALDKKIAEFD 218
Qy 168 TLEDLIRYLEPERWQDLEDYRPTWQLLGAFFGRKSRVDNLNLTVEEVLVYSCTPRN 227
Db 219 TVEDLLKYFNPESWQEDLENMYLTPRYGRSY-HDRKSK-VDLRLNDKAKRYSCTPRN 276
Qy 228 FSVSIRREELARTDTIFWPGLLVKRCGNCACCLHNCNCCVPSKVKYHEVLQLRP- 286
Db 277 YSVNIREEKLNAVVPFPRCLLVQRCGNGCGGTNNWRSCTNSGKTKYKHYHEVLQFEPG 336

RESULT 15
US-09-540-224-2
; Sequence 2, Application US/09540224
; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-540-224-2

Query Match 42.7%; Score 741; DB 4; Length 370;
Best Local Similarity 46.6%; Pred. No. 4.7e-72;
Matches 153; Conservative 52; Mismatches 93; Indels 30; Gaps 9;
```

Qy	10	BONGVQD-PQHERITVSTNGSIHSPRPHYTPRNTVLVRLVAEENWVIOLTDFDERG	68
Db	42	ESNHLTDIYRRDETIQVKGNGVQSPFNPSYPRNLLTWRUHS-QENTRIQLVFDNQFG	100
Qy	69	LEDPEDDICKDFVEVEBPSDGT--ILGRWCOSGTVPGQISKGNQIRIRFVSDEFPSSE	126
Db	101	LEEAENDICRYDFVEVEDISETSTIIRGWCGHKEVPRIKSRWQIKITFKSDDDYFVAK	160
Qy	127	PGFCIHYNVMPQFTEAV-----SPSVLPSPSALPLDLNNAITAPS	167
Db	161	PGFKIYLSL-LEDFOPAAASETNWESVTSSISGVSYNPSFVDTPT-LTADALDKXIAEED	218
Qy	168	TLEDLIRLEPERWQDLEDLYRPTWQLIGKAFVFCRKSRYVDLMLLTBEVLYSCTPRN	227
Db	219	TVEDLLKYFNPESWQEDLENMYLDPTRYGRSY-HDRKSK-VDLDRLNDDAKRYSTCPRN	276
Qy	228	FSVSTIRELKTDTFIWPGCLLVKRCGGNCACCLHNCNECQVPSKVYKKYHEVILQLRP-	286
Db	277	YSVNIARELKUANVFFPRCLLVQRCCGGCGGTVNRSTCNSGKTVKKYHEVILQFBFG	336
Qy	287	--KTGVRGLHKSLTDVALEHHEECDCVC	312
Db	337	HIKRGRAKTWALVDIQLDHHERCDCIC	364

Search completed: November 25, 2003, 21:06:21  
Job time : 12.9881 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 21:04:39 ; Search time 22.3988 Seconds  
(without alignments)  
2618.575 Million cell updates/sec

Title: US-09-852-209A-5  
Perfect score: 1734  
Sequence: 1 GKFQSSNKEQNGVDPQHE.....DVALEHHECDVCVRGSGG 318

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 673684 seqs, 18443283 residues

Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES									
Result No.	Score	Query Match	Length	DB ID	Description				
1	1734	100.0	318	10	US-09-852-209A-5	Sequence 5, Appli			
2	1734	100.0	318	15	US-10-131-600-5	Sequence 5, Appli			
3	1728	99.7	345	9	US-09-823-033-2	Sequence 2, Appli			
4	1728	99.7	345	9	US-09-818-943-1	Sequence 1, Appli			
5	1728	99.7	345	9	US-09-823-995-4	Sequence 4, Appli			
6	1728	99.7	345	10	US-09-795-006A-149	Sequence 149, App			
7	1728	99.7	345	10	US-09-978-295A-488	Sequence 488, App			
8	1728	99.7	345	10	US-09-852-209A-3	Sequence 3, Appli			
9	1728	99.7	345	10	US-09-978-697-488	Sequence 488, App			
10	1728	99.7	345	10	US-09-978-192A-488	Sequence 488, App			
11	1728	99.7	345	10	US-09-999-832A-488	Sequence 488, App			
12	1728	99.7	345	11	US-09-978-189-488	Sequence 488, App			
13	1728	99.7	345	11	US-09-976-753-6	Sequence 6, Appli			
14	1728	99.7	345	11	US-09-978-608A-488	Sequence 488, App			
15	1728	99.7	345	11	US-09-978-585A-488	Sequence 488, App			

16	1728	99.7	345	11	US-09-978-191A-488	Sequence 488, App
17	1728	99.7	345	11	US-09-978-403A-488	Sequence 488, App
18	1728	99.7	345	11	US-09-978-564A-488	Sequence 488, App
19	1728	99.7	345	11	US-09-999-833A-488	Sequence 488, App
20	1728	99.7	345	11	US-09-981-915A-488	Sequence 488, App
21	1728	99.7	345	11	US-09-978-824-488	Sequence 488, App
22	1728	99.7	345	11	US-09-918-585A-488	Sequence 488, App
23	1728	99.7	345	11	US-09-978-423A-488	Sequence 488, App
24	1728	99.7	345	11	US-09-978-193A-488	Sequence 488, App
25	1728	99.7	345	11	US-09-999-830A-488	Sequence 488, App
26	1728	99.7	345	11	US-09-978-757A-488	Sequence 488, App
27	1728	99.7	345	11	US-09-978-187B-488	Sequence 488, App
28	1728	99.7	345	11	US-09-978-643A-488	Sequence 488, App
29	1728	99.7	345	12	US-09-978-375A-488	Sequence 488, App
30	1728	99.7	345	12	US-09-978-188A-488	Sequence 488, App
31	1728	99.7	345	12	US-09-978-298A-488	Sequence 488, App
32	1728	99.7	345	12	US-10-137-870-286	Sequence 286, App
33	1728	99.7	345	12	US-10-140-018-286	Sequence 286, App
34	1728	99.7	345	12	US-10-140-021-286	Sequence 286, App
35	1728	99.7	345	12	US-10-140-27A-286	Sequence 286, App
36	1728	99.7	345	12	US-10-140-471-286	Sequence 286, App
37	1728	99.7	345	12	US-10-140-807-286	Sequence 286, App
38	1728	99.7	345	12	US-10-140-922-286	Sequence 286, App
39	1728	99.7	345	12	US-10-140-924-286	Sequence 286, App
40	1728	99.7	345	12	US-10-140-926-286	Sequence 286, App
41	1728	99.7	345	12	US-10-141-702-286	Sequence 286, App
42	1728	99.7	345	12	US-10-141-703-286	Sequence 286, App
43	1728	99.7	345	12	US-10-141-704-286	Sequence 286, App
44	1728	99.7	345	12	US-10-142-421-286	Sequence 286, App
45	1728	99.7	345	12	US-10-142-432-286	Sequence 286, App

ALIGNMENTS

RESULT 1

US-09-852-209A-5  
; Sequence 5, Application US/09852209A  
; Patent No. US20020164687A1  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: AASE, Karin  
; APPLICANT: LEE, Xuri  
; APPLICANT: PONTEN, Annica  
; APPLICANT: UTELA, Marko  
; APPLICANT: ALITALO, Kari  
; APPLICANT: ORSTMAN, Arne  
; APPLICANT: HELDIN, Carl-Henrik  
; APPLICANT: BEISHOLTZ, Christer  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING  
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF  
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740  
; CURRENT APPLICATION NUMBER: US/09/852,209A  
; CURRENT FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: 09/410,349  
; PRIOR FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: 60/110,749  
; PRIOR FILING DATE: 1998-12-03  
; PRIOR APPLICATION NUMBER: 60/113,002  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 60/135,426  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: 60/144,022  
; PRIOR FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 318  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-852-209A-5

Query Match 100.0%; Score 1734; DB 10; Length 318;

Best Local Similarity 100.0%; Pred. No. 1.2e-166;  
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GKQFSSNKEQNGVDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWVIQ 60  
1 GKQFSSNKEQNGVDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWVIQ 60

61 LTFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 120  
61 LTFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 120

121 EYFSPGFCIHYNIVMPQFTEAVSPVLPSPALPLDLLNNAITAFSTLEDLIRYLEPER 180  
121 EYFSPGFCIHYNIVMPQFTEAVSPVLPSPALPLDLLNNAITAFSTLEDLIRYLEPER 180

181 WQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLTEEVRLYSCTPRNFSVSIREELKRTD 240  
181 WQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLTEEVRLYSCTPRNFSVSIREELKRTD 240

241 TIFWPGCLLVKRCGNCACCLHNCNECCQVPSKVTKKYHEVLQRLPKTGVRGLHKS LTDV 300  
241 TIFWPGCLLVKRCGNCACCLHNCNECCQVPSKVTKKYHEVLQRLPKTGVRGLHKS LTDV 300

301 ALEHHEECDCVCRGSTGG 318  
301 ALEHHEECDCVCRGSTGG 318

## RESULT 2

US-10-131-600-5  
; Sequence 5, Application US/10131600  
; Publication No. US20030082670A1  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: AASE, Karin  
; APPLICANT: LEE, Xuri  
; APPLICANT: PONTEN, Annica  
; APPLICANT: UUTELA, Marko  
; APPLICANT: ALITALO, Karl  
; APPLICANT: OESTMAN, Arne  
; APPLICANT: HELDIN, Carl-Henrik  
; APPLICANT: BETSHOUTZ, Christen  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING  
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740  
; CURRENT APPLICATION NUMBER: US/10/131,600  
; CURRENT FILING DATE: 2002-04-25  
; PRIOR APPLICATION NUMBER: US/09/410,349  
; PRIOR FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: 60/108,109  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: 60/110,749  
; PRIOR FILING DATE: 1998-12-03  
; PRIOR APPLICATION NUMBER: 60/113,002  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 60/135,426  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: 60/144,022  
; PRIOR FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 318  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-131-600-5

Query Match 100.0%; Score 1734; DB 15; Length 318;  
Best Local Similarity 100.0%; Pred. No. 1.2e-166;  
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GKQFSSNKEQNGVDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWVIQ 60  
|||||

Db 1 GKQFSSNKEQNGVDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWVIQ 60  
Qy 61 LTFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 120  
Db 61 LTFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 120  
Qy 121 EYFSPGFCIHYNIVMPQFTEAVSPVLPSPALPLDLLNNAITAFSTLEDLIRYLEPER 180  
Db 121 EYFSPGFCIHYNIVMPQFTEAVSPVLPSPALPLDLLNNAITAFSTLEDLIRYLEPER 180  
Qy 181 WQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLTEEVRLYSCTPRNFSVSIREELKRTD 240  
Db 181 WQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLTEEVRLYSCTPRNFSVSIREELKRTD 240  
Qy 241 TIFWPGCLLVKRCGNCACCLHNCNECCQVPSKVTKKYHEVLQRLPKTGVRGLHKS LTDV 300  
Db 241 TIFWPGCLLVKRCGNCACCLHNCNECCQVPSKVTKKYHEVLQRLPKTGVRGLHKS LTDV 300  
Qy 301 ALEHHEECDCVCRGSTGG 318  
Db 301 ALEHHEECDCVCRGSTGG 318

## RESULT 3

US-09-823-033-2  
; Sequence 2, Application US/09823033  
; Patent No. US20020004225A1  
; GENERAL INFORMATION:  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Gilbertson, Debra G.  
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,  
; FILE REFERENCE: 00-12  
; CURRENT APPLICATION NUMBER: US/09/823,033  
; CURRENT FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-823-033-2

Query Match 99.7%; Score 1728; DB 9; Length 345;  
Best Local Similarity 100.0%; Pred. No. 5.3e-166;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KQFSSNKEQNGVDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWVIQ 61  
Db 29 KQFSSNKEQNGVDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWVIQ 88  
Qy 62 TFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 121  
Db 89 TFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 148  
Qy 122 YFSPGFCIHYNIVMPQFTEAVSPVLPSPALPLDLLNNAITAFSTLEDLIRYLEPER 181  
Db 149 YFSPGFCIHYNIVMPQFTEAVSPVLPSPALPLDLLNNAITAFSTLEDLIRYLEPER 208  
Qy 182 QDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLTEEVRLYSCTPRNFSVSIREELKRTD 241  
Db 209 QDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLTEEVRLYSCTPRNFSVSIREELKRTD 268  
Qy 242 TIFWPGCLLVKRCGNCACCLHNCNECCQVPSKVTKKYHEVLQRLPKTGVRGLHKS LTDV 301  
Db 269 TIFWPGCLLVKRCGNCACCLHNCNECCQVPSKVTKKYHEVLQRLPKTGVRGLHKS LTDV 328  
Qy 302 LEHHEECDCVCRGSTGG 318  
Db 329 LEHHEECDCVCRGSTGG 345

## RESULT 4

```
US-09-818-943-1
; Sequence 1, Application US/09818943
; Patent No. US20020049987A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: LI, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: AASE, Karin
; APPLICANT: LI, Hong
; TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMALS EXPRESSING PLATELET-DERIVED GROWTH F
; FILE REFERENCE: 1064/48487
; CURRENT APPLICATION NUMBER: US/09/818,943
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/192,507
; PRIOR FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 345
; TYPE: PR
; ORGANISM: Homo sapiens
US-09-818-943-1

Query Match      99.7%; Score 1728; DB 9; Length 345;
Best Local Similarity 100.0%; Pred. No. 5.3e-166;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVVIQL 61
DB  29 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVVIQL 88
QY  62 TFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPKGQISKGNQIRIRFVSDE 121
DB  89 TFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPKGQISKGNQIRIRFVSDE 148
QY  122 YFPSEPGFCIHYNIVMPQFTVAVSPVLPPSALPLDLNNAITAFSTLEDLIRYLEPERW 181
DB  149 YFPSEPGFCIHYNIVMPQFTVAVSPVLPPSALPLDLNNAITAFSTLEDLIRYLEPERW 208
QY  182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNNLTTEEVRVLYSCTPRNFSVSIREELKRTDT 241
DB  209 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNNLTTEEVRVLYSCTPRNFSVSIREELKRTDT 268
QY  242 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDVA 301
DB  269 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDVA 328
QY  302 LEHHECDCVCRGSGTG 318
DB  329 LEHHECDCVCRGSGTG 345

RESULT 6
US-09-795-006A-149
; Sequence 149, Application US/09795006A
; Patent No. US20020151680A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAS AND PROTEINS
; FILE REFERENCE: 28967/3597B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 149
; LENGTH: 345
; TYPE: PR
; ORGANISM: Homo sapiens
US-09-795-006A-149

Query Match      99.7%; Score 1728; DB 10; Length 345;
Best Local Similarity 100.0%; Pred. No. 5.3e-166;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVVIQL 61
DB  29 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVVIQL 88
QY  62 TFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPKGQISKGNQIRIRFVSDE 121
DB  89 TFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPKGQISKGNQIRIRFVSDE 148
QY  122 YFPSEPGFCIHYNIVMPQFTVAVSPVLPPSALPLDLNNAITAFSTLEDLIRYLEPERW 181
DB  149 YFPSEPGFCIHYNIVMPQFTVAVSPVLPPSALPLDLNNAITAFSTLEDLIRYLEPERW 208
QY  182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNNLTTEEVRVLYSCTPRNFSVSIREELKRTDT 241
DB  209 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNNLTTEEVRVLYSCTPRNFSVSIREELKRTDT 268
QY  242 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDVA 301
```

```
US-09-818-943-1
; Sequence 1, Application US/09818943
; Patent No. US20020049987A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: LI, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: AASE, Karin
; APPLICANT: LI, Hong
; TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMALS EXPRESSING PLATELET-DERIVED GROWTH F
; FILE REFERENCE: 1064/48487
; CURRENT APPLICATION NUMBER: US/09/818,943
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/192,507
; PRIOR FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 345
; TYPE: PR
; ORGANISM: Homo sapiens
US-09-818-943-1

Query Match      99.7%; Score 1728; DB 9; Length 345;
Best Local Similarity 100.0%; Pred. No. 5.3e-166;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVVIQL 61
DB  29 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVVIQL 88
QY  62 TFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPKGQISKGNQIRIRFVSDE 121
DB  89 TFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPKGQISKGNQIRIRFVSDE 148
QY  122 YFPSEPGFCIHYNIVMPQFTVAVSPVLPPSALPLDLNNAITAFSTLEDLIRYLEPERW 181
DB  149 YFPSEPGFCIHYNIVMPQFTVAVSPVLPPSALPLDLNNAITAFSTLEDLIRYLEPERW 208
QY  182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNNLTTEEVRVLYSCTPRNFSVSIREELKRTDT 241
DB  209 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNNLTTEEVRVLYSCTPRNFSVSIREELKRTDT 268
QY  242 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDVA 301
DB  269 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDVA 328
QY  302 LEHHECDCVCRGSGTG 318
DB  329 LEHHECDCVCRGSGTG 345

RESULT 5
US-09-923-995-4
; Sequence 4, Application US/09923995
; Patent No. US20020081700A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: SNAKE VENOM POLYPEPTIDE ZSNK1
; FILE REFERENCE: 00-47
; CURRENT APPLICATION NUMBER: US/09/923,995
; CURRENT FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 60/223,164
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 345
; TYPE: PR
; ORGANISM: Homo sapiens
US-09-923-995-4
```

Db 269 IFWPGCLLVKRCGCGNACCLHNCNECCQVSKVTKKYHEVLQLRPKTVGRGLHSLTDA 328  
QY 302 LEHHEBCDCVCRGSTGG 318  
Db 329 LEHHEBCDCVCRGSTGG 345

RESULT 7  
US-09-978-295A-488  
; Sequence 488, Application US/09978295A  
; Patent No. US20020156006A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Eilen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Oiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gottard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C11  
; CURRENT APPLICATION NUMBER: US/09/978,295A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/077450  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 60/077632  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077641  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077649  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077791  
; PRIOR FILING DATE: 1998-03-12  
; PRIOR APPLICATION NUMBER: 60/078004  
; PRIOR FILING DATE: 1998-03-13  
; PRIOR APPLICATION NUMBER: 60/078886  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078936  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078939  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079664  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079663  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079786  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079920  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 60/079923  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 60/080105  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080107  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080165  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080194  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080327  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080328  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080333  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080334  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/081070  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081049  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081071  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081195  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081203  
; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 60/081229  
; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 60/081955  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081817  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081819  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081952  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081838  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/082568  
; PRIOR FILING DATE: 1998-04-21  
; PRIOR APPLICATION NUMBER: 60/082569  
; PRIOR FILING DATE: 1998-04-21  
; PRIOR APPLICATION NUMBER: 60/082704  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082804  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082700  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082797  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082796  
; PRIOR FILING DATE: 1998-04-23  
; PRIOR APPLICATION NUMBER: 60/083336

Qy	62	TFDERFGLDPEDDICKYDFVEVEEESDGTILGRWCGSGTVPKGKQISKGNQIRIRFVSDE	12
Db	89	TFDERFGLDPEDDICKYDFVEVEEESDGTILGRWCGSGTVPKGKQISKGNQIRIRFVSDE	148
Qy	122	YFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPSALPLDLLNNAITAFSTLEDLIRYLEPERW	181
Db	149	YFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPSALPLDLLNNAITAFSTLEDLIRYLEPERW	208
Qy	182	OLDLEDLYRETWQLLGKAFVGRKSRVDNLNLTTEVRVLYSCTTPRNFVSISREELKRTDT	241
Db	209	OLDLEDLYRETWQLLGKAFVGRKSRVDNLNLTTEVRVLYSCTTPRNFVSISREELKRTDT	268
Qy	242	IFWPGCLLVKRCGNCACCLHNCNECQCVPFSKVTKKYKHEVLQRLPXTGVRGLHKSJTDVA	301
Db	269	IFWPGCLLVKRCGNCACCLHNCNECQCVPFSKVTKKYKHEVLQRLPXTGVRGLHKSJTDVA	328
Qy	302	LEHHECDCVCRGSTGG 318	
Db	329	LEHHECDCVCRGSTGG 345	
RESULT 8			
US-09-852-209A-3			
; Sequence 3, Application US/09852209A			
; Patent No. US20020164687A1			
; GENERAL INFORMATION:			
; APPLICANT: ERIKSSON, Ulf			
; APPLICANT: AASE, Karin			
; APPLICANT: LEE, Xuri			
; APPLICANT: PONTEN, Annica			
; APPLICANT: UUTELA, Marko			
; APPLICANT: ALITALO, Kari			
; APPLICANT: OESTMAN, Arne			
; APPLICANT: HELDIN, Carl-Henrik			
; APPLICANT: BETSHOLTZ, Christer			
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING			
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF			
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740			
; CURRENT APPLICATION NUMBER: US/09/852,209A			
; CURRENT FILING DATE: 2001-05-10			
; PRIOR APPLICATION NUMBER: 09/410,349			
; PRIOR FILING DATE: 1999-09-30			
; PRIOR APPLICATION NUMBER: 60/110,749			
; PRIOR FILING DATE: 1998-12-03			
; PRIOR APPLICATION NUMBER: 60/113,002			
; PRIOR FILING DATE: 1998-12-18			
; PRIOR APPLICATION NUMBER: 60/135,426			
; PRIOR FILING DATE: 1999-05-21			
; PRIOR APPLICATION NUMBER: 60/144,022			
; PRIOR FILING DATE: 1999-07-15			
; NUMBER OF SEQ ID NOS: 39			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 3			
; LENGTH: 345			
; TYPE: PRM			
; ORGANISM: Homo sapiens			
US-09-852-209A-3			
Query Match 99.7%; Score 1728; DB 10; Length 345;			
Best Local Similarity 100.0%; Pred. No. 5.3e-166;			
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	2	KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWVQL	61
Db	29	KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWVQL	88
Qy	62	TFDERFGLDPEDDICKYDFVEVEEESDGTILGRWCGSGTVPKGKQISKGNQIRIRFVSDE	121
Db	89	TFDERFGLDPEDDICKYDFVEVEEESDGTILGRWCGSGTVPKGKQISKGNQIRIRFVSDE	148
Qy	122	YFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPSALPLDLLNNAITAFSTLEDLIRYLEPERW	181
Db	149	YFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPSALPLDLLNNAITAFSTLEDLIRYLEPERW	208

Qy	182	Q L D E D L Y R P T W L L G K A F V G R K S R V D L N L L T E E V R L Y S C T P R N F S V S I B E E L K R T D T	241
Db	209	Q L D E D L Y R P T W L L G K A F V G R K S R V D L N L L T E E V R L Y S C T P R N F S V S I B E E L K R T D T	268
Qy	242	I F W P G C L L V R K C G G N C A C C L H N C N E C Q V P S K V T K Y K Y H E V L Q R P K T G V R G L H K S L T D V A	301
Db	269	I F W P G C L L V R K C G G N C A C C L H N C N E C Q V P S K V T K Y K Y H E V L Q R P K T G V R G L H K S L T D V A	328
Qy	302	L E H H E E C D C V C R G S T G G	318
Db	329	L E H H E E C D C V C R G S T G G	345

RESIST. T. 9

```

US-09-978-697-488
; Sequence 488, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoli, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C27
; CURRENT APPLICATION NUMBER: US/09/978,697
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13

```







```

; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match          99.7%; Score 1728; DB 10; Length 345;
Best Local Similarity 100.0%; Pred. No. 5.3e-166;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSRPFPHYPRNTVLVWRLVAEENWVQL 61
Db 29 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSRPFPHYPRNTVLVWRLVAEENWVQL 88
QY 62 TDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPKQISKGNQIRIRFVSDE 121
Db 89 TDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPKQISKGNQIRIRFVSDE 148
QY 122 YPSEPGFCIHYNVMPQTEAVSPVLPPSALPLDLNNAITAFSTLEDLIRYLEPERW 181
Db 149 YPSEPGFCIHYNVMPQTEAVSPVLPPSALPLDLNNAITAFSTLEDLIRYLEPERW 208
QY 182 QLDLEDLYRPTWQLLKGAFVFGKRSRVVDNLNLTTEEVRLYSCTPRNFSVSIREELKRTDT 241
Db 209 QLDLEDLYRPTWQLLKGAFVFGKRSRVVDNLNLTTEEVRLYSCTPRNFSVSIREELKRTDT 268
QY 242 IFWPGCLLVKRCGNCACCLHNCNECCVPSKTKKYHYEVLQRPKTVGRGLHKSITDVA 301
Db 269 IFWPGCLLVKRCGNCACCLHNCNECCVPSKTKKYHYEVLQRPKTVGRGLHKSITDVA 328
QY 302 LEHHEECDCVCRGSTGG 318
Db 329 LEHHEECDCVCRGSTGG 345

RESULT 11
US-09-999-832A-488
; Sequence 488, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC63
; CURRENT APPLICATION NUMBER: US/09/999,832A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/079923
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/080105
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080334
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081071
```



APPLICANT: Hillan, Kenneth J  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC7  
CURRENT APPLICATION NUMBER: US/09/978,189  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004  
PRIOR FILING DATE: 1998-03-13  
PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078936  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078939  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079664  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079663  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079786  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079920  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/079923  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/080105  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080107  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080194  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080327  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080328  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080333  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080334  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/081070  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081049  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081071  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081195  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081203  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081229  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081955  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081817  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081819  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081952  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081838  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/082568  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082569  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082704  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082700  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082796  
PRIOR FILING DATE: 1998-04-23  
PRIOR APPLICATION NUMBER: 60/083336  
PRIOR FILING DATE: 1998-04-27  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/083392  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083495  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083496  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083499  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083545  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083554  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083558  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083559  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083500  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742  
PRIOR FILING DATE: 1998-04-30  
PRIOR APPLICATION NUMBER: 60/084366  
PRIOR FILING DATE: 1998-05-05  
PRIOR APPLICATION NUMBER: 60/084414  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084441

;  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/084637  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084639  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084640  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084598  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084627  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084643  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/085339  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085338  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085323  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085582  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085700  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085689  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085579  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085580  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085573  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.7%; Score 1728; DB 11; Length 345;  
Best Local Similarity 100.0%; Pred. No. 5.3e-166;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAVEENVWVQL 61  
DB 29 KQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAVEENVWVQL 88  
QY 62 TFDERFGLDEDDICKYDFVEVEEPPSDGTILGRWCGSGTVPGKQISKGNOIRIRFVSD 121  
DB 89 TFDERFGLDEDDICKYDFVEVEEPPSDGTILGRWCGSGTVPGKQISKGNOIRIRFVSD 148  
QY 122 YFPSPGFCIHNVMPQTEAVSPVLPSPALPLDLLNNAITAFSTLEDLIRYLEPERW 181  
DB 149 YFPSPGFCIHNVMPQTEAVSPVLPSPALPLDLLNNAITAFSTLEDLIRYLEPERW 208  
QY 182 QLDLEDLIRPTWQLGKAFVFGKRSVVDLNLITTEVRVLYSCTPRNFSVSIREEKRTDT 241  
DB 209 QLDLEDLIRPTWQLGKAFVFGKRSVVDLNLITTEVRVLYSCTPRNFSVSIREEKRTDT 268  
QY 242 IFWPGLLVKRCGNCACCLHNCNECCQVPSKVTKYKHEVLQRLPKTVGRGLHKSITDVA 301  
DB 269 IFWPGLLVKRCGNCACCLHNCNECCQVPSKVTKYKHEVLQRLPKTVGRGLHKSITDVA 328  
QY 302 LEHHEEDCVCRGSTGG 318  
DB 329 LEHHEEDCVCRGSTGG 345

RESULT 13  
US-09-796-753-6  
; Sequence 6, Application US/09796753  
; Publication No. US20030027998A1  
; GENERAL INFORMATION:  
; APPLICANT: McCarthy, Sean A.  
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF

;  
; FILE REFERENCE: 7853-227-999  
; CURRENT APPLICATION NUMBER: US/09/796,753  
; CURRENT FILING DATE: 2001-03-01  
; PRIOR APPLICATION NUMBER: 09/183,175  
; PRIOR FILING DATE: 1998-10-30  
; PRIOR APPLICATION NUMBER: 09/223,094  
; PRIOR FILING DATE: 1998-12-30  
; PRIOR APPLICATION NUMBER: 09/223,546  
; PRIOR FILING DATE: 1998-12-30  
; PRIOR APPLICATION NUMBER: 09/224,246  
; PRIOR FILING DATE: 1998-12-30  
; PRIOR APPLICATION NUMBER: 09/259,388  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/122,458  
; PRIOR FILING DATE: 1999-03-01  
; PRIOR APPLICATION NUMBER: 09/312,359  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: 09/336,536  
; PRIOR FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: 09/342,687  
; PRIOR FILING DATE: 1999-06-29  
; PRIOR APPLICATION NUMBER: 09/345,464  
; PRIOR FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: 09/365,164  
; PRIOR FILING DATE: 1999-07-30  
; PRIOR APPLICATION NUMBER: 09/399,723  
; PRIOR FILING DATE: 1999-09-20  
; PRIOR APPLICATION NUMBER: 09/409,634  
; PRIOR FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: 09/471,179  
; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 09/474,071  
; PRIOR FILING DATE: 1999-12-29  
; PRIOR APPLICATION NUMBER: 09/474,072  
; PRIOR FILING DATE: 1999-12-29  
; PRIOR APPLICATION NUMBER: 09/514,010  
; PRIOR FILING DATE: 2000-02-25  
; PRIOR APPLICATION NUMBER: 09/516,745  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: 09/572,002  
; PRIOR FILING DATE: 2000-05-14  
; PRIOR APPLICATION NUMBER: 09/597,993  
; PRIOR FILING DATE: 2000-06-19  
; PRIOR APPLICATION NUMBER: 09/599,596  
; PRIOR FILING DATE: 2000-06-22  
; PRIOR APPLICATION NUMBER: 09/630,334  
; PRIOR FILING DATE: 2000-07-31  
; PRIOR APPLICATION NUMBER: 09/606,565  
; PRIOR FILING DATE: 2000-06-29  
; PRIOR APPLICATION NUMBER: 09/606,317  
; PRIOR FILING DATE: 2000-06-29  
; PRIOR APPLICATION NUMBER: 09/665,666  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: 09/677,751  
; PRIOR FILING DATE: 2000-09-30  
; NUMBER OF SEQ ID NOS: 162  
; SEQ ID NO 6  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-796-753-6

Query Match 99.7%; Score 1728; DB 11; Length 345;  
Best Local Similarity 100.0%; Pred. No. 5.3e-166;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAVEENVWVQL 61  
DB 29 KQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAVEENVWVQL 88  
QY 62 TFDERFGLDEDDICKYDFVEVEEPPSDGTILGRWCGSGTVPGKQISKGNOIRIRFVSD 121  
DB 89 TFDERFGLDEDDICKYDFVEVEEPPSDGTILGRWCGSGTVPGKQISKGNOIRIRFVSD 148

QY 122 YFPSEPGFCIHYNIVMPQTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181  
DB 149 YFPSEPGFCIHYNIVMPQTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208  
QY 182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLITTEVRLYSCTPRNFSVSIREELKRTDT 241  
DB 209 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLITTEVRLYSCTPRNFSVSIREELKRTDT 268  
QY 242 IFWPGCLLVKRCGNCACCLHNCNECQCVPSKVTKYHVLQRLPKTGVRGLHKSITDVA 301  
DB 269 IFWPGCLLVKRCGNCACCLHNCNECQCVPSKVTKYHVLQRLPKTGVRGLHKSITDVA 328  
QY 302 LEHHEBCDCVCRGSTGG 318  
DB 329 LEHHEBCDCVCRGSTGG 345

## RESULT 14

US-09-978-608A-488  
; Sequence 488, Application US/09978608A  
; Publication No. US20030045462A1

GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630PIC22  
; CURRENT APPLICATION NUMBER: US/09/978,608A  
; CURRENT FILING DATE: 2001-10-16  
; NUMBER OF SEQ ID NOS: 624  
; Prior Application removed - See File Wrapper or Palm  
; SEQ ID NO 488  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-978-608A-488

Query Match 99.7%; Score 1728; DB 11; Length 345;  
Best Local Similarity 100.0%; Pred. No. 5.3e-166;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPFTYPRNTVLVWRLVAEENWVQL 61  
DB 29 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPFTYPRNTVLVWRLVAEENWVQL 88  
QY 62 TFERFGLPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPKGKQISKNQIRIRFVSDE 121

DB 89 TFERFGLPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPKGKQISKNQIRIRFVSDE 148  
QY 122 YFPSEPGFCIHYNIVMPQTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181  
DB 149 YFPSEPGFCIHYNIVMPQTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208  
QY 182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLITTEVRLYSCTPRNFSVSIREELKRTDT 241  
DB 209 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLITTEVRLYSCTPRNFSVSIREELKRTDT 268  
QY 242 IFWPGCLLVKRCGNCACCLHNCNECQCVPSKVTKYHVLQRLPKTGVRGLHKSITDVA 301  
DB 269 IFWPGCLLVKRCGNCACCLHNCNECQCVPSKVTKYHVLQRLPKTGVRGLHKSITDVA 328  
QY 302 LEHHEBCDCVCRGSTGG 318  
DB 329 LEHHEBCDCVCRGSTGG 345

## RESULT 15

US-09-978-585A-488  
; Sequence 488, Application US/09978585A  
; Publication No. US20030049633A1

GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630PIC15  
; CURRENT APPLICATION NUMBER: US/09/978,585A  
; CURRENT FILING DATE: 2001-10-16  
; NUMBER OF SEQ ID NOS: 624  
; Prior Application removed - See File Wrapper or Palm  
; SEQ ID NO 488  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-978-585A-488

Query Match 99.7%; Score 1728; DB 11; Length 345;  
Best Local Similarity 100.0%; Pred. No. 5.3e-166;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPFTYPRNTVLVWRLVAEENWVQL 61  
DB 29 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPFTYPRNTVLVWRLVAEENWVQL 88  
QY 62 TFERFGLPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPKGKQISKNQIRIRFVSDE 121

Db	89	TFDERGLEDPEDDICKYDFVEVEEFS	DTILGRWCGSGTVPGKQISKGNQIRIRFVSDE	148
QY	122	YFSEBFGFCHYNI	VMPQFTEAVSPVLPPSALPLDLLANNAITAFSTLEDLIRYLEPERW	181
Db	149	YFSEBFGFCHYNI	VMPQFTEAVSPVLPPSALPLDLLANNAITAFSTLEDLIRYLEPERW	208
QY	182	QLELEDLYRPTWOLLGKAFV	GRKSRVVDNLLTTEEVRLYSCTPRNFSVSIREELKRTDT	241
Db	209	QLELEDLYRPTWOLLGKAFV	GRKSRVVDNLLTTEEVRLYSCTPRNFSVSIREELKRTDT	268
QY	242	IFWPGCLLVKRCGNCACCLHNC	NECQVPSKVKYHEVQLRPKTGVRGLHKS	301
Db	269	IFWPGCLLVKRCGNCACCLHNC	NECQVPSKVKYHEVQLRPKTGVRGLHKS	328
QY	302	LEHHECDCVCRGSTGG		318
Db	329	LEHHECDCVCRGSTGG		345

Search completed: November 25, 2003, 21:17:05  
Job time : 23.3988 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 21:02:19 ; Search time 156.161 Seconds  
(without alignments)  
1852.926 Million cell updates/sec

Title: US-09-852-209A-5  
Perfect score: 1734  
Sequence: 1 GKFQSSNKEQGVDPQHE.....DVALEHHECDVCVRGSGG 318

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents AA Main:\*

1: /cgn2\_6/ptodata/1/paa/PCTUS\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/paa/US06\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/paa/US07\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/paa/US080\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/paa/US081\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/paa/US082\_COMB.pep.\*  
7: /cgn2\_6/ptodata/1/paa/US083\_COMB.pep.\*  
8: /cgn2\_6/ptodata/1/paa/US084\_COMB.pep.\*  
9: /cgn2\_6/ptodata/1/paa/US085\_COMB.pep.\*  
10: /cgn2\_6/ptodata/1/paa/US086\_COMB.pep.\*  
11: /cgn2\_6/ptodata/1/paa/US087\_COMB.pep.\*  
12: /cgn2\_6/ptodata/1/paa/US088\_COMB.pep.\*  
13: /cgn2\_6/ptodata/1/paa/US089\_COMB.pep.\*  
14: /cgn2\_6/ptodata/1/paa/US090\_COMB.pep.\*  
15: /cgn2\_6/ptodata/1/paa/US091\_COMB.pep.\*  
16: /cgn2\_6/ptodata/1/paa/US092\_COMB.pep.\*  
17: /cgn2\_6/ptodata/1/paa/US093\_COMB.pep.\*  
18: /cgn2\_6/ptodata/1/paa/US094\_COMB.pep.\*  
19: /cgn2\_6/ptodata/1/paa/US095\_COMB.pep.\*  
20: /cgn2\_6/ptodata/1/paa/US096\_COMB.pep.\*  
21: /cgn2\_6/ptodata/1/paa/US097A\_COMB.pep.\*  
22: /cgn2\_6/ptodata/1/paa/US097B\_COMB.pep.\*  
23: /cgn2\_6/ptodata/1/paa/US098\_COMB.pep.\*  
24: /cgn2\_6/ptodata/1/paa/US099A\_COMB.pep.\*  
25: /cgn2\_6/ptodata/1/paa/US099B\_COMB.pep.\*  
26: /cgn2\_6/ptodata/1/paa/US100\_COMB.pep.\*  
27: /cgn2\_6/ptodata/1/paa/US101\_COMB.pep.\*  
28: /cgn2\_6/ptodata/1/paa/US102\_COMB.pep.\*  
29: /cgn2\_6/ptodata/1/paa/US103\_COMB.pep.\*  
30: /cgn2\_6/ptodata/1/paa/US104\_COMB.pep.\*  
31: /cgn2\_6/ptodata/1/paa/US106\_COMB.pep.\*  
32: /cgn2\_6/ptodata/1/paa/US60\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1734	100.0	318	1	PCT-US99-22668-5 Sequence 5, Appli

2	1734	100.0	318	18	US-09-410-349A-5	Sequence 5, Appli
3	1734	100.0	318	23	US-09-852-209-5	Sequence 5, Appli
4	1734	100.0	318	23	US-09-852-209A-5	Sequence 5, Appli
5	1734	100.0	318	27	US-10-131-600-5	Sequence 5, Appli
6	1734	100.0	318	29	US-10-303-997B-5	Sequence 5, Appli
7	1728	99.7	323	1	PCT-US99-31025-29	Sequence 23, Appli
8	1728	99.7	323	18	US-09-471-179-29	Sequence 29, Appli
9	1728	99.7	345	1	PCT-US01-43523-286	Sequence 286, App
10	1728	99.7	345	1	PCT-US02-24563-286	Sequence 34, Appl
11	1728	99.7	345	1	PCT-US03-04213-34	Sequence 2, Appli
12	1728	99.7	345	1	PCT-US99-01574-2	Sequence 4, Appli
13	1728	99.7	345	1	PCT-US99-15783-4	Sequence 2, Appli
14	1728	99.7	345	1	PCT-US99-22668-3	Sequence 3, Appli
15	1728	99.7	345	1	PCT-US99-31025-2	Sequence 2, Appli
16	1728	99.7	345	15	US-09-184-216-2	Sequence 2, Appli
17	1728	99.7	345	16	US-09-207-120-2	Sequence 2, Appli
18	1728	99.7	345	16	US-09-223-546-2	Sequence 2, Appli
19	1728	99.7	345	16	US-09-237-705-2	Sequence 2, Appli
20	1728	99.7	345	16	US-09-267-213-2	Sequence 2, Appli
21	1728	99.7	345	17	US-09-304-216-33	Sequence 33, Appl
22	1728	99.7	345	17	US-09-380-138-488	Sequence 488, App
23	1728	99.7	345	18	US-09-410-349A-3	Sequence 4, Appli
24	1728	99.7	345	18	US-09-458-690A-4	Sequence 2, Appli
25	1728	99.7	345	18	US-09-471-179-2	Sequence 2, Appli
26	1728	99.7	345	19	US-09-540-703-2	Sequence 2, Appli
27	1728	99.7	345	19	US-09-541-752-2	Sequence 2, Appli
28	1728	99.7	345	19	US-09-599-596-2	Sequence 2, Appli
29	1728	99.7	345	20	US-09-663-783-24	Sequence 24, Appl
30	1728	99.7	345	20	US-09-685-310-24	Sequence 24, Appl
31	1728	99.7	345	20	US-09-688-312-51	Sequence 51, Appl
32	1728	99.7	345	20	US-09-691-200-32	Sequence 32, Appl
33	1728	99.7	345	20	US-09-695-121-2	Sequence 2, Appli
34	1728	99.7	345	21	US-09-723-749-2	Sequence 2, Appli
35	1728	99.7	345	21	US-09-723-749-2	Sequence 2, Appli
36	1728	99.7	345	22	US-09-795-006A-149	Sequence 149, App
37	1728	99.7	345	22	US-09-796-753-6	Sequence 6, Appli
38	1728	99.7	345	23	US-09-818-943-1	Sequence 1, Appli
39	1728	99.7	345	23	US-09-823-033-2	Sequence 2, Appli
40	1728	99.7	345	23	US-09-852-209-3	Sequence 3, Appli
41	1728	99.7	345	23	US-09-852-209A-3	Sequence 3, Appli
42	1728	99.7	345	24	US-09-918-585A-488	Sequence 488, App
43	1728	99.7	345	24	US-09-923-995-4	Sequence 4, Appli
44	1728	99.7	345	24	US-09-929-404-2	Sequence 2, Appli
45	1728	99.7	345	25	US-09-978-187B-488	Sequence 488, App

ALIGNMENTS

RESULT 1  
PCT-US99-22668-5  
; Sequence 5, Application PC/TUS9922668B  
; GENERAL INFORMATION:  
; APPLICANT: LUDWIG INSTITUTE FOR CANCER RESEARCH  
; APPLICANT: HELSINKI UNIVERSITY LICENSING LTD.  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C,  
; FILE OF INVENTION: THEREFOR, AND USES THEREOF  
; TITLE REFERENCE: PCT/US99/22669-LUDWIG INST FOR CANCER  
; CURRENT APPLICATION NUMBER: PCT/US99/22668B  
; CURRENT FILING DATE: 1999-09-30  
; EARLIER APPLICATION NUMBER: 60/102,461  
; EARLIER FILING DATE: 1998-09-30  
; EARLIER APPLICATION NUMBER: 60/108,109  
; EARLIER FILING DATE: 1998-11-12  
; EARLIER APPLICATION NUMBER: 60/110,749  
; EARLIER FILING DATE: 1998-12-03  
; EARLIER APPLICATION NUMBER: 60/113,002  
; EARLIER FILING DATE: 1998-12-18  
; EARLIER APPLICATION NUMBER: 60/135,426  
; EARLIER FILING DATE: 1999-05-21  
; EARLIER APPLICATION NUMBER: 60/144,022  
; EARLIER FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 39

DNA CODING

```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-22668-5

Query Match      100.0%; Score 1734; DB 1; Length 318;
Best Local Similarity 100.0%; Pred. No. 1.9e-165;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWVIQ 60
   |||
Db 1 GKQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWVIQ 60
   |||

QY 61 LTFDERFGLDEPDDICKYDFVEVEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 120
   |||
Db 61 LTFDERFGLDEPDDICKYDFVEVEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 120
   |||

QY 121 EYFPSEPGFCIHNIYVMPQTEAVSPSVLPSPALPLDLLNNAITAFSTLEDLIRYLEPER 180
   |||
Db 121 EYFPSEPGFCIHNIYVMPQTEAVSPSVLPSPALPLDLLNNAITAFSTLEDLIRYLEPER 180
   |||

QY 181 WQDLEDLVPTWQLLGKAFVGRKSRVVDNLNLTTEVRVLYSCTPRNFSVSIREELKRTD 240
   |||
Db 181 WQDLEDLVPTWQLLGKAFVGRKSRVVDNLNLTTEVRVLYSCTPRNFSVSIREELKRTD 240
   |||

QY 241 TIFWPGCLLVKRCGNCACCLHNCNECCQVPSKVTKYKHYEVLQRPKTGVRGLHKSITDV 300
   |||
Db 241 TIFWPGCLLVKRCGNCACCLHNCNECCQVPSKVTKYKHYEVLQRPKTGVRGLHKSITDV 300
   |||

QY 301 ALEHHEECDCVCRGSTGG 318
   |||
Db 301 ALEHHEECDCVCRGSTGG 318
   |||

RESULT 2
US-09-410-349A-5
; Sequence 5, Application US/09410349A
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UTELA, Marko
; APPLICANT: ALITALO, Karl
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: BETSHOLTZ, Christer
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
; CURRENT FILING DATE: 1999-09-30
; PRIOR FILING DATE: 1998-11-12
; PRIOR FILING DATE: 1998-12-03
; PRIOR FILING DATE: 1998-12-18
; PRIOR FILING DATE: 1999-05-21
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-410-349A-5

Query Match      100.0%; Score 1734; DB 18; Length 318;
Best Local Similarity 100.0%; Pred. No. 1.9e-165;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWVIQ 60
   |||
Db 1 GKQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWVIQ 60
   |||

QY 61 LTFDERFGLDEPDDICKYDFVEVEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 120
   |||
Db 61 LTFDERFGLDEPDDICKYDFVEVEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 120
   |||

QY 121 EYFPSEPGFCIHNIYVMPQTEAVSPSVLPSPALPLDLLNNAITAFSTLEDLIRYLEPER 180
   |||
Db 121 EYFPSEPGFCIHNIYVMPQTEAVSPSVLPSPALPLDLLNNAITAFSTLEDLIRYLEPER 180
   |||

QY 181 WQDLEDLVPTWQLLGKAFVGRKSRVVDNLNLTTEVRVLYSCTPRNFSVSIREELKRTD 240
   |||
Db 181 WQDLEDLVPTWQLLGKAFVGRKSRVVDNLNLTTEVRVLYSCTPRNFSVSIREELKRTD 240
   |||

QY 241 TIFWPGCLLVKRCGNCACCLHNCNECCQVPSKVTKYKHYEVLQRPKTGVRGLHKSITDV 300
   |||
Db 241 TIFWPGCLLVKRCGNCACCLHNCNECCQVPSKVTKYKHYEVLQRPKTGVRGLHKSITDV 300
   |||

QY 301 ALEHHEECDCVCRGSTGG 318
   |||
Db 301 ALEHHEECDCVCRGSTGG 318
   |||

RESULT 3
US-09-852-209-5
; Sequence 5, Application US/09852209
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UTELA, Marko
; APPLICANT: ALITALO, Karl
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: BETSHOLTZ, Christer
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
; CURRENT FILING DATE: 2001-05-10
; PRIOR FILING DATE: 1999-09-30
; PRIOR FILING DATE: 1999-09-30
; PRIOR FILING DATE: 1998-12-03
; PRIOR FILING DATE: 1998-12-18
; PRIOR FILING DATE: 1999-05-21
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-209-5

Query Match      100.0%; Score 1734; DB 23; Length 318;
Best Local Similarity 100.0%; Pred. No. 1.9e-165;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWVIQ 60
   |||
Db 1 GKQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWVIQ 60
   |||

QY 61 LTFDERFGLDEPDDICKYDFVEVEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 120
   |||
```

Db 61 LTFDERFGLDEPDDICKYDFVEVEPESDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 120  
QY 121 EYPPSPGFCIHYNIVMPQFTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPER 180  
Db 121 EYPPSPGFCIHYNIVMPQFTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPER 180  
QY 181 WQDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEVRLYSTCTPRNFSVSIREEKRTD 240  
Db 181 WQDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEVRLYSTCTPRNFSVSIREEKRTD 240  
QY 241 TIFWPGCLLVKRCGGNCACCLHNCNECQCVPVKTKYKHYEVLQRLPKTGVRLHKSITDV 300  
Db 241 TIFWPGCLLVKRCGGNCACCLHNCNECQCVPVKTKYKHYEVLQRLPKTGVRLHKSITDV 300  
QY 301 ALEHHEECDCVCRGSGTG 318  
Db 301 ALEHHEECDCVCRGSGTG 318

RESULT 4  
US-09-852-209A-5  
; Sequence 5, Application US/09852209A  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: AASE, Karin  
; APPLICANT: LEE, Xuri  
; APPLICANT: PONTEN, Annica  
; APPLICANT: UUTELA, Marko  
; APPLICANT: ALITALO, Kari  
; APPLICANT: OESTMAN, Arne  
; APPLICANT: HELDIN, Carl-Henrik  
; APPLICANT: BETSHOLTZ, Christer  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING  
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740  
; CURRENT APPLICATION NUMBER: US/09/852,209A  
; CURRENT FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: 09/410,349  
; PRIOR FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: 60/110,749  
; PRIOR FILING DATE: 1998-12-03  
; PRIOR APPLICATION NUMBER: 60/113,002  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 60/135,426  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: 60/144,022  
; PRIOR FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 318  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-852-209A-5

Query Match 100.0%; Score 1734; DB 23; Length 318;  
Best Local Similarity 100.0%; Pred. No. 1.9e-165;  
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GKQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWVIQ 60  
Db 1 GKQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWVIQ 60  
QY 61 LTFDERFGLDEPDDICKYDFVEVEPESDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 120  
Db 61 LTFDERFGLDEPDDICKYDFVEVEPESDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 120  
QY 121 EYPPSPGFCIHYNIVMPQFTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPER 180  
Db 121 EYPPSPGFCIHYNIVMPQFTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPER 180  
QY 181 WQDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEVRLYSTCTPRNFSVSIREEKRTD 240  
Db 181 WQDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEVRLYSTCTPRNFSVSIREEKRTD 240

Db 181 WQDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEVRLYSTCTPRNFSVSIREEKRTD 240  
QY 241 TIFWPGCLLVKRCGGNCACCLHNCNECQCVPVKTKYKHYEVLQRLPKTGVRLHKSITDV 300  
Db 241 TIFWPGCLLVKRCGGNCACCLHNCNECQCVPVKTKYKHYEVLQRLPKTGVRLHKSITDV 300  
QY 301 ALEHHEECDCVCRGSGTG 318  
Db 301 ALEHHEECDCVCRGSGTG 318

RESULT 5  
US-10-131-600-5  
; Sequence 5, Application US/10131600  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: AASE, Karin  
; APPLICANT: LEE, Xuri  
; APPLICANT: PONTEN, Annica  
; APPLICANT: UUTELA, Marko  
; APPLICANT: ALITALO, Kari  
; APPLICANT: OESTMAN, Arne  
; APPLICANT: HELDIN, Carl-Henrik  
; APPLICANT: BETSHOLTZ, Christer  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING  
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740  
; CURRENT APPLICATION NUMBER: US/10/131,600  
; CURRENT FILING DATE: 2002-04-25  
; PRIOR APPLICATION NUMBER: US/09/410,349  
; PRIOR FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: 60/108,109  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: 60/110,749  
; PRIOR FILING DATE: 1998-12-03  
; PRIOR APPLICATION NUMBER: 60/113,002  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 60/135,426  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: 60/144,022  
; PRIOR FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 318  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-131-600-5

Query Match 100.0%; Score 1734; DB 27; Length 318;  
Best Local Similarity 100.0%; Pred. No. 1.9e-165;  
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GKQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWVIQ 60  
Db 1 GKQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENWVIQ 60  
QY 61 LTFDERFGLDEPDDICKYDFVEVEPESDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 120  
Db 61 LTFDERFGLDEPDDICKYDFVEVEPESDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 120  
QY 121 EYPPSPGFCIHYNIVMPQFTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPER 180  
Db 121 EYPPSPGFCIHYNIVMPQFTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPER 180  
QY 181 WQDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEVRLYSTCTPRNFSVSIREEKRTD 240  
Db 181 WQDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEVRLYSTCTPRNFSVSIREEKRTD 240  
QY 241 TIFWPGCLLVKRCGGNCACCLHNCNECQCVPVKTKYKHYEVLQRLPKTGVRLHKSITDV 300  
Db 241 TIFWPGCLLVKRCGGNCACCLHNCNECQCVPVKTKYKHYEVLQRLPKTGVRLHKSITDV 300

```
QY 301 ALEHHECDCVCRGSTGG 318
Db 301 ALEHHECDCVCRGSTGG 318

RESULT 6
US-10-303-997B-5
; Sequence 5, Application US/10303997B
; GENERAL INFORMATION:
; APPLICANT: LI, Xuri
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: CARMELIET, Peter
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR MODULATING VASCULOGENESIS AND ANGIOGEN
; FILE REFERENCE: 029065.44740C3
; CURRENT APPLICATION NUMBER: US/10/303,997B
; PRIOR FILING DATE: 2002-11-26
; PRIOR FILING DATE: 1999-09-30
; PRIOR FILING DATE: 1999-09-30
; PRIOR FILING DATE: 1998-09-30
; PRIOR FILING DATE: 1998-11-12
; PRIOR FILING DATE: 1998-11-12
; PRIOR FILING DATE: 1998-12-03
; PRIOR FILING DATE: 1998-12-03
; PRIOR FILING DATE: 1998-12-18
; PRIOR FILING DATE: 1998-12-18
; PRIOR FILING DATE: 1999-05-21
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-303-997B-5

Query Match 100.0%; Score 1734; DB 29; Length 318;
Best Local Similarity 100.0%; Pred. No. 1.9e-165;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPFTYPRNTVLVWRLVAEENWVIQ 60
Db 1 GKQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPFTYPRNTVLVWRLVAEENWVIQ 60
QY 61 LTFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 120
Db 61 LTFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 120
QY 121 EYFPSEPGFCIHYNVMPQTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPER 180
Db 121 EYFPSEPGFCIHYNVMPQTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPER 180
QY 181 WQDLEDLYRPTWQLGKAFVFGKRSRVLDNLITTEVRVLYSCTPRNFSVSIREEKRTD 240
Db 181 WQDLEDLYRPTWQLGKAFVFGKRSRVLDNLITTEVRVLYSCTPRNFSVSIREEKRTD 240
QY 241 TIFWPGCLLVKRCGNCACCLHNCNECQCVPKVKYKHYEVLQRLPKTGVRLHKSITDV 300
Db 241 TIFWPGCLLVKRCGNCACCLHNCNECQCVPKVKYKHYEVLQRLPKTGVRLHKSITDV 300
QY 301 ALEHHECDCVCRGSTGG 318
Db 301 ALEHHECDCVCRGSTGG 318

RESULT 7
PCT-US99-31025-29
; Sequence 29, Application PC/TUS9931025
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: 7853-173-228
; CURRENT APPLICATION NUMBER: PCT/US99/31025
; CURRENT FILING DATE: 1999-12-23
; EARLIER APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-31025-29

Query Match 99.7%; Score 1728; DB 1; Length 323;
Best Local Similarity 100.0%; Pred. No. 8e-165;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPFTYPRNTVLVWRLVAEENWVIQ 61
Db 7 KQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPFTYPRNTVLVWRLVAEENWVIQ 66
QY 62 TFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 121
Db 67 TFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 126
QY 122 YFPSEPGFCIHYNVMPQTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPER 181
Db 127 YFPSEPGFCIHYNVMPQTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPER 186
QY 182 QDLEDLYRPTWQLGKAFVFGKRSRVLDNLITTEVRVLYSCTPRNFSVSIREEKRTD 241
Db 187 QDLEDLYRPTWQLGKAFVFGKRSRVLDNLITTEVRVLYSCTPRNFSVSIREEKRTD 246
QY 242 IFWPGCLLVKRCGNCACCLHNCNECQCVPKVKYKHYEVLQRLPKTGVRLHKSITDVA 301
Db 247 IFWPGCLLVKRCGNCACCLHNCNECQCVPKVKYKHYEVLQRLPKTGVRLHKSITDVA 306
QY 302 LEHHECDCVCRGSTGG 318
Db 307 LEHHECDCVCRGSTGG 323

RESULT 8
US-09-471-179-29
; Sequence 29, Application US/09471179
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas
; TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 7853-173
; CURRENT APPLICATION NUMBER: US/09/471,179
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-471-179-29

Query Match 99.7%; Score 1728; DB 18; Length 323;
Best Local Similarity 100.0%; Pred. No. 8e-165;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPFTYPRNTVLVWRLVAEENWVIQ 61
Db 7 KQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPFTYPRNTVLVWRLVAEENWVIQ 66
QY 62 TFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 121
```

Db 67 TFDERFGLPEDDICKYDFVEVEEPPSDGTLGRWCGSGVPGKQISKGNQIRIRFVSDE 126  
QY 122 YFPSEPGFCIHYNVMPQFTEAVSPSVLPSPALPDLNNNAITAFSTLEDLIRYLEPERW 181  
Db 127 YFPSEPGFCIHYNVMPQFTEAVSPSVLPSPALPDLNNNAITAFSTLEDLIRYLEPERW 186  
QY 182 QLDLEDLYRPTWLLGKAFVFGKRSRVVDNLNLTTEEVRVLYSCTPRNFSVSIREEELKRTDT 241  
Db 187 QLDLEDLYRPTWLLGKAFVFGKRSRVVDNLNLTTEEVRVLYSCTPRNFSVSIREEELKRTDT 246  
QY 242 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTKKYHEVQLRPKTGVRGLHKSLLTDVA 301  
Db 247 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTKKYHEVQLRPKTGVRGLHKSLLTDVA 306  
QY 302 LEHHECDCVCRGSTGG 318  
Db 307 LEHHECDCVCRGSTGG 323

## RESULT 9

PCT-US01-43523-286  
; Sequence 286, Application PC/TUS0143523  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: Deforge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tamas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C331  
; CURRENT APPLICATION NUMBER: PCT/US01/43523  
; CURRENT FILING DATE: 2002-10-02  
; PRIOR APPLICATION NUMBER: 60/049911  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: 60/056974  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059115  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059117  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059122  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059184  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059352  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/059588  
; PRIOR FILING DATE: 1997-09-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 286  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
PCT-US01-43523-286

Query Match 99.7%; Score 1728; DB 1; Length 345;  
Best Local Similarity 100.0%; Pred. No. 8.e-165;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 KFOFSSNKONGVQDPOHERIITVSTNGSIHSRPFPHYPRNTTVLVRWVAEENVMQL 61  
Db 29 KFOFSSNKONGVQDPOHERIITVSTNGSIHSRPFPHYPRNTTVLVRWVAEENVMQL 88  
QY 62 TFDERFGLPEDDICKYDFVEVEEPPSDGTLGRWCGSGVPGKQISKGNQIRIRFVSDE 121  
Db 89 TFDERFGLPEDDICKYDFVEVEEPPSDGTLGRWCGSGVPGKQISKGNQIRIRFVSDE 148  
QY 122 YFPSEPGFCIHYNVMPQFTEAVSPSVLPSPALPDLNNNAITAFSTLEDLIRYLEPERW 181  
Db 149 YFPSEPGFCIHYNVMPQFTEAVSPSVLPSPALPDLNNNAITAFSTLEDLIRYLEPERW 208  
QY 182 QLDLEDLYRPTWLLGKAFVFGKRSRVVDNLNLTTEEVRVLYSCTPRNFSVSIREEELKRTDT 241  
Db 209 QLDLEDLYRPTWLLGKAFVFGKRSRVVDNLNLTTEEVRVLYSCTPRNFSVSIREEELKRTDT 268  
QY 242 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTKKYHEVQLRPKTGVRGLHKSLLTDVA 301  
Db 269 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTKKYHEVQLRPKTGVRGLHKSLLTDVA 328  
QY 302 LEHHECDCVCRGSTGG 318  
Db 329 LEHHECDCVCRGSTGG 345  
RESULT 10  
PCT-US02-24563-286  
; Sequence 286, Application PC/TUS0224563  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: Deforge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tamas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C331  
; CURRENT APPLICATION NUMBER: PCT/US02/24563  
; CURRENT FILING DATE: 2002-08-02  
; PRIOR APPLICATION NUMBER: 60/049911  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: 60/056974  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059115  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059117  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059122  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059184  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059352

```
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 286
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo Sapien
PCT-US02-24563-286

Query Match
  Query Match          99.7%; Score 1728; DB 1; Length 345;
  Best Local Similarity 100.0%; Pred. No. 8.8e-165;
  Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      149 YFPSEPGFCIHYNIVMPQFTEAVSPSVLPDNLNNAITAFSTLEDLIRYLEPERW 208
Qy      182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEEVRLYSCTPRNFVSISIRELKRDT 241
Db      209 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEEVRLYSCTPRNFVSISIRELKRDT 268
Qy      242 IFWPGCLLVKRCGNCACCLHNCNECQVPSVLPDNLNNAITAFSTLEDLIRYLEPERW 301
Db      269 IFWPGCLLVKRCGNCACCLHNCNECQVPSVLPDNLNNAITAFSTLEDLIRYLEPERW 328
Qy      302 LEHHECDVCRCSTGG 318
Db      329 LEHHECDVCRCSTGG 345

RESULT 12
PCT-US99-01574-2
; Sequence 2, Application PC/TUS9901574A
; GENERAL INFORMATION:
; APPLICANT: Song, Ho Yeong
; APPLICANT: Na, Songqing
; APPLICANT: Dou, Shengnan
; TITLE OF INVENTION: VEGF Related Gene and Protein
; FILE REFERENCE: X-11851
; CURRENT APPLICATION NUMBER: PCT/US99/01574A
; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-01574-2

Query Match          99.7%; Score 1728; DB 1; Length 345;
Best Local Similarity 100.0%; Pred. No. 8.8e-165;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      2 KQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVMQ 61
Qy      29 KQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVMQ 88
Db      62 TDFERFGLPEDDICKYDFVEVEEPPSDGTILGRWCGSGTVPKGQISKGQIRIRFVSDE 121
Qy      89 TDFERFGLPEDDICKYDFVEVEEPPSDGTILGRWCGSGTVPKGQISKGQIRIRFVSDE 148
Db      122 YFPSEPGFCIHYNIVMPQFTEAVSPSVLPDNLNNAITAFSTLEDLIRYLEPERW 181
Qy      149 YFPSEPGFCIHYNIVMPQFTEAVSPSVLPDNLNNAITAFSTLEDLIRYLEPERW 208
Db      182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEEVRLYSCTPRNFVSISIRELKRDT 241
Qy      209 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDNLNLTTEEVRLYSCTPRNFVSISIRELKRDT 268
Db      242 IFWPGCLLVKRCGNCACCLHNCNECQVPSVLPDNLNNAITAFSTLEDLIRYLEPERW 301
Qy      269 IFWPGCLLVKRCGNCACCLHNCNECQVPSVLPDNLNNAITAFSTLEDLIRYLEPERW 328
Db      302 LEHHECDVCRCSTGG 318
Qy      329 LEHHECDVCRCSTGG 345

RESULT 13
PCT-US99-15783-4
; Sequence 4, Application PC/TUS9915783
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Bone Morphogenic Protein
; FILE REFERENCE: PT012.PCT
; CURRENT APPLICATION NUMBER: PCT/US99/15783
; CURRENT FILING DATE: 1999-07-14
; EARLIER APPLICATION NUMBER: 60/092,922
```

```
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-15783-4

Query Match          99.7%; Score 1728; DB 1; Length 345;
Best Local Similarity 100.0%; Pred. No. 8.8e-165;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMQIOL 61
Db 29 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMQIOL 88
QY 62 TFEREGLDEPDDICKYDFVEVEEPSDGTILGRWCSGTVPGKQISKGNQIRIRFVSDE 121
Db 89 TFEREGLDEPDDICKYDFVEVEEPSDGTILGRWCSGTVPGKQISKGNQIRIRFVSDE 148
QY 122 YFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181
Db 149 YFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208
QY 182 QLDLEDLYRPTWQLLGAFAVFGKRSRVVDNLNLTTEEVRLYSCTPRNFSVSIREELKRTDT 241
Db 209 QLDLEDLYRPTWQLLGAFAVFGKRSRVVDNLNLTTEEVRLYSCTPRNFSVSIREELKRTDT 268
QY 242 IFWPGCLLVKRCGNCACCLHNCNECOCVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDVA 301
Db 269 IFWPGCLLVKRCGNCACCLHNCNECOCVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDVA 328
QY 302 LEHHEECDVCVRGSGTG 318
Db 329 LEHHEECDVCVRGSGTG 345

RESULT 15
PCT-US99-31025-2
; Sequence 2, Application PC/TUS9931025
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS
; TITLE OF INVENTION: ENCODING THEM
; FILE REFERENCE: 7853-173-228
; CURRENT APPLICATION NUMBER: PCT/US99/31025
; EARLIER FILING DATE: 1999-12-23
; EARLIER APPLICATION NUMBER: 09/223,546
; EARLIER FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-31025-2

Query Match          99.7%; Score 1728; DB 1; Length 345;
Best Local Similarity 100.0%; Pred. No. 8.8e-165;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMQIOL 61
Db 29 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMQIOL 88
QY 62 TFEREGLDEPDDICKYDFVEVEEPSDGTILGRWCSGTVPGKQISKGNQIRIRFVSDE 121
Db 89 TFEREGLDEPDDICKYDFVEVEEPSDGTILGRWCSGTVPGKQISKGNQIRIRFVSDE 148
QY 122 YFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181
Db 149 YFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208
QY 182 QLDLEDLYRPTWQLLGAFAVFGKRSRVVDNLNLTTEEVRLYSCTPRNFSVSIREELKRTDT 241
Db 209 QLDLEDLYRPTWQLLGAFAVFGKRSRVVDNLNLTTEEVRLYSCTPRNFSVSIREELKRTDT 268
QY 242 IFWPGCLLVKRCGNCACCLHNCNECOCVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDVA 301
Db 269 IFWPGCLLVKRCGNCACCLHNCNECOCVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDVA 328
QY 302 LEHHEECDVCVRGSGTG 318
Db 329 LEHHEECDVCVRGSGTG 345

Query Match          99.7%; Score 1728; DB 1; Length 345;
Best Local Similarity 100.0%; Pred. No. 8.8e-165;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMQIOL 61
Db 29 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMQIOL 88
QY 62 TFEREGLDEPDDICKYDFVEVEEPSDGTILGRWCSGTVPGKQISKGNQIRIRFVSDE 121
Db 89 TFEREGLDEPDDICKYDFVEVEEPSDGTILGRWCSGTVPGKQISKGNQIRIRFVSDE 148
QY 122 YFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181
Db 149 YFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208
QY 182 QLDLEDLYRPTWQLLGAFAVFGKRSRVVDNLNLTTEEVRLYSCTPRNFSVSIREELKRTDT 241
Db 209 QLDLEDLYRPTWQLLGAFAVFGKRSRVVDNLNLTTEEVRLYSCTPRNFSVSIREELKRTDT 268
QY 242 IFWPGCLLVKRCGNCACCLHNCNECOCVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDVA 301
Db 269 IFWPGCLLVKRCGNCACCLHNCNECOCVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDVA 328
QY 302 LEHHEECDVCVRGSGTG 318
Db 329 LEHHEECDVCVRGSGTG 345

PCT-US99-22668-3
; Sequence 3, Application PC/TUS9922668B
; GENERAL INFORMATION:
; APPLICANT: LUDWIG INSTITUTE FOR CANCER RESEARCH
; APPLICANT: HELSINKI UNIVERSITY LICENSING LTD.
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF
; FILE REFERENCE: PCT/US99/22669-IUDWIG INST FOR CANCER
; CURRENT APPLICATION NUMBER: PCT/US99/22668B
; EARLIER FILING DATE: 1998-09-30
; EARLIER APPLICATION NUMBER: 60/102,461
; EARLIER FILING DATE: 1998-09-30
; EARLIER APPLICATION NUMBER: 60/108,109
; EARLIER FILING DATE: 1998-11-12
; EARLIER FILING DATE: 1998-11-12
; EARLIER FILING DATE: 1998-11-12
; EARLIER FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 60/113,002
; EARLIER FILING DATE: 1998-12-18
; EARLIER APPLICATION NUMBER: 60/135,426
; EARLIER FILING DATE: 1999-05-21
; EARLIER APPLICATION NUMBER: 60/144,022
; EARLIER FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-22668-3

Query Match          99.7%; Score 1728; DB 1; Length 345;
Best Local Similarity 100.0%; Pred. No. 8.8e-165;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Search completed: November 25, 2003, 21:14:49  
Job time : 157.494 secs

---



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 21:02:59 ; Search time 12.619 Seconds  
(without alignments)  
1293.384 Million cell updates/sec

Title: US-09-852-209A-5

Perfect score: 1734

Sequence: 1 GKQFSSNKQNGVQDPQHE.....DVALEHHECDVCVRGSGTG 318

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 271250 seqs, 51324744 residues

Total number of hits satisfying chosen parameters: 271250

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New:  
1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep.\*  
7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1728	99.7	345	1	PCT-US03-26491-191
2	1728	99.7	345	5	US-09-457-066-2
3	1728	99.7	345	5	US-09-876-813-33
4	1728	99.7	345	6	US-10-648-593-191
5	1728	99.7	345	6	US-10-471-221-1
6	1728	99.7	345	7	US-60-487-610-1644
7	1728	99.7	345	7	US-60-485-450-1042
8	1720	99.2	345	5	US-09-830-320A-4
9	1559	89.9	345	5	US-09-457-066-43
10	1559	89.9	345	5	US-09-876-813-35
11	1325	76.4	302	5	US-09-876-813-54
12	1320.5	76.2	282	6	US-10-471-221-5
13	1266.5	73.0	303	5	US-09-876-813-57
14	1107	63.8	305	1	PCT-US00-28803-7
15	1098	63.3	316	5	US-09-876-813-55
16	1051.5	60.6	317	5	US-09-876-813-56
17	741	42.7	370	5	US-09-457-066-37
18	741	42.7	370	5	US-09-876-813-2
19	741	42.7	370	6	US-10-321-962-4
20	741	42.7	370	6	US-10-606-055-2
21	736	42.4	370	5	US-09-876-813-53
22	736	42.4	370	6	US-10-321-962-8
23	736	42.4	370	6	US-10-606-055-4
24	684	39.4	167	6	US-10-471-221-6
25	604	34.8	111	6	US-10-471-221-2
26	431	24.9	261	6	US-10-321-962-10

27	328.5	18.9	132	6	US-10-321-962-6	Sequence 6, Appli
28	320.5	18.5	154	6	US-10-321-962-12	Sequence 12, Appli
29	187	10.8	726	7	US-60-495-114-2251	Sequence 2251, Ap
30	181.5	10.5	730	5	US-09-830-320A-12	Sequence 12, Appli
31	181.5	10.5	730	7	US-60-495-114-2257	Sequence 2257, Ap
32	181.5	10.5	730	7	US-60-495-114-2260	Sequence 2260, Ap
33	181.5	10.5	730	7	US-60-495-114-2268	Sequence 2268, Ap
34	174	10.0	110	6	US-10-321-962-14	Sequence 14, Appli
35	173	10.0	823	7	US-60-495-114-2259	Sequence 2259, Ap
36	173	10.0	823	7	US-60-495-114-2266	Sequence 2266, Ap
37	173	10.0	823	7	US-60-495-114-2267	Sequence 2267, Ap
38	171	9.9	1015	7	US-60-495-114-1841	Sequence 1841, Ap
39	169	9.7	466	7	US-60-495-114-2262	Sequence 2262, Ap
40	169	9.7	717	7	US-60-495-114-2252	Sequence 2252, Ap
41	169	9.7	717	7	US-60-495-114-2253	Sequence 2253, Ap
42	169	9.7	717	7	US-60-495-114-2263	Sequence 2263, Ap
43	169	9.7	986	6	US-10-474-794-242	Sequence 242, App
44	169	9.7	986	7	US-60-495-114-2254	Sequence 2254, Ap
45	169	9.7	986	7	US-60-495-114-2264	Sequence 2264, Ap

ALIGNMENTS

RESULT 1  
PCT-US03-26491-191  
; Sequence 191, Application PC/TUS0326491  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS TH  
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR  
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS  
; FILE REFERENCE: D0273 PCT  
; CURRENT APPLICATION NUMBER: PCT/US03/26491  
; CURRENT FILING DATE: 2003-08-26  
; PRIOR APPLICATION NUMBER: 60/406,385  
; PRIOR FILING DATE: 2002-08-27  
; NUMBER OF SEQ ID NOS: 557  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 191  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US03-26491-191

Query Match		99.7%	Score 1728;	DB 1;	Length 345;
Best Local Similarity		100.0%	Pred. No. 2.8e-139;	Mismatches 0;	Gaps 0;
Matches 317;		Conservative 0;	Indels 0;		
Qy	2	KQFSSNKQNGVQDPQHE	IIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVTQL	61	
Db	29	KQFSSNKQNGVQDPQHE	IIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVTQL	88	
Qy	62	TFDRFGLPEDDICKYDFVEE	PSDGTILGWCSGTVPGKQISKGNQIRFVSDE	121	
Db	89	TFDRFGLPEDDICKYDFVEE	PSDGTILGWCSGTVPGKQISKGNQIRFVSDE	148	
Qy	122	YFSEPFCHYNTVMPQFTEA	VSPLPPSALPLDLNNAITAFSTLEDLIRYLEPRW	181	
Db	149	YFSEPFCHYNTVMPQFTEA	VSPLPPSALPLDLNNAITAFSTLEDLIRYLEPRW	208	
Qy	182	QLDLEDYRPTWLLGKAFV	FGKRSRVVDLNLITVEEVLVYSCTPRNFVSIREELKRTDT	241	
Db	209	QLDLEDYRPTWLLGKAFV	FGKRSRVVDLNLITVEEVLVYSCTPRNFVSIREELKRTDT	268	
Qy	242	IFWPGCLLVKRCGNCACCL	HCNCCVSKTKKHEVLOLRPKTVRGHLKSLTDA	301	
Db	269	IFWPGCLLVKRCGNCACCL	HCNCCVSKTKKHEVLOLRPKTVRGHLKSLTDA	328	
Qy	302	LEHHECDVCVRGSGTG	318		
Db	329	LEHHECDVCVRGSGTG	345		

```
RESULT 2
US-09-457-066-2
; Sequence 2, Application US/09457066
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-457-066-2

Query Match          99.7%; Score 1728; DB 5; Length 345;
Best Local Similarity 100.0%; Pred. No. 2.8e-139;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 KQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPFTYPRNTVLVWRLVAEENVMIQL 61
Db  29 KQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPFTYPRNTVLVWRLVAEENVMIQL 88
Qy  62 TFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCSGTVPKGQISKGNQIRIRFVSDE 121
Db  89 TFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCSGTVPKGQISKGNQIRIRFVSDE 148
Qy  122 YFPSEPGFCHYNIWMPQFTEAVSPVLPSPALPLDLLNNAITAFSTLEDLIRYLEPERW 181
Db  149 YFPSEPGFCHYNIWMPQFTEAVSPVLPSPALPLDLLNNAITAFSTLEDLIRYLEPERW 208
Qy  182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLITVEVRLYSCTPRNFVSISREELKRTDT 241
Db  209 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLITVEVRLYSCTPRNFVSISREELKRTDT 268
Qy  242 IFWPGCLLVKRCGNCACCLHNCNECCVPSKVTCKYHEVLQLRPKTGVRGLHKS LTDVA 301
Db  269 IFWPGCLLVKRCGNCACCLHNCNECCVPSKVTCKYHEVLQLRPKTGVRGLHKS LTDVA 328
Qy  302 LEHHECDCVCRGSTGG 318
Db  329 LEHHECDCVCRGSTGG 345

RESULT 3
US-09-876-813-33
; Sequence 33, Application US/09876813
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/876,813
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US/09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57

Query Match          99.7%; Score 1728; DB 6; Length 345;
Best Local Similarity 100.0%; Pred. No. 2.8e-139;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 KQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPFTYPRNTVLVWRLVAEENVMIQL 61
Db  29 KQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPFTYPRNTVLVWRLVAEENVMIQL 88
Qy  62 TFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCSGTVPKGQISKGNQIRIRFVSDE 121
Db  89 TFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCSGTVPKGQISKGNQIRIRFVSDE 148
Qy  122 YFPSEPGFCHYNIWMPQFTEAVSPVLPSPALPLDLLNNAITAFSTLEDLIRYLEPERW 181
Db  149 YFPSEPGFCHYNIWMPQFTEAVSPVLPSPALPLDLLNNAITAFSTLEDLIRYLEPERW 208
Qy  182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLITVEVRLYSCTPRNFVSISREELKRTDT 241
Db  209 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLITVEVRLYSCTPRNFVSISREELKRTDT 268
Qy  242 IFWPGCLLVKRCGNCACCLHNCNECCVPSKVTCKYHEVLQLRPKTGVRGLHKS LTDVA 301
Db  269 IFWPGCLLVKRCGNCACCLHNCNECCVPSKVTCKYHEVLQLRPKTGVRGLHKS LTDVA 328
Qy  302 LEHHECDCVCRGSTGG 318
Db  329 LEHHECDCVCRGSTGG 345

RESULT 4
US-10-648-593-191
; Sequence 191, Application US/10648593
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS TH
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
; FILE REFERENCE: D0273 NP
; CURRENT APPLICATION NUMBER: US/10/648,593
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 60/406,385
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 557
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 191
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-593-191

Query Match          99.7%; Score 1728; DB 6; Length 345;
Best Local Similarity 100.0%; Pred. No. 2.8e-139;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 KQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPFTYPRNTVLVWRLVAEENVMIQL 61
Db  29 KQFSSNKEQGVQDPQHERIITVSTNGSIHSPRPFTYPRNTVLVWRLVAEENVMIQL 88
Qy  62 TFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCSGTVPKGQISKGNQIRIRFVSDE 121
Db  89 TFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCSGTVPKGQISKGNQIRIRFVSDE 148
Qy  122 YFPSEPGFCHYNIWMPQFTEAVSPVLPSPALPLDLLNNAITAFSTLEDLIRYLEPERW 181
Db  149 YFPSEPGFCHYNIWMPQFTEAVSPVLPSPALPLDLLNNAITAFSTLEDLIRYLEPERW 208
Qy  182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLITVEVRLYSCTPRNFVSISREELKRTDT 241
Db  209 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLITVEVRLYSCTPRNFVSISREELKRTDT 268
Qy  242 IFWPGCLLVKRCGNCACCLHNCNECCVPSKVTCKYHEVLQLRPKTGVRGLHKS LTDVA 301
Db  269 IFWPGCLLVKRCGNCACCLHNCNECCVPSKVTCKYHEVLQLRPKTGVRGLHKS LTDVA 328
Qy  302 LEHHECDCVCRGSTGG 318
Db  329 LEHHECDCVCRGSTGG 345
```

QY 182 QLDLEDLYRPTWQLLGFVGRKSRVVDLNLITVEVRLYSCVTPRNFVSIRBELKRTDT 241  
DB 209 QLDLEDLYRPTWQLLGFVGRKSRVVDLNLITVEVRLYSCVTPRNFVSIRBELKRTDT 268  
QY 242 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTYKHYEVLQRLPKTGVRGLHKS LTDVA 301  
DB 269 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTYKHYEVLQRLPKTGVRGLHKS LTDVA 328  
QY 302 LEHHECDVCVCRGSGTG 318  
DB 329 LEHHECDVCVCRGSGTG 345  
RESULT 5  
US-10-471-221-1  
; Sequence 1, Application US/10471221  
; GENERAL INFORMATION:  
; APPLICANT: Janssen Pharmaceutica N.V.  
; TITLE OF INVENTION: Modulation Of Smooth Muscle Cell Proliferation  
; FILE REFERENCE: JAB 1687  
; CURRENT APPLICATION NUMBER: US/10/471,221  
; CURRENT FILING DATE: 2003-09-05  
; PRIOR APPLICATION NUMBER: US 60/274901  
; PRIOR FILING DATE: 2001-03-09  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 1  
; TYPE: PRT  
; LENGTH: 345  
; ORGANISM: Homo sapiens  
US-10-471-221-1

Query Match 99.7%; Score 1728; DB 6; Length 345;  
Best Local Similarity 100.0%; Pred. No. 2.8e-139;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVWIQL 61  
DB 29 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVWIQL 88  
QY 62 TDFERFGLDEPDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNIIRFVSDE 121  
DB 89 TDFERFGLDEPDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNIIRFVSDE 148  
QY 122 YFPSEPGFCIHYNVMPQFTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181  
DB 149 YFPSEPGFCIHYNVMPQFTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208  
QY 182 QLDLEDLYRPTWQLLGFVGRKSRVVDLNLITVEVRLYSCVTPRNFVSIRBELKRTDT 241  
DB 209 QLDLEDLYRPTWQLLGFVGRKSRVVDLNLITVEVRLYSCVTPRNFVSIRBELKRTDT 268  
QY 242 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTYKHYEVLQRLPKTGVRGLHKS LTDVA 301  
DB 269 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTYKHYEVLQRLPKTGVRGLHKS LTDVA 328  
QY 302 LEHHECDVCVCRGSGTG 318  
DB 329 LEHHECDVCVCRGSGTG 345

RESULT 6  
US-60-487-610-1644  
; Sequence 1644, Application US/60487610  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; APPLICANT: HUANG, Honglin  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,  
; TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001469  
; CURRENT APPLICATION NUMBER: US/60/487,610  
; CURRENT FILING DATE: 2003-07-17

; NUMBER OF SEQ ID NOS: 97101  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1644  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-60-487-610-1644

Query Match 99.7%; Score 1728; DB 7; Length 345;  
Best Local Similarity 100.0%; Pred. No. 2.8e-139;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVWIQL 61  
DB 29 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVWIQL 88  
QY 62 TDFERFGLDEPDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNIIRFVSDE 121  
DB 89 TDFERFGLDEPDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNIIRFVSDE 148  
QY 122 YFPSEPGFCIHYNVMPQFTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181  
DB 149 YFPSEPGFCIHYNVMPQFTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208  
QY 182 QLDLEDLYRPTWQLLGFVGRKSRVVDLNLITVEVRLYSCVTPRNFVSIRBELKRTDT 241  
DB 209 QLDLEDLYRPTWQLLGFVGRKSRVVDLNLITVEVRLYSCVTPRNFVSIRBELKRTDT 268  
QY 242 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTYKHYEVLQRLPKTGVRGLHKS LTDVA 301  
DB 269 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTYKHYEVLQRLPKTGVRGLHKS LTDVA 328  
QY 302 LEHHECDVCVCRGSGTG 318  
DB 329 LEHHECDVCVCRGSGTG 345

RESULT 7  
US-60-485-450-1042  
; Sequence 1042, Application US/60485450  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; APPLICANT: CHANG, Sheng-Yung  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C  
; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001470  
; CURRENT APPLICATION NUMBER: US/60/485,450  
; CURRENT FILING DATE: 2003-07-09  
; NUMBER OF SEQ ID NOS: 47859  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1042  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-60-485-450-1042

Query Match 99.7%; Score 1728; DB 7; Length 345;  
Best Local Similarity 100.0%; Pred. No. 2.8e-139;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVWIQL 61  
DB 29 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVWIQL 88  
QY 62 TDFERFGLDEPDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNIIRFVSDE 121  
DB 89 TDFERFGLDEPDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNIIRFVSDE 148  
QY 122 YFPSEPGFCIHYNVMPQFTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181  
DB 149 YFPSEPGFCIHYNVMPQFTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208

Qy 182 QLDLEDLYRPTWQLLKGAFVFGKRSRVVDLNLTEEVRLYSCTPRNFVSISREELKRTDT 241  
Db 209 QLDLEDLYRPTWQLLKGAFVFGKRSRVVDLNLTEEVRLYSCTPRNFVSISREELKRTDT 268  
Qy 242 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDVA 301  
Db 269 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDVA 328  
Qy 302 LEHHECDCVCRGSTGG 318  
Db 329 LEHHECDCVCRGSTGG 345  
RESULT 8  
US-09-830-320A-4  
; Sequence 4, Application US/09830320A  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: TANG, Y. Tom  
; APPLICANT: YUE, Henry  
; APPLICANT: HILLMAN, Jennifer L.  
; APPLICANT: CORLEY, Neil C.  
; APPLICANT: GUEGLER, Karl J.  
; APPLICANT: BAUGHER, Mariah R.  
; APPLICANT: AU-YOUNG, Janice K.  
; TITLE OF INVENTION: GROWTH FACTOR RELATED MOLECULES  
; FILE REFERENCE: PF-0627 USN  
; CURRENT APPLICATION NUMBER: US/09/830,320A  
; CURRENT FILING DATE: 2003-04-29  
; PRIOR FILING DATE: 1999-10-28  
; PRIOR APPLICATION NUMBER: PCT/US99/25458  
; PRIOR FILING DATE: 1998-10-28  
; PRIOR APPLICATION NUMBER: US 60/183,024  
; PRIOR FILING DATE: 1998-10-28  
; PRIOR APPLICATION NUMBER: US 60/155,216  
; PRIOR FILING DATE: 1998-12-11  
; PRIOR APPLICATION NUMBER: US 60/172,233  
; PRIOR FILING DATE: 1999-05-17  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PERL Program  
; SEQ ID NO 4  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No.: 4163378CD1  
US-09-830-320A-4

Query Match 99.2%; Score 1720; DB 5; Length 345;  
Best Local Similarity 99.7%; Pred. No. 1.3e-138;  
Matches 316; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 2 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVMQL 61  
Db 29 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVMQL 88  
Qy 62 TFDERFGLDPEDDICKYDFVEVEEPSDGTILGRWCSGTVPKGQISKGNQIRIRFVSDE 121  
Db 89 TFDERFGLDPEDDICKYDFVEVEEPSDGTILGRWCSGTVPKGQISKGNQIRIRFVSDE 148  
Qy 122 YFPSEPGFCHYNTVMQFTAVSPVLPSPALPDLNNAITAFSTLEDLIRYLEPERW 181  
Db 149 YFPSEPGFCHYNTVMQFTAVSPVLPSPALPDLNNAITAFSTLEDLIRYLEPERW 208  
Qy 182 QLDLEDLYRPTWQLLKGAFVFGKRSRVVDLNLTEEVRLYSCTPRNFVSISREELKRTDT 241  
Db 209 QLDLEDLYRPTWQLLKGAFVFGKRSRVVDLNLTEEVRLYSCTPRNFVSISREELKRTDT 268  
Qy 242 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDVA 301  
Db 269 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDVA 328

Qy 302 LEHHECDCVCRGSTGG 318  
Db 329 LEHHECDCVCRGSTGG 345  
RESULT 9  
US-09-457-066-43  
; Sequence 43, Application US/09457066  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60  
; CURRENT APPLICATION NUMBER: US/09/457,066  
; CURRENT FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 43  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-457-066-43  
Query Match 89.9%; Score 1559; DB 5; Length 345;  
Best Local Similarity 87.1%; Pred. No. 6.7e-125;  
Matches 276; Conservative 26; Mismatches 15; Indels 0; Gaps 0;  
Qy 2 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVMQL 61  
Db 29 KQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVMQL 88  
Qy 62 TFDERFGLDPEDDICKYDFVEVEEPSDGTILGRWCSGTVPKGQISKGNQIRIRFVSDE 121  
Db 89 TFDERFGLDPEDDICKYDFVEVEEPSDGTILGRWCSGTVPKGQISKGNQIRIRFVSDE 148  
Qy 122 YFPSEPGFCHYNTVMQFTAVSPVLPSPALPDLNNAITAFSTLEDLIRYLEPERW 181  
Db 149 YFPSEPGFCHYNTVMQFTAVSPVLPSPALPDLNNAITAFSTLEDLIRYLEPERW 208  
Qy 182 QLDLEDLYRPTWQLLKGAFVFGKRSRVVDLNLTEEVRLYSCTPRNFVSISREELKRTDT 241  
Db 209 QLDLEDLYRPTWQLLKGAFVFGKRSRVVDLNLTEEVRLYSCTPRNFVSISREELKRTDT 268  
Qy 242 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDVA 301  
Db 269 IFWPGCLLVKRCGNCACCLHNCNECQVPSKVTKKYHEVLQLRPKTGVRGLHKS LTDVA 328  
Qy 302 LEHHECDCVCRGSTGG 318  
Db 329 LEHHECDCVCRGNAGG 345  
RESULT 10  
US-09-876-813-35  
; Sequence 35, Application US/09876813  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4  
; FILE REFERENCE: 99-19  
; CURRENT APPLICATION NUMBER: US/09/876,813  
; CURRENT FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: US/09/564,595  
; PRIOR FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: US 09/304,216  
; PRIOR FILING DATE: 1999-05-03  
; PRIOR APPLICATION NUMBER: US 60/164,463

```

; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-876-813-35

Query Match      89.9%; Score 1559; DB 5; Length 345;
Best Local Similarity 87.1%; Pred. No. 6.7e-125;
Matches 276; Conservative 26; Mismatches 15; Indels 0; Gaps 0;

QY 2 KFOFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMWL 61
DB 29 KLQSSDKQNGVQDPQHERVITVSTNGSIHSPKPHYPRNMVLVWRLVAVDENRVL 88
QY 62 TPDREGLDEPDDICKYDFVEVEBPDSGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE 121
DB 89 TPDREGLDEPDDICKYDFVEVEBPDSGTILGRWCGSGTVPGKQISKGNHIRIRFVSDE 148
QY 122 YPSEPGFCIHYNIMVQPTAVSPVLPSPALPLDLNNAITAFSTLEDLIRVLEPERW 181
DB 149 YPSEPGFCIHYSILNPQVETTSVLPSPSLDLDLNNATVATSTLEELIRVLEPERW 208
QY 182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLITBEVRLYSTPRNFSVSIRELKRDT 241
DB 209 QVLDLSLYRPTWQLLGKAFYLGKSKVNLNLLKEVKLYSCTPRNFSVSIRELKRDT 268
QY 242 IFWPGCLLVKRCGNCACCLHNCQCVPSKVTKYKHVQLRPTGVGRGLHSLTDVA 301
DB 269 IFWPGCLLVKRCGNCACCLHNCQCVPRKVTYKHVQLRPTGVGRGLHSLTDVA 328
QY 302 LEHHEECDCVCRGSGTG 318
DB 329 LEHHEECDCVCRGNAGG 345

RESULT 11
US-09-876-813-54
; Sequence 54; Application US/09876813
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG 2VZGPF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/876,813
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US/09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-876-813-54

Query Match      76.4%; Score 1325; DB 5; Length 302;
Best Local Similarity 82.8%; Pred. No. 4.5e-105;
Matches 246; Conservative 14; Mismatches 33; Indels 4; Gaps 2;

QY 19 HERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMWLQTFDEPFGLEDDEDDICK 78
DB 1 HERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMWLQTFDEPFGLEDDEDDICK 60
QY 79 YDFVEVEBPDSGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSPGFCIHYNIMV 138
DB 61 YDFVEVEBPDSGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSPGFCIHYNIMV 120
QY 139 QFTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRVLEPERWQDLEDLYRPTWQLLGK 198
DB 121 QFTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRVLEPERWQDLEDLYRPTWQLLGK 180
QY 199 AFVFGKRSRVVDLNLITBEVRLYSTPRNFSVSIRELKRDTTFWPGCLLVKRCGNC 258
DB 181 AFVFGKRSRVVDLNLITBEVRLYSTPRNFSVSIRELKRDTTFWPGCLLVKRCGNC 239
QY 259 CCLHNCNECQCVPSKVTKYKHVQLRPTGVGRGLHSLTDVALSHHEECDCVC 312
DB 240 CGTVNWRSTCTNSGKTVKYKHVQLRPTGVGRGLHSLTDVALSHHEECDCVC 296

RESULT 12
US-10-471-221-5
; Sequence 5; Application US/10471221
; GENERAL INFORMATION:
; APPLICANT: Janssen Pharmaceutica N.V.
; TITLE OF INVENTION: Modulation Of Smooth Muscle Cell Proliferation
; FILE REFERENCE: JAB 1687
; CURRENT APPLICATION NUMBER: US/10/471,221
; CURRENT FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: US 60/274901
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-471-221-5

Query Match      76.2%; Score 1320.5; DB 6; Length 282;
Best Local Similarity 80.1%; Pred. No. 9.9e-105;
Matches 254; Conservative 0; Mismatches 0; Indels 63; Gaps 1;

QY 2 KFOFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMWL 61
DB 29 KFOFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMWL 88
QY 62 TPDREGLDEPDDICKYDFVEVEBPDSGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE 121
DB 89 TPDREGLDEPDDICKYDFVEVEBPDSGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE 148
QY 122 YPSEPGFCIHYNIMVQPTAVSPVLPSPALPLDLNNAITAFSTLEDLIRVLEPERW 181
DB 149 YPSEPGFCIHYNIMVQPTAVSPVLPSPALPLDLNNAITAFSTLEDLIRVLEPERW 208
QY 182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLITBEVRLYSTPRNFSVSIRELKRDT 241
DB 209 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLITBEVRLYSTPRNFSVSIRELKRDT 243
QY 242 IFWPGCLLVKRCGNCACCLHNCQCVPSKVTKYKHVQLRPTGVGRGLHSLTDVA 301
DB 244 -----EVLQRPKTVGRGLHSLTDVA 265
QY 302 LEHHEECDCVCRGSGTG 318
DB 266 LEHHEECDCVCRGSGTG 282

RESULT 13
US-09-876-813-57
; Sequence 57; Application US/09876813
; GENERAL INFORMATION:

```

```
/ APPLICANT: Gilbert, Teresa
/ APPLICANT: Hart, Charles E.
/ APPLICANT: Shepard, Paul O.
/ TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
/ FILE REFERENCE: 99-19
/ CURRENT APPLICATION NUMBER: US/09/876,813
/ PRIOR FILING DATE: 2001-06-06
/ PRIOR FILING DATE: 2000-05-03
/ PRIOR FILING DATE: 1999-05-03
/ PRIOR FILING DATE: 1999-11-10
/ PRIOR FILING DATE: 2000-02-04
/ NUMBER OF SEQ ID NOS: 57
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 57
/ LENGTH: 303
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: fusion polypeptide
US-09-876-813-57

Query Match 73.0%; Score 1266.5; DB 5; Length 303;
Best Local Similarity 78.9%; Pred. No. 4.3e-100;
Matches 240; Conservative 24; Mismatches 33; Indels 7; Gaps 4;

QY 20 ERITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMQLTFDERFGLEDPEDDICKY 79
DB 2 DETIQVKGNGVQSPFPNSYPRNLLTWRLHS-QENTRIQLVFDNQFGLSEAEINDICRY 60
QY 80 DFEVEEPPSDGT--ILGRWCGSGTVPGKQISKGNQIRIRFVSDYEPSPGFCIHYNIVM 137
DB 61 DFEVEEDISTSIIRGWCCHKEVPPRIKSRNQIKITKSDDYFVAKGPKIYSL-L 119
QY 138 PQTEA---VSPVLPSPALPLDLNNAITAFSTLEDLIRLYLSPERWQLEDLYRPTWQ 194
DB 120 EDQPAASVSPVLPSPALPLDLNNAITAFSTLEDLIRLYLSPERWQLEDLYRPTWQ 179
QY 195 LLGKAFVGRKSRVDNLITTEVRLYSCPTPRNFSVIRELKRDTTFWPGCLLVKRCG 254
DB 180 LLGKAFVGRKSRVDNLITTEVRLYSCPTPRNFSVIRELKRDTTFWPGCLLVKRCG 239
QY 255 GNCACCLHNCNCCQVPSKTKYKHEVLQLRPKTGVRLHSLTDVALEHHEECDCVCRG 314
DB 240 GNCACCLHNCNCCQVPSKTKYKHEVLQLRPKTGVRLHSLTDVALEHHEECDCVCRG 299
QY 315 STGG 318
DB 300 STGG 303

RESULT 14
PCT-US00-28803-7
/ Sequence 7, Application PC/TUS0028803
/ GENERAL INFORMATION:
/ APPLICANT: Turner, C. Alexander Jr.
/ APPLICANT: Donoho, Gregory
/ APPLICANT: Nehls, Michael
/ APPLICANT: Hilbun, Erin
/ APPLICANT: Zambrowicz, Brian
/ APPLICANT: Sands, Arthur T.
/ TITLE OF INVENTION: Novel Human Proteins and Polynucleotides
/ FILE REFERENCE: LEX-0070-PCT
/ CURRENT APPLICATION NUMBER: PCT/US00/28803
/ CURRENT FILING DATE: 2000-12-18
/ PRIOR FILING DATE: 1999-10-16
/ PRIOR FILING DATE: 1999-10-18
/ PRIOR FILING DATE: 1999-10-29

/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 7
/ LENGTH: 305
/ TYPE: PRT
/ ORGANISM: Homo sapiens
PCT-US00-28803-7

Query Match 63.8%; Score 1107; DB 1; Length 305;
Best Local Similarity 100.0%; Pred. No. 1.6e-86;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KFOFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMQL 61
DB 29 KFOFSSNKEQNGVQDPQHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMQL 88
QY 62 TFDERRFGLEDPEDDICKYDFVEVEEESDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE 121
DB 89 TFDERRFGLEDPEDDICKYDFVEVEEESDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE 148
QY 122 YFPSEPGFCIHYNIVMPQFTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRLYLEPERW 181
DB 149 YFPSEPGFCIHYNIVMPQFTEAVSPVLPSPALPLDLNNAITAFSTLEDLIRLYLEPERW 208
QY 182 QLDLEDLYRPTWQLLGAFFVGRKSR 207
DB 209 QLDLEDLYRPTWQLLGAFFVGRKSR 234

RESULT 15
US-09-876-813-55
/ Sequence 55, Application US/09876813
/ GENERAL INFORMATION:
/ APPLICANT: Gilbert, Teresa
/ APPLICANT: Hart, Charles E.
/ APPLICANT: Shepard, Paul O.
/ TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
/ FILE REFERENCE: 99-19
/ CURRENT APPLICATION NUMBER: US/09/876,813
/ CURRENT FILING DATE: 2001-06-06
/ PRIOR FILING DATE: 2000-05-03
/ PRIOR FILING DATE: 1999-05-03
/ PRIOR FILING DATE: 1999-11-10
/ PRIOR FILING DATE: 2000-02-04
/ NUMBER OF SEQ ID NOS: 57
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 55
/ LENGTH: 316
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: fusion polypeptide
US-09-876-813-55

Query Match 63.3%; Score 1098; DB 5; Length 316;
Best Local Similarity 67.1%; Pred. No. 9.7e-86;
Matches 210; Conservative 26; Mismatches 55; Indels 22; Gaps 5;

QY 19 HERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMQLTFDERFGLEDPEDDICK 78
DB 1 HERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMQLTFDERFGLEDPEDDICK 60
QY 79 YDFVEVEEESDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDYFPPSEPGFCIHYNIVMP 138
DB 61 YDFVEVEEESDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDYFPPSEPGFCIHYNIVMP 120
QY 139 QFTEAV-----SPSVLPSPALPLDLNNAITAFSTLEDLIRLYLEPERW 182
DB 121 QFTEAVTWNESVTSISGVSYNSPVTDPDT-LIADALDKKIABFDTVEDLLKFNPSWQ 179
```

QY	183	LDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLTEEVRLYSCTPRNFSVSIREBLKRTDTI	242
Db	180	EDLENNVLDTPRYGRSY-HDRKSK-VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVV	237
QY	243	FWPGCLLVKRCGNCACCLHNCNECQVPSKVTKYHEVLQLRP---KTGVRGLHKS LTD	299
Db	238	FFPRCLLVQRCCGNCGCGTVNWRSCNCGTKVTKYHEVLQFEFGHIKRRGRKTMALVD	297
QY	300	VALEHHEECDCVC	312
Db	298	IQLDHERCDCIC	310

Search completed: November 25, 2003, 21:15:40  
Job time : 13.619 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: November 25, 2003, 20:59:34 ; Search time 13.5655 Seconds  
(without alignments)  
2254.373 Million cell updates/sec

Title: US-09-852-209A-5

Perfect score: 1734

Sequence: 1 GRKFSSNKEQNGVQDPQHE.....DVALEHHECDVCVRGSG 318

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	742	42.8	370	2 JC7591	spinal cord-derive
2	736	42.4	370	2 JC7592	spinal cord-derive
3	181.5	10.5	730	1 BMH1	procollagen C-endo
4	179.5	10.4	927	1 JQ0948	A5 antigen precurs
5	176	10.1	707	2 JC2218	procollagen C-endo
6	173.5	10.0	3623	2 T09456	intrinsic factor-B
7	173	10.0	823	1 A58788	procollagen C-endo
8	169	9.7	986	1 B58788	procollagen C-endo
9	169	9.7	991	2 I49540	procollagen C-endo
10	168	9.7	3623	2 T08618	intrinsic factor-B
11	154	8.9	449	2 A55362	procollagen I C-pr
12	148.5	8.6	1057	1 A39288	dorsal-ventral pat
13	143.5	8.3	686	1 A59271	Ra-reactive factor
14	139.5	8.0	1070	2 T31069	tollid-BMP-1 like
15	138.5	8.0	597	2 T31352	metalloproteinase
16	138	8.0	705	1 C1HURB	complement subcomp
17	137.5	7.9	699	1 I54763	Ra-reactive factor
18	137.5	7.9	1524	2 T30337	polyprotein - Afri
19	133	7.7	1594	2 T30549	hensin - rabbit
20	132	7.6	419	2 S69207	vascular endotheli
21	130.5	7.5	1464	2 S58984	development protei
22	128	7.4	402	2 JH0403	procollagen I C-pr
23	127.5	7.4	767	2 T30018	hypothetical prote
24	127.5	7.4	3871	2 T22812	hypothetical prote
25	125	7.2	198	2 J50735	platelet-derived g
26	123.5	7.1	277	2 A41735	hyaluronate-bindin
27	120.5	6.9	245	1 TVC758	platelet-derived g
28	120.5	6.9	275	2 JVC6506	tumor necrosis fac
29	118.5	6.8	276	2 A47290	TSG-6 homolog p84

30 116.5 6.7 579 2 JC7629 membrane-type friz  
31 114.5 6.6 148 2 D49530 16K vascular endot  
32 114.5 6.6 241 1 PFHUG2 platelet-derived g  
33 112.5 6.5 200 2 IS1551 platelet-derived g  
34 112.5 6.5 215 2 S08220 platelet-derived g  
35 112.5 6.5 226 2 IS1550 platelet-derived g  
36 111.5 6.4 319 2 IS1569 UVS.2 protein - Af  
37 110.5 6.4 2403 2 A59386 sanko - human  
38 110 6.3 166 2 JN0248 platelet-derived g  
39 109 6.3 197 2 S25096 platelet-derived g  
40 108.5 6.3 226 1 TVMVSS PDGF-related trans  
41 108 6.2 196 2 A37359 platelet-derived g  
42 104.5 6.0 232 2 A41551 vascular endotheli  
43 104 6.0 196 2 B28964 platelet-derived g  
44 104 6.0 211 1 PFHUG1 platelet-derived g  
45 103 5.9 770 2 D89447 protein F57C12.1 [

## ALIGNMENTS

## RESULT 1

JC7591  
spinal cord-derived growth factor-B precursor - human  
C;Species: Homo sapiens (man)  
C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 24-Aug-2001  
C;Accession: JC7591  
R;Hamada, T.; Ui-Tei, K.; Imaki, J.; Miyata, Y.  
Biochem. Biophys. Res. Commun. 280, 733-737, 2001  
A;Title: Molecular cloning of SCDGF-B, a novel growth factor homologous to SCDGF/PDGF-  
A;Reference number: JC7591; MUID:2102670; PMID:11162582  
A;Accession: JC7591  
A;Molecule type: DNA  
A;Residues: 1-370 <HAM>  
A;Cross-references: DDBJ:AB033832  
C;Genetics:  
A;Gene: scdgf-B  
F;1-17/Domain: secretory signal sequence #status predicted <SIG>  
F;18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>  
F;52-170/Region: CUB domain #status predicted  
F;272-370/Region: homologous to platelet-derived growth factor/vascular endothelial gr  
F;294-308/Region: conserved motif #status predicted

Query Match 42.8%; Score 742; DB 2; Length 370;

Best Local Similarity 46.6%; Pred. No. 1.2e-56;

Matches 153; Conservative 52; Mismatches 93; Indels 30; Gaps 9;

QY 10 EQNGVQD-PQHERIITVSTNGSIHSRPHPTVPRNTVLVWELVAEENWVQLTDFRFG 68

Db 42 ESNHLDLYRDETQVKGNGYQSPFPNSYPRNLLLTWRLHS-QENTRIQLVFDNQFG 100

QY 69 LEDPEDDICKYDFVEVEEPSDGT--ILGRWCGSGTVFGKQISKGNQIRIRFVSDEYFPSE 126

Db 101 LEEAENDICRYDFVEVEDISSTIIRGRWCGHKEVPPIKSRNTQIKITFKSDDYFAK 160

QY 127 PGCIHYNVMPQTEAV-----SPSVLPSPALPLDLINNAITAFS 167

Db 161 PGFIYYSL-LEDFQPAASSETNWESVTSISGVSNPSVTDPT-LIADALDKKIAEFD 218

QY 168 TLEDLIRYLPERWOLDLXRPWTWLLGKAFVGRKSRVVDNLNLTTEEVRVLSCTPRN 227

Db 219 TVEDLLKYPESWQEDLENNYLDTPYRGSY-HSRKSK-VDLDRLNDDAKRYSCPTPN 276

QY 228 FSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNEQCVSKYTKKTHEVLQRP- 286

Db 277 YSVNIREELKLANVVFPRCLLVQRCGNCGCGVNWRSCTCSGKTKVKYHEVLQPEFG 336

QY 287 --KTGVRLHKLTDVALEHHECDVCV 312

Db 337 HIKRGRGAKTMALVDIQLDHERCDIC 364

## RESULT 2



A: Cross-references: DDBJ:AB052170  
C: Geneticks:  
A: Gene: scdggf-B  
F: 1-17/Domain: secretory signal sequence #status predicted <SR>  
F: 18-370/Product: spinal cord-derived growth factor-B #status predicted <MR>  
F: 52-170/Region: CUB domain #status predicted  
F: 272-370/Region: homologous to platelet-derived growth factor/vascular endothelial growth factor #status predicted  
E: 294-308/Region: conserved motif #status predicted

	Query Match	10.5%;	Score 181.5;	DB 1;	Length 730;
	Best Local Similarity	37.3%;	Pred. No. 1.3e-07;		
	Matches 50;	Conservative	20;	Mismatches 47;	Indels 17; Gaps 7;
Qy	28	NGSTHSFRFHPTYPRNTVLVWRLVA-VEENWVIQLTDERFGLDEDPEDDICKYDFVEVEE	86		
Db	599	NGSTSTSGWPKVEYPPNNKINQLVAPQYRISLQDFPFETEG	653		
Qy	87	--PDGFTILRCWCSGTVPGKQISKGKQAIRFRVSDVEYFSPGPGCIHYNIMPOFTTAV	144		
Db	654	GLTADSKLHGFCGS-EKPEVITQYNNMRVEFKSDNTV-SKKGFKAHF-----FSEK-	704		
Qy	145	SPSVLPPSALPLDL	158		
Db	705	REALQPPRGREPHQL	718		

RESULT 4

QJ00948

A5 antigen precursor - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Jun-2000

C:Accession: JH0466; JQ0948

R:Takagi, S.; Hirata, T.; Agata, K.; Mochii, M.; Eguchi, G.; Fujisawa, H.

Neuron 7, 295-307, 1991

A>Title: The A5 antigen, a candidate for the neuronal recognition molecule, has homology

A:Reference number: JH0466; PMID:91337458; PMID:1908252

A:Accession: JH0466

A:Molecule type: mRNA

A:Residues: 1-927 <TAX>

A:Cross-references: GB:D10467; GB:D01077; NID:g222962; PIDN:BAA01360.1; PID:g222963

A:Experimental source: tadpole, brain

A>Note: This protein has motifs homologous to complement components C1r and C1s and to

C:Comment: This protein is a neuronal cell surface molecule involved in the neuronal r

C:Superfamily: Xenopus A5 antigen; C1r/C1s repeat homology; discoidin I amino-terminal

C:Keywords: duplication; glycoprotein; transmembrane protein

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-927/Product: A5 antigen #status predicted <A5A>

F:27-138/Domain: C1r/C1s repeat homology <C1R1>

F:147-262/Domain: C1r/C1s repeat homology <C1R2>

F:274-424/Domain: discoidin I amino-terminal homology <DN1>

F:430-584/Domain: discoidin I amino-terminal homology <DN2>

F:646-812/Domain: MAM homology <MAM>

F:861-883/Domain: transmembrane #status predicted <TMW>

F:150-263, 300-523 844/Binding site: carboxhydrate (Asn) (covalent) #status predicted

	Query Match	10.4%	Score 179.5	DB 1	Length 927	
	Best Local Similarity	31.6%	Pred. No. 2.7e-07			
	Matches	55	Conservative	29	Mismatches 73	Indels 17
					Gaps	7
Qy	23	ITVSTNGSIHSRPFHTYPRNTVLVWRLVAVENVWLIQTEDERFGLGEDPEDDICKYDEV	82			
Db	31	IKITSPYSYTSAGYSHSPSPSORCEMLIQAPHYQRIIMNFNPHFLEDR---	CKIDYV	87		
Qy	83	EV--EPPSDGTLIGWCGSGTVPGQISKGNQIRIRFVSDYPPSPGFCIHYNVMP--	138			
Db	88	EVIDGNANGQLLKGYCGK-IAPSLVSTGPGSIFIRFVSDYETPG-AGSIRYEVFKTP	145			
Qy	139	-----QFTEA--VSPSVLPSPALPLDILNNNAITAFSTLEDLIRLYLEPERWQLDL	186			

Best Local Similarity 26.4%; Pred. No. 4.8e-06;  
Matches 92; Consensus 39; Mismatches 135; Indels 83; Gaps 22;

QY 3 FQPSKNEQNG-----VDQPOHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAVEEN 56  
DB 910 FVKSSSTENHGFMAKFSADLACGEILTEST-GTIQSPGHVNVYPHGINCTWHIL-VQPN 967  
QY 57 VTIQLFDERFGLDEDDICKYDFVEVEPSDGTILGRWCGSGTVPKGQISKGNQIR 116  
DB 968 HLHLHMF-ETFHLEFHN--CTNDYLEVDYDTSLSLGRYCGK-SIPPSLTSSNSMLV 1023  
QY 117 FVSDYFPPSPGFCIHNV-----MPOFEAVSPSVLPSPALPLDLNNAITAFSTLE 170  
DB 1024 FVTDSDLAYE-GFLINTEALISAACLODYDLDLGTFTSP-----NFPNN----- 1067  
QY 171 DLIRYLEPERWOLDLEDLYR---PTWOLLGKAFVGRKSRVVDLNLLE--EVR----- 219  
DB 1068 -----YPNW---ECIYRITVTRTGLIAVHFTNFSLEAIG-NYVTDLEIRDGGYEK 1116  
QY 220 -----LY--SCTPRNFSVIRELK-RTDTI-----FWPCLAVKRCGGNACCLH 262  
DB 1117 SPLIGIFYGNLPPTIISHNKLWLFKSDQIDTRSGFSAYWDGS--STGGGN-----LT 1170  
QY 263 NCNEQCQVPSKVTKYHE--VLQLRPTKTVRGLHLSLTDLVALEHHBEC 308  
DB 1171 TSGTFTSPNPMYDHSSECYNWLKSHG-SAFELEKDFLHEHPNC 1218

RESULT 7  
A58788  
procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form HIS - human  
N:Alternate names: Bone morphogenic protein splice form BMP-1/His  
C:Species: Homo sapiens (man)  
C:Date: 28-Mar-1998 #sequence\_revision 09-Apr-1998 #text\_change 18-Jun-1999  
C:Accession: A37278; A58788  
E:Wozeny, J.M.; Rosen, V.; Celeste, A.J.; Micsosk, L.M.; Whitters, M.J.; Kriz, R.W.; H:  
Science 242, 1528-1534, 1988  
A:Title: Novel regulators of bone formation: molecular clones and activities.  
A:Reference number: A37278; PMID:89072730; PMID:3201241  
A:Accession: A37278  
A:Molecule type: mRNA  
A:Residues: 1-702, 'EKRPALOPRGRPHQLKFRVQKNRTPQ' <WOZ>  
A:Cross-references: GB:M22488; NID:g179499; PIDN:AAA51833.1; PID:g179500  
R:Takahara, K.; Lyons, G.E.; Greenspan, D.S.  
J. Biol. Chem. 269, 32572-32578, 1994  
A:Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld) are enc:  
A:Reference number: A58788; PMID:95096114; PMID:7798260  
A:Accession: A58788  
A:Molecule type: mRNA  
A:Residues: 703-823 <YAK>  
A:Cross-references: GB:L35278; NID:g619423; PIDN:AAC41703.1; PID:g619424  
C:Genetics:  
A:Gene: GDB:BMPL; BMP-1  
A:Cross-references: GDB:125203; OMIM:112264  
A:Map position: 8p21-8p21  
C:Function:  
A:Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen tyf  
C:Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology;  
C:Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; s  
F:1-823/domain: signal sequence #status predicted <SIG>  
F:2-823/Product: procollagen C-endopeptidase splice form HIS #status predicted <MAT>  
F:130-321/Domain: astacin homology <AST>  
F:322-431/Domain: C1r/C1s repeat homology <CIR1>  
F:435-544/Domain: C1r/C1s repeat homology <CIR2>  
F:551-587/Domain: EGF homology <EGF>  
F:591-700/Domain: C1r/C1s repeat homology <CIR3>  
F:738-752/Region: histidine-rich  
F:91-142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-  
F:213, 217, 223, 272/Binding site: zinc (His, His, His, Tyr) #status predicted  
F:214/Active site: Glu #status predicted  
F:565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

[illegible]

Db 924 KFSDDKLECG-----EVLTAET-GIEBSPGHNVYPRGVNCTHWV-VORGQLIRLF 974  
QY 64 DERFGLDEDDICKYDFVEVEPSDGTILGWCSGTVPQKQISKGNOIRIRFVSDYF 123  
Db 975 SG-FYLEFHYN--CTNDYLEIYDTAQTFLGRYCGK-SIPPSLTNSNSIKLIFVSDSAL 1030  
QY 124 PSEPGFCIHV-----NIVMPOFTEAVSPSLP--PSALPLDL-----LNNAI--- 163  
Db 1031 AHE-GFSINVEALDASSVCLDYDTDFNGMLSPFNPNYPSNWEICIRYITVGLNQIALH 1089  
QY 164 -TAFSTLED-----LIRYLEPERWQDLDDLRPTWQLLGKAPVFGKRSKRVLDNLITTE 217  
Db 1090 FTDF-TLEDYFGSQCDVFE-----IRGGYETSPLVG---IY--CGSVLPPTIISHS 1136  
QY 218 VRLY-----SCTPNFVSIREELKRTDTTFMPGCLLVKRCGNCACCLHNCQCQV 270  
Db 1137 NKLWLKFKSAAUTAGFSA-----YWDGS--STGCGN-----LTPTGVLTS 1178  
QY 271 PSKVTYKHYE--VLOLRPKTGVGRGLHKSILTDVALEHHEEC 308  
Db 1179 PNYPMYVYHSSECYWELEASHG-SPFELEFQDPHLEHPSC 1218  
RESULT 11  
A53362  
procollagen I C-proteinase enhancer protein precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 05-Nov-1999  
C:Accession: A53362  
R:Takahara, K.; Kessler, E.; Biniaminov, L.; Brusel, M.; Eddy, R.L.; Jani-Sait, S.; Show  
J. Biol. Chem. 269, 26280-26285, 1994  
A:Title: Type I procollagen COOH-terminal proteinase enhancer protein: identification, E  
A:Reference number: A53362; MUID:95014462; PMID:7523404  
A:Accession: A53362  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-449 <TAK>  
A:Cross-references: GB:I33799; NID:g642907; PIDN:AAA61949.1; PID:g642908  
C:Genetics:  
A:Gene: GDB:PCOLCE  
A:Cross-references: GDB:305468; OMIM:600270  
A:Map position: 7q21.3-7q22  
C:Superfamily: C1r/C1s repeat homology  
C:Keywords: extracellular protein; glycoprotein; pyroglutamic acid  
F:1-25/Domain: signal sequence #status predicted <SIG>  
F:26-449/Product: #status predicted <MAT>  
F:37-146/Domain: C1r/C1s repeat homology <C1R1>  
F:159-270/Domain: C1r/C1s repeat homology <C1R2>  
F:26/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted  
F:29,431/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 8.9%; Score 154; DB 2; Length 449;  
Best Local Similarity 33.8%; Pred. No. 1.9e-05;  
Matches 48; Conservative 22; Mismatches 50; Indels 22; Gaps 10;  
QY 29 GSTHSRPFPHY-YPRTNVLVRLVAEENWVQLTDFRFGLEDPEDDICKYDFVEY--- 84  
Db 168 GTLTTPNWPSSDYPGIGCSWHIAPPDQV-IALT-F-EKFDLE--PDYCKRYSVSFNG 223  
QY 85 EEFSDGTILGWCSGTVPQKQISKGNOIRIRFVSDYFSEPGFCIHVIVMPQFT--- 141  
Db 224 AVSDDSRRLGKFCGD-AVPGISGSEGNELLVQFVSDLSVTAD-GFSASYK-TLPRGTAK 280  
QY 142 -----EAVSPSV-LPPSALP 155  
Db 281 GQGPGRKRGTEPKYKLPKSP 302  
RESULT 12  
A39288  
dorsal-ventral patterning protein tolloid (EC 3.4.24.-) - fruit fly (Drosophila melanoga  
C:Species: Drosophila melanogaster  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: A39288  
R:Shimell, M.J.; Ferguson, E.L.; Childs, S.R.; O'Connor, M.B.  
Cell 67, 469-481, 1991  
A:Title: The Drosophila dorsal-ventral patterning gene tolloid is related to human bone  
A:Reference number: A39288; MUID:92034970; PMID:1940509  
A:Accession: A39288  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1057 <SHI>  
A:Cross-references: GB:M76976; NID:gi57305; PIDN:AAA28491.1; PID:gi57306  
C:Genetics:  
A:Gene: FlyBase:tld  
A:Cross-references: FlyBase:FBgn0003719  
C:Superfamily: dorsal-ventral patterning protein tolloid; astacin homology; C1r/C1s rei  
C:Keywords: duplication; hydrolase; metalloproteinase; zinc  
F:136-329/Domain: astacin homology <AST>  
F:352-464/Domain: C1r/C1s repeat homology <C1R1>  
F:468-578/Domain: C1r/C1s repeat homology <C1R2>  
F:585-620/Domain: EGF homology <EG1>  
F:624-740/Domain: C1r/C1s repeat homology <C1R3>  
F:747-782/Domain: EGF homology <EG2>  
F:787-896/Domain: C1r/C1s repeat homology <C1R4>  
F:900-1013/Domain: C1r/C1s repeat homology <C1R5>  
F:221,225,231,280/Binding site: zinc (His, His, Tyr) #status predicted  
F:222/Active site: Glu #status predicted  
Query Match 8.6%; Score 148.5; DB 1; Length 1057;  
Best Local Similarity 38.0%; Pred. No. 0.00015;  
Matches 38; Conservative 20; Mismatches 35; Indels 7; Gaps 5;  
QY 23 ITVSTNGSIHSRPFPHYYPRTNVLVRLVAEENWVQLTDFRFGLEDPEDDICKYDFV 82  
Db 472 LKLTQKQSDSPNYPMYDMPDKCVWRITA-PDNHQVALKE--QSFELE--KHDGCAYDFV 527  
QY 83 EVEE--PSDGTILGWCSGTVPQKQISKGNOIRIRFVSD 120  
Db 528 EIRKGNHSDSRLIGRCGDKLPNIK-TRSNQWIRFVSD 566  
RESULT 13  
A59271  
Ra-reactive factor (EC 3.4.21.-) 2 precursor - human  
N:Alternate names: mannose binding protein-associated serine proteinase 2 (MASP-2)  
C:Species: Homo sapiens (man)  
C:Date: 19-May-2000 #sequence\_revision 19-May-2000 #text\_change 16-Jun-2000  
C:Accession: A59271  
R:Thiel, S.; Vorup-Jensen, T.; Stover, C.M.; Schwaeble, W.J.; Laursen, S.B.; Poulsen, I  
Nature 386, 506-510, 1997  
A:Title: A second serine protease associated with mannan-binding lectin that activates  
A:Reference number: A59271; MUID:97242412; PMID:9087411  
A:Accession: A59271  
A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-686 <JEN>  
A:Cross-references: GB:T09926; NID:g4007626; PIDN:CAA71059.1; PID:g4007627  
A:Experimental source: tissue liver  
A:Note: submitted to GenBank, December 1996  
A:Note: parts of this sequence, including the amino end of the mature protein, were det  
C:Genetics:  
A:Gene: GDB:MASP2  
A:Cross-references: GDB:6071500  
A:Map position: 1p36.2-1p36.3  
C:Superfamily: complement subcomponent C1r; C1r/C1s repeat homology; complement factor  
C:Keywords: beta-hydroxyasparagine; complement pathway; duplication; hydrolase; serine  
F:1-15/Domain: signal sequence #status predicted <SIG>  
F:16-444, 445-686/Product: Ra-reactive factor 2 #status predicted <MAT>  
F:19-134/Domain: C1r/C1s repeat homology <C1R1>  
F:142-180/Domain: EGF homology <EGF>  
F:184-293/Domain: C1r/C1s repeat homology <C1R2>  
F:300-361/Domain: complement factor H repeat homology <FHL>  
F:366-430/Domain: complement factor H repeat homology <FH2>  
F:445-679/Domain: trypsin homology <TRY>  
F:72-90, 142-156, 152-165, 167-180, 184-211, 241-259, 300-348, 328-361, 366-412, 396-430, 434-557

F:158/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted  
F:444-445/Cleavage site: Arg-Ile (autolytic) #status predicted  
F:483,532,633/Active site: His, Asp, Ser #status predicted

Query Match 8.3%; Score 143.5; DB 1; Length 686;  
Best Local Similarity 32.1%; Pred. No. 0.00025;  
Matches 34; Conservative 25; Mismatches 42; Indels 5; Gaps 4;

QY 28 NGSIIHSPRPHYPYPRNTVLVRLVAVENWVQLTFDERFGLDEPDDICKYDFVEVEEP 87  
DB 193 SGEISPEYPRYPKSSCTYS-ISLEGFVSILDFVSGFDVTHPETICFYDFLKIQ-- 249  
QY 88 SDGTLGRWCGSGTVPGKIQSKGNQIRIRFVSDEYFSPGFCIH 133  
DB 250 TDRHGGPCGK-TLPHRIETKSNVTIIFVDE-SGDHTGWKIHY 293

RESULT 14  
T31069  
tolloid-BMP-1 like protein 1 - California sea hare  
N/Alternate names: Probable metalloproteinase TBL-1  
C/Species: Aplysia californica (California sea hare)  
C/Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 18-Aug-2000  
R/Accession: T31069  
R/Liu, Q.R.; Hattar, S.; Endo, S.; MacPhee, K.; Zhang, H.; Byrne, J.H.; et al.  
J. Neurosci. 17, 755-764, 1997  
A/Title: A developmental gene (Tolloid/BMP-1) is regulated in Aplysia Neurons by treatment with retinoic acid  
A/Reference number: Z2965; MUID:98007484; PMID:8987797  
A/Accession: T31069  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-1070 <LIU>  
A/Cross-references: EMBL:U57369; NID:G1899041; PID:G1899042; PIDN:AAC47485.1  
C:Superfamily: dorsal-ventral patterning protein tolloid; astacin homology; C1r/C1s repeats

Query Match 8.0%; Score 139.5; DB 2; Length 1070;  
Best Local Similarity 21.9%; Pred. No. 0.00095;  
Matches 70; Conservative 36; Mismatches 102; Indels 111; Gaps 17;

QY 29 GSHTSPRFPHYPNTVLVRLVAVENWVQL--TFDERFGLDEPDDICKYDFVEVE 85  
DB 529 GFLNSPAYDEYSGDKVCEW-VITVREGYVAFEFATFET--DPD---CAIDYVEIR 581  
QY 86 --RPSDGTILGRWCGSGTVPGKIQSKGNQIRIRFVSDEYFSPGFCIH-- 133  
DB 582 DGTGKDSPLVGTTCGRT-PPNALSTRHLVYKVSDESM-QKGFSASYLEVDECEGE 639  
QY 134 -----NIVMPQFTEAVSPSV 148  
DB 640 DHGCEHVCVNTLGSYECTKIGYELHSDGKKCKACGGYLDAPSGTISPSF-----PDL 694  
QY 149 LPSALPLDLLNNAITAFS-----TLEDLRYLEPERWQLDLEDLYRPTWQLLGKAFVFG 203  
DB 695 YFPD-----KNCVWHISAPKGHILTIVNTHMDLE-WRGECEL-----DFRVTVNVG 741  
QY 204 RKSRRVDLNLTEBRLYSTCPNFSVS--IRBELKRTDTIFWPGCLL-----VKRCGGN 256  
DB 742 NKER-----LQGYCGFMAPPSTISLSNELRIEFSDDTLQKTGFSMDYADVDECASS 795  
QY 257 CACCLHNCN-----BCQC 269  
DB 796 NGGCKHCICENTVGSFHCSC 814

RESULT 15  
S71352  
metalloproteinase (EC 3.4.24.-) 10 precursor, blastula - sea urchin (Paracentrotus lividus)  
N/Alternate names: Gene tolloid protein homolog  
C/Species: Paracentrotus lividus (common urchin)  
C/Date: 12-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 17-Mar-1999  
R/Accession: S71352; A44880; S22060  
R/Thomond, G.; Ghiglione, C.; Lepage, T.; Gache, C.  
Eur. J. Biochem. 238, 744-751, 1996

A/Title: Structure of the gene encoding the sea urchin blastula protease 10 (BP10), a metalloproteinase  
A/Reference number: S71352; MUID:96300240; PMID:8706676  
A/Accession: S71352  
A/Molecule type: DNA  
A/Residues: 1-597 <LHO>  
A/Cross-references: EMBL:X65721; NID:e956534; PID:e46942  
A/Experimental source: sperm  
A/Note: the authors translated the codon GCT for residue 11 as Val, AAC for residue 57: R:lepage, T.; Ghiglione, C.; Gache, C.  
Development 114, 147-163, 1992  
A/Title: Spatial and temporal expression pattern during sea urchin embryogenesis of a tolloid patterning gene  
A/Reference number: A44880; MUID:92249197; PMID:1339338  
A/Accession: A44880  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-7, 'S', '9-10, 'V', '12-28, 'H', '30-72, 'D', '74-77, 'SK', '80-81, 'I', '83-232, 'R', '234-2: 9-571, 'N', '573-584, 'D', '586-595, 'D', '597 <LEP>  
A/Cross-references: EMBL:X56224; NID:G10928; PID:G10929  
A/Experimental source: embryo  
A/Note: sequence extracted from NCBI backbone (NCBIP:99979)  
C/Genetics:

A/Gene: BP10  
A/Introns: 30/3; 116/1; 184/3; 252/3; 370/3; 555/2  
C:Superfamily: C1r/C1s repeat homology; astacin homology  
C/Keywords: hydrolase; metalloproteinase; zinc  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-597/Product: metalloproteinase 10, blastula #status predicted <MAT>  
F:102-295/Domain: astacin homology <AST>  
F:339-446/Domain: C1r/C1s repeat homology <CLRI>  
F:484-592/Domain: C1r/C1s repeat homology <CLRI2>  
F:190,194,200/Binding site: zinc (His) #status predicted  
F:191/Active site: Glu #status predicted

Query Match 8.0%; Score 138.5; DB 2; Length 597;  
Best Local Similarity 24.4%; Pred. No. 0.00056;  
Matches 59; Conservative 44; Mismatches 92; Indels 47; Gaps 13;

QY 29 GSHTSPRFPHYPNTVLVRLVAVENWVQLTFDERFGLDEPDDICKYDFVEVEEP- 87  
DB 348 GVITSNPGRYDDNNACVYQEGPGST-IELTFTE---MNIENHACRYDAVEIRKDD 403  
QY 88 --SDGTILGRWCGSGTVPGKIQSKGNQIRIRFVSDEYFSPGFCIHYNIVMPQFTEAVS 145  
DB 404 INSDGE--KFCGN-TLPAVQISSGNQMLVSTSDPSITGR-GFRATYRIVILTTQLPD 458  
QY 146 PSVLPPSALPLDLLNNAIT-----AFSTLEDLI---RYLEPERWQLDLEDLYRPT 192  
DB 459 TTIT-STTTPVPTTQATTDETIVVSGCGRFGTQGRVATPNY--PNYNDNLECVVIE 515  
QY 193 WOLLGKAFVFGKRSRVVDLNLTEBRLYSTCPNFSVSIRBELKRTDTIFWPGCLLVKR 252  
DB 516 VEV-----GRVELDFDFVLEDET--NCRWDSLSINLGDIK-----IDMKM 556  
QY 253 CG 254  
DB 557 CG 558

Search completed: November 25, 2003, 21:05:29  
Job time : 13.5655 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	179.5	10.4	928	1	NRP1_XENLA	P28824 xenopus lae
2	176	10.1	707	1	BMF1_XENLA	P98070 xenopus lae
3	173.5	10.0	616	1	SPAN_STRPU	P98068 strongyloce
4	169	9.7	986	1	BMF1_HUMAN	P13497 homo sapien
5	169	9.7	991	1	BMF1_MOUSE	P98063 mus musculus
6	163.5	9.4	922	1	NRP1_RAT	Q9Gwj9 rattus norv
7	163.5	9.4	931	1	NRP2_HUMAN	O60462 homo sapien
8	163	9.4	925	1	NRP2_RAT	O35276 rattus norv
9	162.5	9.4	326	1	VEGD_RAT	O35251 rattus norv
10	160.5	9.3	923	1	NRP1_MOUSE	P97333 mus musculus
11	159.5	9.2	931	1	NRP2_MOUSE	O53375 mus musculus
12	159	9.2	1022	1	TLD_BRARE	O57460 brachydanio
13	158.5	9.1	923	1	NRP1_HUMAN	O14786 homo sapien
14	157	9.1	914	1	NRP1_CHICK	P73795 gallus gall
15	154	8.9	449	1	PCO1_HUMAN	Q15113 homo sapien
16	148.5	8.6	1057	1	TLD_DROME	P25723 drosophila
17	147	8.5	354	1	VEGD_HUMAN	O43915 homo sapien
18	143.5	8.3	686	1	MAGE_HUMAN	O00187 homo sapien
19	140	8.1	358	1	VEGD_MOUSE	P97946 mus musculus
20	139.5	8.0	597	1	BP10_PARLI	P42674 paracentrot
21	138.5	8.0	704	1	CRAR_MOUSE	P98064 mus musculus
22	138	8.0	639	1	BMFH_STRPU	P98069 strongyloce
23	138	8.0	705	1	CLR_HUMAN	P00736 homo sapien
24	137.5	7.9	699	1	CRAR_HUMAN	P48740 h complemen
25	132	7.6	419	1	VEGC_HUMAN	P49767 homo sapien
26	128	7.4	468	1	PCO1_MOUSE	Q61398 mus musculus
27	128	7.4	468	1	PCO1_RAT	O08628 rattus norv
28	125	7.2	213	1	PDGA_RABIT	P34007 oryctolagus
29	125	7.2	415	1	VEGC_MOUSE	P97953 mus musculus
30	123.5	7.1	277	1	TSGG_HUMAN	P98066 homo sapien
31	120.5	6.9	245	1	PDGB_FELCA	P12919 felis silve
32	120.5	6.9	275	1	TSGE_MOUSE	O08859 mus musculus
33	118.5	6.8	276	1	TSGG_RABIT	P98065 oryctolagus

```

DR PROSITE; PS01285; FA58C_1; 2.
DR PROSITE; PS01286; FA58C_2; 2.
DR PROSITE; PS50022; FA58C_3; 2.
DR PROSITE; PS00740; MAM_1; 1.
DR PROSITE; PS50060; MAM_2; 1.
KW Angiogenesis; Transmembrane; Glycoprotein; Neurone; Signal; Repeat;
KW Receptor; Antigen.
FT SIGNAL 1 21
FT CHAIN 22 928
FT DOMAIN 22 860
FT TRANSMEM 861 883
FT DOMAIN 884 928
FT DOMAIN 27 141
FT DOMAIN 147 265
FT DOMAIN 275 424
FT DOMAIN 431 584
FT DOMAIN 646 812
FT DOMAIN 27 54
FT DISULFID 82 104
FT DISULFID 147 173
FT DISULFID 206 228
FT DISULFID 275 424
FT DISULFID 431 584
FT CARBOHYD 150 161
FT CARBOHYD 261 261
FT CARBOHYD 300 300
FT CARBOHYD 523 523
FT CARBOHYD 844 844
SQ SEQUENCE 928 AA; 103416 MW; AF6B32380A4C789D CRC64;

Query Match 10.4%; Score 179.5; DB 1; Length 928;
Best Local Similarity 31.6%; Pred. No. 1.5e-07;
Matches 55; Conservative 29; Mismatches 73; Indels 17; Gaps 7;

Qy 23 ITVSTNGSIHSPRPHTYPRNTLVRLVAEENVMQLTDFRPLGLEDDEDDICKYDFV 82
Db 31 IKITSPSLTSGYSPSPSCWELIQAPEHYQRIINFNPHDPDLEDRE---CKYDYV 87
Qy 83 EV--EPPSDGTLGRWCGSGTVPQKISQKQIRIRFVSDVEYFPGFCIHYNIVMP-- 138
Db 88 EVIDGNANGQLGKYCK--IAPSLVSTGSPISFIRFVSDYETPG--AGSTRYEVFKTP 145
Qy 139 ---QFTRA---VSPSLVPPSALPLDNLNNAITAFSTLEDLIRYLPFRWQDLE 186
Db 146 ECSRNTSSNGVKSPPKYPKYPNALECTYIIFAPKMQEIV--LRFESFELEAD 197

RESULT 2
ID -BMP1_XENLA STANDARD; PRT; 707 AA.
AC P98070.
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bone morphogenetic protein 1 precursor (BC 3.4.24.-) (BMP-1).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=94085787; PubMed=8262384;
RA Maeno M., Xue Y., Wood T.I., Ong R.C., Kung H.F.;
RT "Cloning and expression of cDNA encoding Xenopus laevis bone
RL morphogenetic protein-1 during early embryonic development.";
RL Gene 134:257-261(1993).
CC -!- FUNCTION: INVOLVED IN PATTERN FORMATION IN GASTRULA AND LATER
CC DIFFERENTIATION OF DEVELOPING ORGANS.
CC -!- DEVELOPMENTAL STAGE: BLASTULA, EARLY GASTRULA AND HATCHED
CC TADPOLES; LITTLE OR NO EXPRESSION IN MORULA AND LATE GASTRULA.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.

```

---

```

CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 3 CUB domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L12249; AAA16313.1; -.
CC PIR; JC2218; JC2218.
CC HSP; P00736; IAPQ.
CC MEROPS; M12.005; -.
CC InterPro; IPR001506; Astacin.
CC InterPro; IPR000152; Asx_Hydroxyl.
CC InterPro; IPR000859; CUB_Domain.
CC InterPro; IPR01881; EGF_Ca.
CC InterPro; IPR006209; EGF_Like.
CC InterPro; IPR006026; Nzn_Mtpeptidse.
CC InterPro; IPR006025; Zn_Mtpeptidse.
CC Pfam; PF01400; Astacin; 1.
CC Pfam; PF00431; CUB; 3.
CC Pfam; PF00008; EGF; 1.
CC PRINTS; PR00480; ASTACIN.
CC SMART; SM00042; CUB; 3.
CC SMART; SM00179; EGF_CA; 1.
CC SMART; SM00235; ZnMC; 1.
CC PROSITE; PS00142; ZINC_PROTEASE; 1.
CC PROSITE; PS01180; CUB; 3.
CC PROSITE; PS00010; ASX_HYDROXYL; 1.
CC PROSITE; PS00022; EGF_1; FALSE_NEG.
CC PROSITE; PS01186; EGF_2; 1.
CC PROSITE; PS01187; EGF_CA; 1.
KW Growth factor; Cytokine; Repeat; Bone; Cartilage; Hydrolase; Protease;
KW Metalloprotease; EGF-like domain; Zinc; Calcium; Signal;
KW Glycoprotein.
FT SIGNAL 1 ?
FT PROPEP ? 83
FT CHAIN 84 707
FT DOMAIN 84 284
FT DOMAIN 285 397
FT DOMAIN 398 509
FT DOMAIN 510 551
FT DOMAIN 554 666
FT METAL 176 176
FT ACT_SITE 177 177
FT METAL 180 180
FT METAL 186 186
FT DISULFID 146 149
FT DISULFID 514 526
FT DISULFID 522 535
FT DISULFID 537 550
FT CARBOHYD 62 62
FT CARBOHYD 105 105
FT CARBOHYD 295 295
FT CARBOHYD 326 326
FT CARBOHYD 562 562
SQ SEQUENCE 707 AA; 80673 MW; 1B980D716DC3B8D CRC64;

Query Match 10.1%; Score 176; DB 1; Length 707;
Best Local Similarity 43.3%; Pred. No. 2.1e-07;
Matches 45; Conservative 15; Mismatches 36; Indels 8; Gaps 5;

Qy 28 NGSISPPPHPTYPNTVLVWELVAEENVMQLTDFRPLGLEDDEDDICKYDFVEEB- 86
Db 562 NGSINSPGWKPEYPPNKNICWQLVAPTQ--YRISLXFDQ---FETEDNCKYDFVEVRSG 617
Qy 87 -PSDGTILGRWCGSGTVPQKISQKQIRIRFVSDVEYFPGFCIHYNIVMP- 129
Db 618 LTSDSKLHGKFCGS--ELPAVITISQYNNRIEFKSDNTV--SKKGF 659

```

RESULT 3  
 SPAN\_STRPU STANDARD; PRT; 616 AA.  
 AC P98068;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE SPAN protein precursor (EC 3.4.24.-)  
 GN SPAN.  
 OS Strongylocentrotus purpuratus (Purple sea urchin).  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Echinoida; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;  
 OC Strongylocentrotus.  
 OX NCBI\_TaxID=7668;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92315921; PubMed=1618141;  
 RA Reynolds S.D., Angerer L.M., Palis J., Nasir A., Angerer R.C.;  
 RT "Early mRNAs, spatially restricted along the animal-vegetal axis of  
 RT sea urchin embryos, include one encoding a protein related to tolloid  
 RT and BMP-1.";  
 RL Development 114:769-786(1992).  
 CC -1- TISSUE SPECIFICITY: ASYMMETRICALLY ALONG THE ANIMAL-VEGETAL AXIS  
 CC OF THE BLASTULA.  
 CC -1- DEVELOPMENTAL STAGE: VERY EARLY BLASTULA (BETWEEN 16-CELL STAGE  
 CC AND HATCHING).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.  
 CC -1- SIMILARITY: Contains 1 EGF-like domain.  
 CC -1- SIMILARITY: Contains 2 CUB domains.  
 CC  
 CC -----  
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use, by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; M84144; AAA30072.1; -;  
 CC HSPSP; P28825; 11AF.  
 CC MEROPS; M12.013; -;  
 CC InterPro; IPR001506; Astacin.  
 CC InterPro; IPR000859; CUB domain.  
 CC InterPro; IPR006209; EGF-like.  
 CC InterPro; IPR006210; IEGF.  
 CC InterPro; IPR006026; Zn MPepptidse.  
 CC InterPro; IPR006025; Zn MPepptidse.  
 CC Pfam; PF01400; Astacin; 1.  
 CC Pfam; PF00431; CUB; 2.  
 CC PRINTS; PR00480; ASTACIN.  
 CC SMART; SM00042; CUB; 2.  
 CC SMART; SM00181; EGF; 1.  
 CC SMART; SM00235; Zmcg; 1.  
 CC PROSITE; PS00142; ZINC\_PROTEASE; 1.  
 CC PROSITE; PS01180; CUB; 2.  
 CC PROSITE; PS00022; EGF 1; 1.  
 CC PROSITE; PS01186; EGF 2; FALSE NEG.  
 CC Developmental protein; Repeat; Hydrolase; Protease; Zinc; Embryo;  
 KW Metalloprotease; EGF-like domain; Signal.  
 FT SIGNAL 1 16  
 FT 16  
 FT 17 93 ACTIVATION PEPTIDE (POTENTIAL).  
 FT CHAIN 94 616  
 FT DOMAIN 89 93 ARG/LYS-RICH (BASIC).  
 FT DOMAIN 94 295 METALLOPROTEASE.  
 FT DOMAIN 295 329 EGF-LIKE.  
 FT DOMAIN 340 450 CUB 1.  
 FT DOMAIN 451 502 THR-RICH.  
 FT DOMAIN 503 614 CUB 2.  
 FT METAL 190 190 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT ACT SITE 191 191 BY SIMILARITY.  
 FT METAL 194 194 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT METAL 200 200 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT METAL

FT DISULFID 299 315 BY SIMILARITY.  
 FT DISULFID 305 317 BY SIMILARITY.  
 FT DISULFID 319 328 BY SIMILARITY.  
 SQ SEQUENCE 616 AA; 67902 MW; 397CD923FFB9B98 CRC64;  
 Query Match 10.0%; Score 173.5; DB 1; Length 616;  
 Best Local Similarity 27.0%; Pred. No. 2.9e-07;  
 Matches 70; Conservative 33; Mismatches 93; Indels 63; Gaps 14;  
 QY 29 GSISPRFPHTYPRNTVLVRLVAEENVMQLTFDERFGLDEDDICKYDFVEVEPS 88  
 Db 349 GEITSPNYPNVEDNTACVIEGPGYST-IELTF---LDMEIETELCRYDAVEVRKDD 404  
 QY 89 DGTILGWCSGTVPGKQISKGNIRIRFVSDVEYPPS--EPGCIHYNVMPQTFEAVSP 146  
 Db 405 INSIGKFCGN-TLPPVQISSNQMVSTSD---PSITRRGFKATYVIII-QTTTFST 459  
 QY 147 SVL---PPSALPLDLLNNAITAFSTLEDLYLPERWQLDLEDLYRPTWLLGKAFVFG 203  
 Db 460 TTLQTPPSTTTLQTPNPSTTLQT-----TNPSTTLQTTD--TPVSCGGTFV-G 509  
 QY 204 RKSRLVDNLNLTREVRVLYSCTPRNFVSIR-----BELKRTDTIF-----W 244  
 Db 510 VEGRVASPNY-----PNYDMSLQCDYVIEDGRRVELIFEDFGLDETTCRM 558  
 QY 245 PGCLL-----VKRCG 254  
 Db 559 DSLMLNLNGIKVGMKMG 577  
 RESULT 4  
 BMP1 HUMAN  
 ID BMP1\_HUMAN STANDARD; PRT; 986 AA.  
 AC P13497; Q13292; Q13872; Q14874; Q99421; Q99423; Q9UL38;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 16-OCT-2001 (Rel. 49, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bone morphogenetic protein 1 precursor (EC 3.4.24.19) (BMP-1)  
 DE (Procollagen C-proteinase) (PCP) (Mammalian tolloid protein) (mtld).  
 GN BMP1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM BMP1-3).  
 RC TISSUE=Skin;  
 RX MEDLINE=96209868; PubMed=8643539;  
 RA Li S.W., Sieron A.L., Fertaia A., Hojima Y., Arnold W.V.,  
 RA Prockop D.J.;  
 RA "The C-proteinase that processes procollagens to fibrillar collagens  
 RT is identical to the protein previously identified as bone morphogenic  
 RT protein-1.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:5127-5130(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM BMP1-1).  
 RX MEDLINE=89072730; PubMed=3201241;  
 RA Wozney J.M., Rosen V., Celeste A.J., Mitsock L.M., Whitters M.J.,  
 RA Kriz R.W., Hewick R.M., Wang E.A.;  
 RA "Novel regulators of bone formation: molecular clones and  
 RT activities.";  
 RL Science 242:1528-1534(1988).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS BMP1-4; BMP1-5 AND BMP1-6).  
 RC TISSUE=Placenta;  
 RX MEDLINE=98160316; PubMed=9500680;  
 RA Janitz M., Heiser V., Boettcher U., Landt O., Lauster R.;  
 RT "Three alternatively spliced variants of the gene coding for the human  
 RT bone morphogenetic protein-1.";  
 RL J. Mol. Med. 76:141-146(1998).  
 RN [4]  
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS BMP1-3 AND BMP1-7).  
 RC TISSUE=Placenta;



DR	PFam; PF01400; Astacin; 1.	DR	PFam; PF00431; CUB; 5.	DR	PFam; PF00008; EGF; 2.	DR	PRINTS; PR00480; ASTACIN.	DR	SMART; SM00042; CUB; 5.	DR	SMART; SM00179; EGF_CA; 2.	DR	SMART; SM00235; ZMNC; 1.	DR	PROSITE; PS00142; ZINC_PROTEASE; 1.	DR	PROSITE; PS01180; CUB; 5.	DR	PROSITE; PS00010; ASX_HYDROXYL; 2.	DR	PROSITE; PS00022; EGF_1; FALSE_NEG.	DR	PROSITE; PS01186; EGF_2; 2.	DR	PROSITE; PS01187; EGF_CA; 2.	KW	Growth factor; Cytokine; Repeat; Bone; Cartilage; Hydrolase;	KW	Metalloprotease; EGF-like domain; Zinc; Calcium; Signal;	KW	Glycoprotein; Zymogen; Alternative splicing.	FT	SIGNAL	1	22	POTENTIAL.	FT	PROPEP	23	120	POTENTIAL.	FT	CHAIN	121	986	BONE MORPHOGENETIC PROTEIN 1.	FT	DOMAIN	121	321	METALLOPROTEASE.	FT	DOMAIN	322	434	CUB 1.	FT	DOMAIN	435	546	CUB 2.	FT	DOMAIN	547	588	EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).	FT	DOMAIN	591	703	CUB 3.	FT	DOMAIN	704	743	EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).	FT	DOMAIN	747	859	CUB 4.	FT	DOMAIN	860	976	CUB 5.	FT	METAL	213	213	ZINC (CATALYTIC) (BY SIMILARITY).	FT	ACT SITE	214	214	BY SIMILARITY.	FT	METAL	217	217	ZINC (CATALYTIC) (BY SIMILARITY).	FT	METAL	223	223	ZINC (CATALYTIC) (BY SIMILARITY).	FT	DISULFID	183	186	BY SIMILARITY.	FT	DISULFID	322	348	BY SIMILARITY.	FT	DISULFID	375	397	BY SIMILARITY.	FT	DISULFID	435	461	BY SIMILARITY.	FT	DISULFID	488	510	BY SIMILARITY.	FT	DISULFID	551	563	BY SIMILARITY.	FT	DISULFID	559	572	BY SIMILARITY.	FT	DISULFID	574	587	BY SIMILARITY.	FT	DISULFID	591	617	BY SIMILARITY.	FT	DISULFID	644	666	BY SIMILARITY.	FT	DISULFID	707	718	BY SIMILARITY.	FT	DISULFID	714	727	BY SIMILARITY.	FT	DISULFID	729	742	BY SIMILARITY.	FT	CARBOHYD	91	91	N-LINKED (GLCNAC. .) (POTENTIAL).	FT	CARBOHYD	142	142	N-LINKED (GLCNAC. .) (POTENTIAL).	FT	CARBOHYD	332	332	N-LINKED (GLCNAC. .) (POTENTIAL).	FT	CARBOHYD	363	363	N-LINKED (GLCNAC. .) (POTENTIAL).	FT	CARBOHYD	599	599	N-LINKED (GLCNAC. .) (POTENTIAL).	FT	VARSPPLIC	703	730	KRDECSKONGGQQDCQVTFGSYECOCR -> EKRPALQPP KGRPQLKFRVQKRNRTQ (in isoform BMP1-1). /FTID=VSP 005461. Missing (in isoform BMP1-1). /FTID=VSP 005462. QBYNFKMFPQVESLGETYDFDSIMHYARNTFSRGIFLDT IVPKYEVNGKRPPIGR -> VHSLSLHSCSNGASFP CSLESSTHALCWTGLFRLPSPFPRLPLAAPTRLRAGV (in isoform BMP1-4). /FTID=VSP 005463. Missing (in isoform BMP1-4). /FTID=VSP 005464. AACGGFLTKINGSITSPGPKKYPNNKNIQWLV -> GCY DLQVGKLLMDRHCFLRSLTHGEMGLTALRG (in isoform BMP1-5). /FTID=VSP 005465. Missing (in isoform BMP1-5). /FTID=VSP 005466. DKDECSKONGGQQDD -> GGSLFGLLGHPPRRP (in isoform BMP1-6). /FTID=VSP 005467. Missing (in isoform BMP1-6). /FTID=VSP 005468. DKDECSKONGGQQDCQVTFGSYECOCRGSFVLHDKHDCQ
DR	PFam; PF00431; CUB; 5.	DR	PFam; PF00008; EGF; 2.	DR	PRINTS; PR00480; ASTACIN.	DR	SMART; SM00042; CUB; 5.	DR	SMART; SM00179; EGF_CA; 2.	DR	SMART; SM00235; ZMNC; 1.	DR	PROSITE; PS00142; ZINC_PROTEASE; 1.	DR	PROSITE; PS01180; CUB; 5.	DR	PROSITE; PS00010; ASX_HYDROXYL; 2.	DR	PROSITE; PS00022; EGF_1; FALSE_NEG.	DR	PROSITE; PS01186; EGF_2; 2.	DR	PROSITE; PS01187; EGF_CA; 2.	KW	Growth factor; Cytokine; Repeat; Bone; Cartilage; Hydrolase;	KW	Metalloprotease; EGF-like domain; Zinc; Calcium; Signal;	KW	Glycoprotein; Zymogen; Alternative splicing.	FT	SIGNAL	1	22	POTENTIAL.	FT	PROPEP	23	120	POTENTIAL.	FT	CHAIN	121	986	BONE MORPHOGENETIC PROTEIN 1.	FT	DOMAIN	121	321	METALLOPROTEASE.	FT	DOMAIN	322	434	CUB 1.	FT	DOMAIN	435	546	CUB 2.	FT	DOMAIN	547	588	EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).	FT	DOMAIN	591	703	CUB 3.	FT	DOMAIN	704	743	EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).	FT	DOMAIN	747	859	CUB 4.	FT	DOMAIN	860	976	CUB 5.	FT	METAL	213	213	ZINC (CATALYTIC) (BY SIMILARITY).	FT	ACT SITE	214	214	BY SIMILARITY.	FT	METAL	217	217	ZINC (CATALYTIC) (BY SIMILARITY).	FT	METAL	223	223	ZINC (CATALYTIC) (BY SIMILARITY).	FT	DISULFID	183	186	BY SIMILARITY.	FT	DISULFID	322	348	BY SIMILARITY.	FT	DISULFID	375	397	BY SIMILARITY.	FT	DISULFID	435	461	BY SIMILARITY.	FT	DISULFID	488	510	BY SIMILARITY.	FT	DISULFID	551	563	BY SIMILARITY.	FT	DISULFID	559	572	BY SIMILARITY.	FT	DISULFID	574	587	BY SIMILARITY.	FT	DISULFID	591	617	BY SIMILARITY.	FT	DISULFID	644	666	BY SIMILARITY.	FT	DISULFID	707	718	BY SIMILARITY.	FT	DISULFID	714	727	BY SIMILARITY.	FT	DISULFID	729	742	BY SIMILARITY.	FT	CARBOHYD	91	91	N-LINKED (GLCNAC. .) (POTENTIAL).	FT	CARBOHYD	142	142	N-LINKED (GLCNAC. .) (POTENTIAL).	FT	CARBOHYD	332	332	N-LINKED (GLCNAC. .) (POTENTIAL).	FT	CARBOHYD	363	363	N-LINKED (GLCNAC. .) (POTENTIAL).	FT	CARBOHYD	599	599	N-LINKED (GLCNAC. .) (POTENTIAL).	FT</						

FT FT EAGCDHKVTSSTGTTSPNNPKYPSKXECTWAISSTPGHR  
FT FT VKLTFTMEMDIESCEAYDHLVEFDGRDAKAPVIGRFG  
FT FT -> VLKAGADRHSHLSGLLELLCPHALVDVTPAPPALHGD  
FT FT THAHTHTVHTCPHQAETCRGPEPLGASRLSPQPGHLTIA  
FT FT PQGSGYLDWDTHRGDPKFRKRRKSLKTSLSLTPATFRGIWA  
FT FT L (in isoform BMP1-7).  
FT FT /FTId-VSP 005469.  
FT FT Missing (in isoform BMP1-7).  
FT FT /FTId-VSP 005470.  
FT FT D -> N (IN REF. 4).  
FT FT CONFLICT 748 748  
FT FT CONFLICT 934 934 R -> S (IN REF. 4).  
SQ SEQUENCE 986 AA; 111248 MW; F89201913AC3CBEA CRC64;  
  
Query Match 9.7%; Score 169; DB 1; Length 986;  
Best Local Similarity 39.4%; Pred. No. 1.3e-06;  
Matches 43; Conservative 17; Mismatches 39; Indels 10; Gaps 5;  
  
QY 28 NGSIHSRPFHTYPRNTVLVRLVA-VEENVWVQLTFDERFGLDEDDICKYDFVEVEE 86  
Db 599 NGSIHSRPFHTYPRNTVLVRLVA-VEENVWVQLTFDERFGLDEDDICKYDFVEVEE 86  
QY 87 --PSDGTILGRWCGSGTVPGKQISKGQIRIRFVSDYFSPGFCIH 133  
Db 654 GLTADSKLHGKFGCS-EKPEVITSQNNMVEPKSDNTV-SKKGFKAHF 700  
  
RESULT 5  
BMP1\_MOUSE STANDARD; PRT; 991 AA.  
ID BMP1\_MOUSE  
AC P98063;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bone morphogenetic protein 1 precursor (EC 3.4.24.19) (BMP-1)  
DE (Procollagen C-proteinase) (PCP) (Mammalian tolloid protein) (mtld).  
GN BMP1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Embryo;  
RX MEDLINE=94229342; PubMed=8174772;  
RA Fukagawa M., Noboru S., Hogan B.L.M., Jones C.M.;  
RT "Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1),  
RT which is related to the Drosophila dorsoventral gene tolloid and  
RT encodes a putative astacin metalloendopeptidase.";  
RL Dev. Biol. 163:175-183(1994).  
CC -I- FUNCTION: CLEAVES THE C-TERMINAL PROPEPTIDES OF PROCOLLAGEN I, II  
CC AND II. INDUCES CARTILAGE AND BONE FORMATION.  
CC -I- CATALYTIC ACTIVITY: Cleavage of the C-terminal propeptide at  
CC Ala-[Asp in type I and II procollagens and at Arg-[Asp in type  
CC III.  
CC -I- COFACTOR: Binds 1 zinc ion per subunit (By similarity).  
CC -I- ENZYME REGULATION: ACTIVITY IS INCREASED BY THE PROCOLLAGEN C-  
CC ENDOPEPTIDASE ENHANCER PROTEIN.  
CC -I- TISSUE SPECIFICITY: AT HIGH LEVELS IN EMBRYONIC MATERNAL DECIDUUM  
CC AND FLOOR PLATE REGION OF THE NEURAL TUBE. LESS IN DEVELOPING  
CC MEMBRANOUS AND ENDOCHONDRAL BONE, SUBMUCOSA OF INTESTINE, DERMIS  
CC OF SKIN AND THE MESENCHYME OF SPLEEN AND LUNG.  
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.  
CC -I- SIMILARITY: Contains 2 EGF-like domains.  
CC -I- SIMILARITY: Contains 5 CUB domains.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----

DR EMBL; L24755; AAA37306.1; -.  
DR PIR; I49540; I49540.  
DR HSSP; P00736; IAPQ.  
DR MEROPS; M12.005; -.  
DR MGD; MGI:89176; Bmp1.  
DR InterPro; IPR001506; Astacin.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR000859; CUB domain.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR006026; Nzn\_Mtpeptdse.  
DR InterPro; IPR006025; Zn\_Mtpeptdse.  
DR Pfam; PF01400; Astacin; 1.  
DR Pfam; PF00431; CUB; 5.  
DR Pfam; PF00008; EGF; 2.  
DR PRINTS; PR00480; ASTACIN.  
DR SMART; SM00042; CUB; 5.  
DR SMART; SM00179; EGF\_Ca; 2.  
DR SMART; SM00235; ZNMG; 1.  
DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
DR PROSITE; PS01180; CUB; 5.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 2.  
DR PROSITE; PS00022; EGF\_1; FALSE\_NEG.  
DR PROSITE; PS01186; EGF\_2; 2.  
DR PROSITE; PS01187; EGF\_Ca; 2.  
KW Growth factor; Cytokine; Repeat; Bone; Cartilage; Hydrolase;  
KW Metalloprotease; EGF-like domain; Zinc; Calcium; Signal;  
KW Glycoprotein; Zymogen.  
FT SIGNAL 1 25 POTENTIAL.  
FT PROPEP 26 125 POTENTIAL..  
FT CHAIN 126 991 BONE MORPHOGENETIC PROTEIN 1.  
FT DOMAIN 126 326 METALLOPROTEASE.  
FT DOMAIN 327 439 CUB 1.  
FT DOMAIN 440 551 CUB 2.  
FT DOMAIN 552 593 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 596 707 CUB 3.  
FT DOMAIN 708 748 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).  
FT DOMAIN 752 864 CUB 4.  
FT DOMAIN 865 981 CUB 5.  
FT METAL 218 218 ZINC (CATALYTIC) (BY SIMILARITY).  
FT ACT SITE 219 219 BY SIMILARITY.  
FT METAL 222 222 ZINC (CATALYTIC) (BY SIMILARITY).  
FT METAL 228 228 ZINC (CATALYTIC) (BY SIMILARITY).  
FT DISULFID 188 191 BY SIMILARITY.  
FT DISULFID 327 353 BY SIMILARITY.  
FT DISULFID 380 402 BY SIMILARITY.  
FT DISULFID 440 466 BY SIMILARITY.  
FT DISULFID 493 515 BY SIMILARITY.  
FT DISULFID 556 568 BY SIMILARITY.  
FT DISULFID 564 577 BY SIMILARITY.  
FT DISULFID 579 592 BY SIMILARITY.  
FT DISULFID 596 622 BY SIMILARITY.  
FT DISULFID 649 671 BY SIMILARITY.  
FT DISULFID 712 723 BY SIMILARITY.  
FT DISULFID 719 732 BY SIMILARITY.  
FT DISULFID 734 747 BY SIMILARITY.  
FT CARBOHYD 96 96 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 147 147 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 337 337 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 368 368 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 604 604 N-LINKED (GLCNAC. .) (POTENTIAL).  
SQ SEQUENCE 991 AA; 111607 MW; 68A1847783A0BB9E CRC64;  
  
Query Match 9.7%; Score 169; DB 1; Length 991;  
Best Local Similarity 39.4%; Pred. No. 1.3e-06;  
Matches 43; Conservative 17; Mismatches 39; Indels 10; Gaps 5;  
  
QY 28 NGSIHSRPFHTYPRNTVLVRLVA-VEENVWVQLTFDERFGLDEDDICKYDFVEVEE 86  
Db 604 NGSIHSRPFHTYPRNTVLVRLVA-VEENVWVQLTFDERFGLDEDDICKYDFVEVEE 86  
QY 87 --PSDGTILGRWCGSGTVPGKQISKGQIRIRFVSDYFSPGFCIH 133  
Db 87 --PSDGTILGRWCGSGTVPGKQISKGQIRIRFVSDYFSPGFCIH 133  
-----

659 GLTADSKLHGKFGS-EKPEVITQNNRVFKSDNTV-SKKGPKAHF 705

DB

RESULT 6  
NRPI\_RAT  
ID NRPI\_RAT STANDARD; PRT; 922 AA.  
AC Q9QWJ9;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Neuropilin-1 precursor (Vascular endothelial cell growth factor 165 receptor).  
DE NRPI.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RN SEQUENCE FROM N.A.  
RP STRAIN=Sprague-Dawley;  
RX MEDLINE=97433085; PubMed=9288754;  
RA Kolodkin A.L., Levengood D.V., Rowe E.G., Tai Y.-T., Giger R.J.,  
RA Ginty D.D.;  
RT "Neuropilin is a semaphorin III receptor."  
RT Cell 90:753-762(1997)  
CC -1- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE  
CC CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF  
CC CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS  
CC SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS. IT  
CC BINDS TO SEMAPHORIN 3A, THE PLGF-2 ISOFORM OF PGF, THE VEGF-165  
CC ISOFORM OF VEGF AND VEGF-B. COEXPRESSION WITH KDR RESULTS IN  
CC INCREASED VEGF-165 BINDING TO KDR AS WELL AS INCREASED CHEMOTAXIS.  
CC IT MAY REGULATE VEGF-INDUCED ANGIOGENESIS (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- TISSUE SPECIFICITY: FOUND IN THE EMBRYONIC NERVOUS SYSTEM.  
CC -1- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.  
CC -1- SIMILARITY: Contains 2 CUB domains.  
CC -1- SIMILARITY: Contains 2 F5/8 type C domains.  
CC -1- SIMILARITY: Contains 1 MAM domain.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; AF016296; AAC53337.1; -  
CC HGSP; P12259; 1CZT.  
CC InterPro; IPR000859; CUB domain.  
CC InterPro; IPR000421; FAS8 C.  
CC InterPro; IPR000998; MAM domain.  
CC Pfam; PF00431; CUB; 2.  
CC Pfam; PF00754; F5/F8 type C; 2.  
CC Pfam; PF00629; MAM; 1.  
CC PRINTS; PR00020; MAMDOMAIN.  
CC SMART; SM00042; CUB; 2.  
CC SMART; SM00231; FAS8C; 2.  
CC SMART; SM00137; MAM; 1.  
CC PROSITE; PS01180; CUB; 2.  
CC PROSITE; PS01285; FAS8C 1; 2.  
CC PROSITE; PS01286; FAS8C 2; 2.  
CC PROSITE; PS00022; FAS8C 3; 2.  
CC PROSITE; PS00740; MAM 1; 1.  
CC PROSITE; PS00060; MAM 2; 1.  
KW Angiogenesis; Transmembrane; Glycoprotein; Neuron; Signal; Repeat;  
Receptor.  
FT SIGNAL 1 21 POTENTIAL.  
FT CHAIN 22 922 NEUROPILIN-1.  
FT DOMAIN 22 855 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 856 880 POTENTIAL.  
FT DOMAIN 881 922 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 141 CUB 1.  
FT DOMAIN 147 CUB 2.  
FT DOMAIN 275 F5/8 TYPE C 1.  
FT DOMAIN 431 F5/8 TYPE C 2.  
FT DOMAIN 645 MAM.  
FT DISULFID 27 54 PROBABLE.  
FT DISULFID 82 104 PROBABLE.  
FT DISULFID 147 173 PROBABLE.  
FT DISULFID 206 228 PROBABLE.  
FT DISULFID 275 424 BY SIMILARITY.  
FT DISULFID 431 583 BY SIMILARITY.  
FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 522 522 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 841 841 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 922 AA; 103082 MW; CC6F82AD098B0F2E CRC64;  
Query Match 9.4%; Score 163.5; DB 1; Length 922;  
Best Local Similarity 36.5%; Pred. No. 3.5e-06;  
Matches 42; Conservative 16; Mismatches 50; Indels 7; Gaps 4;  
QY 23 ITVSTNGSIHSPRPHTYPRNTVLVRLVAVENWVLIQTFDERRGLEDDEDDICKYDFV 82  
DB 31 IKIENFGYLTSPGPHSYHPSEKCEWLIOAPEYQIRIMINFNHFDLEDKRD---CKYD 87  
QY 83 EV--EPPSDGTILGRWCGSGTVFGKQISKGNQIRIRFVSDEYFSPSEFGCIHYNI 135  
DB 88 EVIDGENEGRLNGKFCGK-IAFSPVSSGPFIFIRFVSD-YETHGAGFSIRVEI 140  
RESULT 7  
NRPI\_HUMAN STANDARD; PRT; 931 AA.  
ID NRPI\_HUMAN STANDARD; PRT; 931 AA.  
AC OC04E2; O14820; O14821;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Neuropilin-2 precursor (Vascular endothelial cell growth factor 165 receptor 2).  
DE NRPI OR VEGF165R2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RN SEQUENCE FROM N.A. (ISOFORMS A0 AND A17).  
RP MEDLINE=97470886; PubMed=9333348;  
RA Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.;  
RT "Neuropilin-2, a novel member of the neuropilin family, is a high  
RT affinity receptor for the semaphorins Sema E and Sema IV but not Sema  
RT III."  
RL Neuron 19:547-559(1997).  
RN [2]  
RN SEQUENCE FROM N.A. (ISOFORM A22).  
RP TISSUE=Breast;  
RX MEDLINE=98188099; PubMed=9529250;  
RA Soker S., Takashima S., Miao H.-Q., Neufeld G., Klagsbrun M.;  
RT "Neuropilin-1 is expressed by endothelial and tumor cells as an  
RT isoform-specific receptor for vascular endothelial growth factor."  
RL Cell 92:735-745(1998).  
RN [3]  
RN CHARACTERIZATION.  
RX MEDLINE=20309748; PubMed=10748121;  
RA Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;  
RT "Neuropilin-2 and neuropilin-1 are receptors for the 165-amino acid  
RT form of vascular endothelial growth factor (VEGF) and of placenta  
RT growth factor-2, but only neuropilin-2 functions as a receptor for  
RT the 145-amino acid form of VEGF."  
RL J. Biol. Chem. 275:18040-18045(2000).  
CC -1- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165  
CC AND VEGF-145 ISOFORMS OF VEGF. AND THE PLGF-2 ISOFORM OF PGF.  
CC -1- SUBUNIT: NEUROPILIN-2 PROBABLY FORMS AN HETEROMERIC COMPLEX WITH

CC NEUROPILIN-1 IN ORDER TO BE A FUNCTIONAL SEMAPHORIN 3C RECEPTOR.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- ALTERNATIVE PRODUCTS: Type I membrane protein.  
CC Name=A22;  
CC IsoId=060462-1; Sequence=Displayed;  
CC Name=A0;  
CC IsoId=060462-2; Sequence=VSP\_004342;  
CC Name=A17;  
CC IsoId=060462-3; Sequence=VSP\_004341;  
CC -1- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.  
CC -1- SIMILARITY: Contains 2 CUB domains.  
CC -1- SIMILARITY: Contains 2 F5/8 type C domains.  
CC -1- SIMILARITY: Contains 1 MAM domain.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; AF022859; AAC51788.1; -;  
CC EMBL; AF022860; AAC51789.1; -;  
CC EMBL; AF016098; AAC12922.1; -;  
CC HSP; P12259; 1CZT.  
CC Genew; HGNC:8005; NRP2.  
CC MIM; 602070; -;  
CC GO; GO:0005624; C:membrane fraction; TAS.  
CC GO; GO:0004872; F:receptor activity; TAS.  
CC GO; GO:0005021; F:vascular endothelial growth factor receptor. .; TAS.  
CC GO; GO:0007411; P:axon guidance; TAS.  
CC InterPro; IPR000859; CUB domain.  
CC InterPro; IPR000421; FA58\_C.  
CC Pfam; PF00431; CUB; 2.  
CC Pfam; PF00754; F5 F8 type C; 2.  
CC Pfam; PF00629; MAM; 1.  
CC PRINTS; PR00020; MAMDOMAIN.  
CC SMART; SM00042; CUB; 2.  
CC SMART; SM00231; FA58C; 2.  
CC SMART; SM00137; MAM; 1.  
CC PROSITE; PS01180; CUB; 2.  
CC PROSITE; PS01285; FA58C\_1; 2.  
CC PROSITE; PS01286; FA58C\_2; 2.  
CC PROSITE; PS50022; FA58C\_3; 2.  
CC PROSITE; PS50060; MAM\_2; 1.  
CC Transmembrane; Glycoprotein; Neuron; Signal; Repeat; Receptor;  
KW Alternative splicing.  
FT SIGNAL 1 20  
FT CHAIN 21 931  
FT DOMAIN 21 864  
FT TRANSMEM 865 889  
FT DOMAIN 890 931  
FT DOMAIN 149 267  
FT DOMAIN 277 427  
FT DOMAIN 434 592  
FT DOMAIN 642 802  
FT DOMAIN 671 674  
FT DISULFID 28 55  
FT DISULFID 83 105  
FT DISULFID 149 175  
FT DISULFID 208 230  
FT DISULFID 277 427  
FT DISULFID 434 592  
FT CARBOHYD 152 152  
FT CARBOHYD 157 157  
FT CARBOHYD 629 629  
FT CARBOHYD 839 839  
FT VARSPLIC 809 813  
/FTID=VSP\_004341.

FT VARSPLIC 809 830 Missing (in isoform A0).  
FT CONFLICT 602 602 /FTID=VSP\_004342.  
FT SEQUENCE 931 AA; 104830 MW; 270CBA569A0A797C CRC64;  
SQ  
Query Match 9.4%; Score 163.5; DB 1; Length 931;  
Best Local Similarity 32.3%; Pred. No. 3.6e-06;  
Matches 43; Conservative 19; Mismatches 64; Indels 7; Gaps 4;  
Qy 5 FSSNKEQGVDPQHERIITVSTNGSIHSRPFHTYPRNTVLVWRLVAEENVMITLTFD 64  
Db 14 YFSHQVRGQDPDPCGGRLNSKAGYITSPGYPDYSHQNCENVIVAPENQKIVLNFN 73  
Qy 65 ERFGLEDPEDDICKYDFEVE--EPSDGTILGRWCGSGTVEGKQISGNQIRIRFVSDEY 122  
Db 74 PHFEIKHD--CKYDFEIRDGSEADLKGHCN-IAPPTIISGSMLYIKFTSD-Y 128  
Qy 123 FSPSPGFCIHNI 135  
Db 129 ARQAGFSLRYEI 141  
RESULT 8  
NRP2\_RAT STANDARD; PRT; 925 AA.  
AC O35276;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Neuropilin-2 precursor (Vascular endothelial cell growth factor 165  
DE receptor 2).  
GN NRP2.  
OS Rattus norvegicus (Rat).  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
ON NCBI\_TaxID=10116;  
RX [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley;  
EX MEDLINE=97433085; PubMed=9288754;  
RA Kolodkin A.L., Levengood D.V., Rowe E.G., Tai Y.-T., Giger R.J.,  
RA Ginty D.D.;  
RL Cell 90:753-762(1997).  
CC -1- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165  
CC AND VEGF-145 ISOFORMS OF VEGF. AND THE PLGF-2 ISOFORM OF PGF.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- TISSUE SPECIFICITY: FOUND IN CERTAIN NEURONAL POPULATIONS OF THE  
CC CNS AND IN OTHER NONNEURONAL TISSUES INCLUDING MESENCHYMAL TISSUE  
CC LINING IN THE RIBS.  
CC -1- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.  
CC -1- SIMILARITY: Contains 2 CUB domains.  
CC -1- SIMILARITY: Contains 2 F5/8 type C domains.  
CC -1- SIMILARITY: Contains 1 MAM domain.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; AF016297; AAC53338.1; -;  
CC HSP; P12259; 1CZT.  
CC InterPro; IPR000859; CUB domain.  
CC InterPro; IPR000421; FA58\_C.  
CC InterPro; IPR000998; MAM domain.  
CC Pfam; PF00431; CUB; 2.  
CC Pfam; PF00754; F5 F8 type C; 2.  
CC Pfam; PF00629; MAM; 1.  
CC PRINTS; PR00020; MAMDOMAIN.  
CC SMART; SM00042; CUB; 2.

RESULT 10

```

NRP1_MOUSE
ID NRP1_MOUSE STANDARD; PRT; 923 AA.
AC P97333;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropilin-1 precursor (A5 protein).
DN NRPI OR NRP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=BALB/c; TISSUE=Embryonic brain;
RC MEDLINE=96353149; PubMed=8748368;
RX Kawakami A., Kitsuoka T., Takagi S., Fujisawa H.;
RA "Developmentally regulated expression of a cell surface protein,
RT Neuropilin, in the mouse nervous system.";
RL J. Neurobiol. 29:1-17(1996).
CC -!- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE
CC CARDIOVASCULAR SYSTEM. IN ANGIOGENESIS. IN THE FORMATION OF
CC CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS
CC SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS. IT
CC BINDS TO SEMAPHORIN 3A, THE PLGF-2 ISOFORM OF PGF, THE VEGF-165
CC ISOFORM OF VEGF AND VEGF-B. COEXPRESSION WITH KDR RESULTS IN
CC INCREASED VEGF-165 BINDING TO KDR AS WELL AS INCREASED CHEMOTAXIS.
CC IT MAY REGULATE VEGF-INDUCED ANGIOGENESIS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC -!- TISSUE SPECIFICITY: NERVOUS SYSTEM.
CC -!- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
CC -!- SIMILARITY: Contains 2 CUB domains.
CC -!- SIMILARITY: Contains 2 F5/8 type C domains.
CC -!- SIMILARITY: Contains 1 MAM domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D50086; BAA08789.1; -.
DR HSP; P12259; 1CZT.
DR MGP; MGI:106206; NRP.
DR InterPro; IPR000859; CUB domain.
DR InterPro; IPR000421; FAS8 C.
DR InterPro; IPR000998; MAM domain.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00754; F5 F8 type C; 2.
DR PRINTS; PR00020; MAMDOMAIN.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00231; FAS8C; 2.
DR SMART; SM00137; MAM; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01285; FAS8C 1; 2.
DR PROSITE; PS01286; FAS8C 2; 2.
DR PROSITE; PS00022; FAS8C 3; 2.
DR PROSITE; PS00740; MAM 1; 1.
DR PROSITE; PS00600; MAM 2; 1.
DR Angiogenesis; Transmembrane; Glycoprotein; Neurone; Signal; Repeat;
KW Receptor.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 923 NEUROPILIN-1.
FT DOMAIN 22 856 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 857 879 POTENTIAL.
FT DOMAIN 880 923 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 27 141 CUB 1.
FT DOMAIN 147 265 CUB 2.
FT DOMAIN 275 424 F5/8 TYPE C 1.
FT DOMAIN 431 583 F5/8 TYPE C 2.

```

---

```

FT DOMAIN 645 811 MAM.
FT DISULFID 27 54 PROBABLE.
FT DISULFID 82 104 PROBABLE.
FT DISULFID 147 173 PROBABLE.
FT DISULFID 206 228 PROBABLE.
FT DISULFID 275 424 BY SIMILARITY.
FT DISULFID 431 583 BY SIMILARITY.
FT CARBOHYD 150 150 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 522 522 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 842 842 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 923 AA; 103020 MW; 064B8A170796808 CRC64;

Query Match 9.3%; Score 160.5; DB 1; Length 923;
Best Local Similarity 36.5%; Pred. No. 6.4e-06;
Matches 42; Conservative 16; Mismatches 50; Indels 7; Gaps 4;

QY 23 ITVSTNGSIHSPRPHTYPRVTVLVRLVAVENVWVLTDPDERGLEDPEDDICKYDFV 82
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 31 IKIENPGYLTSPGYPHSYHPSEKCEWLIQAPEYQRIIINFNPFDLEDRD---CKYDYV 87
QY 83 EV--EPPSDGTILGRCGSGTVPGKQISKGNQIRIRFVSDYFPPSEPGFCIHVNI 135
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 88 EVIDGENEGRLWGKFCGK-IAPSPVSSGPFLLFKFVSD-YETHGAGFSIRYEI 140

RESULT 11
NRP2_MOUSE
ID NRP2_MOUSE STANDARD; PRT; 931 AA.
AC O35375; O35373; O35374; O35376; O35377; O35378;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropilin-2 precursor (Vascular endothelial cell growth factor 165
DE receptor 2).
DE receptor 2).
GN NRP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A. (ISOFORMS A0; A17; A22; A5; B0 AND B5).
RC STRAIN=BALB/c;
RX MEDLINE=97470888; PubMed=9331348;
RA Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.;
RT "Neuropilin-2, a novel member of the neuropilin family, is a high
RT affinity receptor for the semaphorins Sema 5 and Sema IV but not Sema
RT III.";
RL Neuron 19:547-559(1997).
CC -!- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165
CC AND VEGF-145 ISOFORMS OF VEGF, AND THE PLGF-2 ISOFORM OF PGF.
CC -!- SUBUNIT: NEUROPILIN-2 PROBABLY FORMS AN HETEROMERIC COMPLEX WITH
CC NEUROPILIN-1 IN ORDER TO BE A FUNCTIONAL SEMAPHORIN E RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=6;
CC Name=A22;
CC IsoId=O35375-1; Sequence=Displayed;
CC Name=A0;
CC IsoId=O35375-2; Sequence=VSP_004344;
CC Name=A5;
CC IsoId=O35375-3; Sequence=VSP_004345;
CC Name=A17;
CC IsoId=O35375-4; Sequence=VSP_004343;
CC Name=B0;
CC IsoId=O35375-5; Sequence=VSP_004346;
CC Name=B5;
CC IsoId=O35375-6; Sequence=VSP_004347;
CC -!- TISSUE SPECIFICITY: EXPRESSED IN DEVELOPING CNS, PNS AND IN SOME
CC NONNEURAL TISSUES INCLUDING LIMB BUDS, DEVELOPING BONES, MUSCLES,
CC INTESTINAL EPITHELIUM, KIDNEY LUNG AND SUBMANDIBULAR GLAND.
CC -!- DEVELOPMENTAL STAGE: THE EXPRESSION PATTERN IS VERY DYNAMIC AND IS

```









use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; D45416; BAA08256.1; -.  
 CC HSSP; P12259; 1C2T.  
 DR InterPro; IPR000859; CUB domain.  
 DR InterPro; IPR000421; FA5B\_C.  
 DR InterPro; IPR000938; MAM\_domain.  
 DR Pfam; PF00431; CUB; 2.  
 DR Pfam; PF00754; F5\_F8\_type\_C; 2.  
 DR Pfam; PF00629; MAM; 1.  
 DR PRINTS; PR00020; MAMDOMAIN.  
 DR SMART; SM00042; CUB; 2.  
 DR SMART; SM00231; FA58C; 2.  
 DR SMART; SM00137; MAM; 1.  
 DR PROSITE; PS01180; CUB; 2.  
 DR PROSITE; PS01285; FA58C\_1; 2.  
 DR PROSITE; PS01286; FA58C\_2; 2.  
 DR PROSITE; PS00022; FA58C\_3; 2.  
 DR PROSITE; PS00740; MAM\_1; 1.  
 DR PROSITE; PS00060; MAM\_2; 1.  
 KW Angiogenesis; Transmembrane; Glycoprotein; Neurone; Signal; Repeat;  
 KW Receptor; Cell adhesion.  
 FT SIGNAL 1 18  
 FT CHAIN 19 914  
 FT DOMAIN 20 847  
 FT TRANSMEM 848 870  
 FT DOMAIN 871 914  
 FT DOMAIN 25 139  
 FT DOMAIN 145 263  
 FT DOMAIN 273 422  
 FT DOMAIN 429 581  
 FT DOMAIN 636 801  
 FT DISULFID 25 52  
 FT DISULFID 80 102  
 FT DISULFID 145 171  
 FT DISULFID 204 226  
 FT DISULFID 273 422  
 FT DISULFID 429 581  
 FT SEQUENCE 914 AA; 102480 MW; DD2EE6D6FCBB68C CRC64;

Query Match 9.1%; Score 157; DB 1; Length 914;  
 Best Local Similarity 29.4%; Pred. No. 1.3e-05;  
 Matches 52; Conservative 27; Mismatches 68; Indels 30; Gaps 9;  
 QY 23 ITVSTGSHSPRPHTYPRNTVLVWELVAEENVVMIQLTFDERFGLDEPDDICKYDFV 82  
 DB 29 IKILSPGLTSPGPOSYHPSQKCEMLIQAPYQRTIMNFPHFDELRD---CKYDYV 85  
 QY 83 EV--EPPSDGTLGRWCGSGTVPKQISKGNQIRIRFVSPSEPGFCIHYNIVM--P 138  
 DB 86 EVIDGNAEGRWKYCGK-IAPPLVSSGPLYFIRKVSVD-YETHGAGFIRYEVFKRGP 143  
 QY 139 Q-----PTEAVSPVLP--PALPLDL-----LNNAITAFSTLEDLIRKLEPE 179  
 DB 144 ECSRNFSTSSGMKSPGPKYPSNLECTYIIFAPKMSIILFESPE-----LEPD 195

RESULT 15  
 ID PC01\_HUMAN STANDARD; PRT; 449 AA.  
 AC Q15113; O14550;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Procollagen C-proteinase enhancer protein precursor (PCPE) (Type I  
 DE of procollagen COOH-terminal proteinase enhancer) (Type 1 procollagen C-  
 DE proteinase enhancer protein).  
 GN PCOLCE.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=95014462; PubMed=7523404;  
 RA Takahara K., Kessler E., Biniaminov L., Brusel M., Eddy R.L.,  
 RA Jani-Sait S., Shows T.B., Greenspan D.S.;  
 RT "Type I procollagen COOH-terminal proteinase enhancer protein:  
 RT identification, primary structure, and chromosomal localization of the  
 RT cognate human gene (PCOLCE).";  
 RL J. Biol. Chem. 269:26280-26285(1994).  
 RN [2]  
 RP REVISIONS TO 56; 154 AND 373.  
 RA Kessler E.;  
 RL Unpublished observations (FEB-2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Heart;  
 RA Hirahara I., Syoufuda K., Harada K., Tomita M., Urakami K., Terai H.,  
 RA Morisaki N., Saito Y.;  
 RT "Smooth muscle cell derived procollagen C-protease enhancer protein.";  
 RL Cell Struct. Funct. 21:662-662(1996).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99018118; PubMed=9799793;  
 RA Gloeckner G., Scherer S., Schattevoy R., Boright A.P., Weber J.,  
 RA Tsui L.-C., Rosenthal A.;  
 RT "Large-scale sequencing of two regions in human chromosome 7q22:  
 RT analysis of 650 KB of genomic sequence around the EPO and CYP11 loci  
 RT reveals 17 genes.";  
 RL Genome Res. 8:1060-1073(1998).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=99134301; PubMed=9933570;  
 RA Scott I.C., Clark T.G., Takahara K., Hoffman G.G., Greenspan D.S.;  
 RT "Structural organization and expression patterns of the human and  
 RT mouse genes for the type I procollagen COOH-terminal proteinase  
 RT enhancer protein.";  
 RL Genomics 55:229-234(1999).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.B.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [7]  
 RP PARTIAL SEQUENCE, AND CHARACTERIZATION OF INHIBITORY ACTIVITY.  
 RX MEDLINE=20092917; PubMed=10625689;  
 RA Mott J.D., Thomas C.L., Rosenbach M.T., Takahara K., Greenspan D.S.,  
 RA Banda M.J.;  
 RT "Post-translational proteolytic processing of procollagen C-terminal  
 RT proteinase enhancer releases a metalloproteinase inhibitor.";  
 RL J. Biol. Chem. 275:1384-1390(2000).

Search completed: November 25, 2003, 21:02:51  
Job time : 8.8869 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model  
Run on: November 25, 2003, 20:58:59 ; Search time 28.0774 Seconds  
(without alignments)  
2922.663 Million cell updates/sec

Title: US-09-852-209A-5  
Perfect score: 1734  
Sequence: 1 GKQFSSKNGVQDPQHE.....DVALEHHECDVCVRGSTGG 318

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues 830525  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL 23.3:

- 1: sp archaea.\*
- 2: sp bacteria.\*
- 3: sp fungi.\*
- 4: sp human.\*
- 5: sp invertebrate.\*
- 6: sp mammal.\*
- 7: sp mbc.\*
- 8: sp organelle.\*
- 9: sp phase.\*
- 10: sp plant.\*
- 11: sp rodent.\*
- 12: sp virus.\*
- 13: sp vertebrate.\*
- 14: sp unclassified.\*
- 15: sp\_virus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1728	99.7	345	4	Q9NRA1	Q9nral homo sapien
2	1728	99.7	345	4	Q9UL22	Q9ul22 homo sapien
3	1559	89.9	345	11	Q9GY71	Q9gy71 mus musculus
4	1557	89.8	345	11	Q8C119	Q8ci19 mus musculus
5	1541	88.9	345	11	Q9EQX6	Q9eqx6 rattus norv
6	1530	88.2	345	11	Q9JHV8	Q9jhv8 mus musculus
7	1524	87.9	345	13	Q91946	Q91946 gallus gall
8	1260	72.7	258	11	Q8K429	Q8k429 rattus norv
9	741	42.7	370	4	Q9GZP0	Q9gzp0 homo sapien
10	739.5	42.6	364	4	Q9BWV5	Q9bwv5 homo sapien
11	736	42.4	370	11	Q9EQT1	Q9eqt1 rattus norv
12	736	42.4	370	11	Q92517	Q92517 mus musculus
13	434	25.0	261	11	Q8K2L3	Q8k2l3 mus musculus
14	184.5	10.6	923	13	Q9QFX6	Q9qfx6 brachydanio
15	184.5	10.6	923	13	Q8AXP1	Q8axp1 brachydanio
16	182	10.5	691	13	O57658	O57658 gallus gall

17	180	10.4	34	11	Q99JM4	Q99jm4 mus musculus
18	176	10.1	977	13	Q91925	Q91925 xenopus lae
19	173.5	10.0	3623	4	O60494	O60494 homo sapien
20	172	9.9	1012	11	Q9WVM6	Q9wvm6 mus musculus
21	171	9.9	735	13	O57381	O57381 xenopus lae
22	171	9.9	926	4	Q9UQ00	Q9uq00 homo sapien
23	171	9.9	1015	4	Q9Y6L7	Q9y6l7 homo sapien
24	169	9.7	241	11	Q9Z135	Q9z135 rattus norv
25	168	9.7	3623	11	O70244	O70244 rattus norv
26	164.5	9.5	145	11	Q8BP20	Q8bp20 mus musculus
27	164.5	9.5	926	11	Q8QZY7	Q8qzy7 mus musculus
28	163.5	9.4	555	4	Q9H2E2	Q9h2e2 homo sapien
29	163.5	9.4	901	4	Q9H2E4	Q9h2e4 homo sapien
30	163.5	9.4	901	4	Q9H2D5	Q9h2d5 homo sapien
31	163.5	9.4	906	4	Q9H2D4	Q9h2d4 homo sapien
32	163.5	9.4	906	4	Q9H2E3	Q9h2e3 homo sapien
33	163.5	9.4	921	11	Q9QX38	Q9qx38 rattus norv
34	160	9.2	1007	13	Q8J128	O8j128 xenopus lae
35	160	9.2	3620	6	Q9TU53	Q9tu53 canis famil
36	158.5	9.1	609	4	Q96190	Q96190 homo sapien
37	158.5	9.1	644	4	Q961H5	Q961h5 homo sapien
38	158.5	9.1	704	4	Q9H2E1	Q9h2e1 homo sapien
39	157.5	9.1	919	13	Q8UVR0	Q8uvr0 gallus gall
40	157.5	9.1	936	13	Q8UVQ9	Q8uvq9 gallus gall
41	154	8.9	1008	13	Q9DER7	Q9der7 gallus gall
42	153	8.8	415	4	Q9UKZ9	Q9ukz9 homo sapien
43	153	8.8	1019	13	O57382	O57382 xenopus lae
44	151.5	8.7	326	11	Q91ZE4	Q91ze4 rattus norv
45	151	8.7	276	4	Q9BRH3	Q9brh3 homo sapien

ALIGNMENTS

RESULT 1

ID	Q9NRA1	PRELIMINARY;	PRT;	345 AA.
AC	Q9NRA1;			
DT	01-OCT-2000	(TRENBLrel. 15, Created)		
DT	01-OCT-2000	(TRENBLrel. 15, Last sequence update)		
DT	01-MAR-2003	(TRENBLrel. 23, Last annotation update)		
DE	Platelet-derived growth factor C.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung;			
RX	MEDLINE=20268201; PubMed=10806482;			
RA	Li X., Ponten A., Aase K., Karlsson L., Abramsson A., Uutela M.,			
RA	Backstrom G., Hellstrom M., Boström H., Li H., Soriano P.,			
RA	Betscholtz C., Heidin C.-H., Alitalo K., Ostman A., Eriksson U.,			
RT	"PDGF-C is a new protease-activated ligand for the PDGF alpha-			
RT	receptor.";			
RL	Nat. Cell Biol. 2:302-309(2000).			
CC	-!- SIMILARITY: CONTAINS 1 CUB DOMAIN.			
DR	EMBL; AF244813; AAF80597.1; -			
DR	Genew; HGNC:8801; PDGFC			
DR	InterPro; IPR000859; CUB_domain.			
DR	InterPro; IPR000072; PD_growth_factor.			
DR	Pfam; PF00431; CUB; 1.			
DR	Pfam; PF00341; PDGF; 1.			
DR	SMART; SM00042; CUB; 1.			
DR	SMART; SM00141; PDGF; 1.			
DR	PROSITE; PS01180; CUB; 1.			
DR	PROSITE; PS0278; PDGF_2; 1.			
SQ	SEQUENCE 345 AA; 39043 MW; 590889CEA55CC5EA CRC64;			

Query Match 99.7%; Score 1728; DB 4; Length 345;  
Best Local Similarity 100.0%; Pred.No. 1.4e-161; Indels 0; Gaps 0;  
Matches 317; Conservative 0; Mismatches 0;

```
QY 2 KFQSSNKEQNGVODPOHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMQIOL 61
Db 29 KFQSSNKEQNGVODPOHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMQIOL 88
QY 62 TFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE 121
Db 89 TFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE 148
QY 122 YFPSEPGFCIHYNIMVPOFTAVSPSVLPSPSALPDLNLNNAITAFSTLEDLIRYLEPERW 181
Db 149 YFPSEPGFCIHYNIMVPOFTAVSPSVLPSPSALPDLNLNNAITAFSTLEDLIRYLEPERW 208
QY 182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLITTEEVRLYSTPRNFSVSIREELKRTDT 241
Db 209 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLITTEEVRLYSTPRNFSVSIREELKRTDT 268
QY 242 IFWPGCLLVKRCGGNCACCLHNCNECQCVPKSVTKKYHEVLQLRPKTVGRGLHKSILTDA 301
Db 269 IFWPGCLLVKRCGGNCACCLHNCNECQCVPKSVTKKYHEVLQLRPKTVGRGLHKSILTDA 328
QY 302 LEHHEECDCVCRGSGTG 318
Db 329 LEHHEECDCVCRGSGTG 345
RESULT 2
Q9UL22 PRELIMINARY; PRT; 345 AA.
AC Q9UL22;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Secretory growth factor-like protein FALLOTEIN (SPINAL CORD-derived
DE growth factor) (Platelet-derived growth factor C).
GN HSCDGF OR PDGFC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Tsai Y.-J., Lee R.K.-K., Lin S.P.;
RA "Fallotein, a novel growth factor like gene identified in human
RT uterus.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20317014; PubMed=10858496;
RA Hamada T., Ui-Tei K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SCDGF, is a unique
RT member of the PDGF/VEGF family.";
RA FEBS Lett. 475:97-102(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21347863; PubMed=11297552;
RA Gilbertson D.G., Duff M.B., West J.W., Kelly J.D., Sheppard P.O.,
RA Hofstrand P.D., Gao Z., Shoemaker K., Bukowski T.R., Moore M.,
RA Feldhaus A.L., Humes J.M., Palmer T.E., Hart C.E.;
RT "Platelet-derived Growth Factor C (PDGF-C), a Novel Growth Factor That
RT Binds to PDGF alpha and beta Receptor.";
RL J. Biol. Chem. 276:27406-27414(2001).
CC -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR ENBL; AF091434; AAF00049.1; -.
DR ENBL; AB033831; BAB03266.1; -.
DR ENBL; AF260738; AAK51637.1; -.
DR InterPro; IPR000859; CUB domain.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
```

```
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF 2; 1.
SQ SEQUENCE 345 AA; 39029 MW; CDE9B51F40633E78 CRC64;
Query Match 99.7%; Score 1728; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 1.4e-161;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 KFQSSNKEQNGVODPOHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMQIOL 61
Db 29 KFQSSNKEQNGVODPOHERIITVSTNGSIHSPRPHTYPRNTVLVWRLVAEENVMQIOL 88
QY 62 TFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE 121
Db 89 TFDERFGLDEPDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE 148
QY 122 YFPSEPGFCIHYNIMVPOFTAVSPSVLPSPSALPDLNLNNAITAFSTLEDLIRYLEPERW 181
Db 149 YFPSEPGFCIHYNIMVPOFTAVSPSVLPSPSALPDLNLNNAITAFSTLEDLIRYLEPERW 208
QY 182 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLITTEEVRLYSTPRNFSVSIREELKRTDT 241
Db 209 QLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLITTEEVRLYSTPRNFSVSIREELKRTDT 268
QY 242 IFWPGCLLVKRCGGNCACCLHNCNECQCVPKSVTKKYHEVLQLRPKTVGRGLHKSILTDA 301
Db 269 IFWPGCLLVKRCGGNCACCLHNCNECQCVPKSVTKKYHEVLQLRPKTVGRGLHKSILTDA 328
QY 302 LEHHEECDCVCRGSGTG 318
Db 329 LEHHEECDCVCRGSGTG 345
RESULT 3
Q9QY71 PRELIMINARY; PRT; 345 AA.
AC Q9QY71;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Fallotein (Platelet-derived growth factor C).
GN PDGFC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Tsai Y.-J., Lee R.K.-K., Chen Y.-H., Lin S.-P., Cheng W.T.-K.;
RT "cDNA Cloning of fallotein from mouse ovary.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Gao Z., Hart C., Piddington C., Sheppard P., Shoemaker K.,
RA Gilbertson D., West J., O'Hara P.J.;
RT "Platelet-derived growth factor C (PDGF-C), a novel growth factor that
RT binds to PDGF alpha receptor.";
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
CC -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR ENBL; AF117608; AAF22516.1; -.
DR ENBL; AF266467; AAK58566.1; -.
DR ENBL; AK033734; BAC28455.1; -.

```

QY	122	YFPSEPGFCIHYNIMVMPQTEAVPSVLPPSALPLDLINNAITAFSTLEDLIRYLEPERW	181
Db	149	YFPSEPGFCIHYSIIMPQVTEITSPSVLPSSLSLDLNNAVTAFSTLEELIRYLEPDRW	208
QY	182	QLDLEDLYRPTWQLLGKAFVFGKRSVVDLNLTEEVRLYSCTPRNFSVSIREELKRTDT	241
Db	209	QVDLDSLYRPTWQLLGKAFVFGKRSVVDLNLTEEVRLYSCTPRNFSVSIREELKRTDT	268
QY	242	IFWPGCLLVKRCGGNCACCLHNCNECCQVPSVKTKYKHEVQLRPKTVGVRGLHKS LTDVA	301
Db	269	IFWPGCLLVKRCGGNCACCLHNCNECCQVPSVKTKYKHEVQLRPKTVGVRGLHKS LTDVA	328
QY	302	LEHHBECDCVCRGSTGG 318	
Db	329	LEHHBECDCVCRGNAGG 345	
RESULT 5			
QY	ID	Q9EQX6 PRELIMINARY; PRF; 345 AA.	
QY	AC	Q9EQX6; 01-MAR-2001 (T-EMBLrel. 16, Created)	
QY	DT	01-MAR-2001 (T-EMBLrel. 16, Last sequence update)	
QY	DT	01-MAR-2003 (T-EMBLrel. 23, Last annotation update)	
QY	DE	Spinal cord-derived growth factor.	
QY	GN	RSCDGF.	
QY	OS	Rattus norvegicus (Rat).	
QY	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
QY	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
QY	OX	NCBI_TaxID=10116;	
QY	RN	[1]	
QY	RP	SEQUENCE FROM N.A.	
QY	RC	STRAIN=Wistar; TISSUE=Kidney;	
QY	RX	MEDLINE=21092670; PubMed=11162582;	
QY	RA	Hamada T., Ui-Tei K., Imaki J., Miyata Y.;	
QY	RT	"Molecular Cloning of SCDF-B, a Novel Growth Factor Homologous to	
QY	RT	SCDGF/PDGF-C/fallosein.";	
QY	RL	Biochem. Biophys. Res. Commun. 280:733-737(2001).	
QY	CC	-1- SIMILARITY: CONTAINS 1 CUB DOMAIN.	
QY	DR	EMBL; AB033830; BAB1969.1; -.	
QY	DR	InterPro; IPR000859; CUB domain.	
QY	DR	InterPro; IPR000072; PD_growth_factor.	
QY	DR	Pfam; PF00431; CUB; 1.	
QY	DR	Pfam; PF00341; PDGF; 1.	
QY	DR	SMART; SM00042; CUB; 1.	
QY	DR	SMART; SM00141; PDGF; 1.	
QY	DR	PROSITE; PS01180; CUB; 1.	
QY	DR	PROSITE; PS0278; PDGF 2; 1.	
QY	SQ	SEQUENCE 345 AA; 38734 MW; F296DA6E9B765D10 CRC64;	
Query Match 88.9%; Score 1541; DB 11; Length 345;			
Best Local Similarity 85.8%; Pred. No. 3.6e-143; Indels 0; Gaps 0;			
Matches 272; Conservative 28; Mismatches 17;			
QY	2	KFOFSSNKEQNGVQDPOHERIITVSTNGSIHSPRPFTYPRNTVLVRLVAEENVIQL	61
Db	29	KLQSSNKEQNGVQDPRHVRVTISNGSIHSPRPFTYPRNTVLVRLVAEENVIQL	88
QY	62	TFDERFGLDEDDICKYDFVEVEEPPSDGTLGRWCGSGTPGKQISKGNQIRIRFVSD	121
Db	89	TFDERFGLDEDDICKYDFVEVEEPPSDGTLGRWCGSGTPGKQISKGNQIRIRFVSD	148
QY	122	YFPSEPGFCIHYNIMVMPQTEAVPSVLPPSALPLDLINNAITAFSTLEDLIRYLEPERW	181
Db	149	YFPSEPGFCIHYSIIMPQVTEITSPSVLPSSLSLDLNNAVTAFSTLEELIRYLEPDRW	208
QY	182	QLDLEDLYRPTWQLLGKAFVFGKRSVVDLNLTEEVRLYSCTPRNFSVSIREELKRTDT	241
Db	209	QVDLDSLYRPTWQLLGKAFVFGKRSVVDLNLTEEVRLYSCTPRNFSVSIREELKRTDT	268
QY	242	IFWPGCLLVKRCGGNCACCLHNCNECCQVPSVKTKYKHEVQLRPKTVGVRGLHKS LTDVA	301

```
Db 269 IFWPGCLLVKRCGGNCACCLHNCNECQVPRKVTYKKYHEVLQLRPKIGVKGHLKSLTDVA 328
QY 302 LEHHECDCVCRGSTGG 318
Db 329 LEHHECDCVCRGNTEG 345

RESULT 6
Q9JHV8 PRELIMINARY; PRT; 345 AA.
AC Q9JHV8;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Platelet-derived growth factor C.
GN PDGFC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss-Webster/NIH;
RX MEDLINE=20417814; PubMed=10960785;
RA Ding H., Wu X., Kim I., Tam P.L., Koh G.Y., Nagy A.;
RT "The mouse pdgfc gene: dynamic expression in embryonic tissues during
RT organogenesis."
RL Mech. Dev. 96:209-213 (2000).
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AF286725; AAF91483.1; -.
DR MGD; MGI:1859631; pdgfc.
DR InterPro; IPR000859; CUB_domain.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF 2; 1.
SQ SEQUENCE 345 AA; 38886 MW; FA1486BED6D362F8 CRC64;

Query Match 88.2%; Score 1530; DB 11; Length 345;
Best Local Similarity 85.8%; Pred. No. 4.4e-142;
Matches 272; Conservative 26; Mismatches 19; Indels 0; Gaps 0;

QY 2 KFPSSNKEQGVDPQHERITVTSGSIHSPRPPTYPRTVLMVRLVAVENVMVQL 61
Db 29 KLPSSNKEQGVDPQHERITVTSGSIHSPRPPTYPRTVLMVRLVAVENVMVQL 88
QY 62 TDFERFGLDEPDDICKYDFVEVEEPPSDGTLGRWCGSGTVPGKQISKGNQIRIRFVSD 121
Db 89 TDFERFGLDEPDDICKYDFVEVEEPPSDGTLGRWCGSGTVPGKQISKGNQIRIRFVSD 148
QY 122 YFPSEPGCIHYNIIMPQVETTSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181
Db 149 YFPSEPGCIHYNIIMPQVETTSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208
QY 182 QLDLEDLYRPTWQLLGKAFVFGKSRVVDLNLLEEVRLYSCTPRNFSVIREELKRTDT 241
Db 209 QVLDLSLYKPTWQLLGKAFVFGKSRVVDLNLLEEVRLYSCTPRNFSVIREELKRTDT 268
QY 242 IFWPGCLLVKRCGGNCACCLHNCNECQVPSKVTKYKHYEVLQLRPKTVGRGLHSLTDVA 301
Db 269 RFWPGCLLVKRCGGNCACCLHNCNECQVPRKVTYKKYHEVLQLRPKTVGRGLHSLTDVA 328

QY 302 LEHHECDCVCRGSTGG 318
Db 329 LEHHECDCVCRGNAGG 345

RESULT 7
Q9I946 PRELIMINARY; PRT; 345 AA.
ID Q9I946
AC Q9I946;
```

```
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Spinal cord-derived growth factor.
GN SCDGF.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=white leghorn; TISSUE=Spinal cord;
RX MEDLINE=20317014; PubMed=10858496;
RA Hamada T., Ui-Tei K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SCDGF, is a unique
RT member of the PDGF/VEGF family."
RL FEBS Lett. 475:97-102 (2000).
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AB033829; BAB03265.1; -.
DR InterPro; IPR000859; CUB_domain.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS50278; PDGF 2; 1.
SQ SEQUENCE 345 AA; 38940 MW; 97ACEA992BF5128C CRC64;

Query Match 87.9%; Score 1524; DB 13; Length 345;
Best Local Similarity 84.9%; Pred. No. 1.7e-141;
Matches 269; Conservative 28; Mismatches 20; Indels 0; Gaps 0;

QY 2 KFPSSNKEQGVDPQHERITVTSGSIHSPRPPTYPRTVLMVRLVAVENVMVQL 61
Db 29 KFPSSNKEQGVDPQHERITVTSGSIHSPRPPTYPRTVLMVRLVAVENVMVQL 88
QY 62 TDFERFGLDEPDDICKYDFVEVEEPPSDGTLGRWCGSGTVPGKQISKGNQIRIRFVSD 121
Db 89 TDFERFGLDEPDDICKYDFVEVEEPPSDGTLGRWCGSGTVPGKQISKGNQIRIRFVSD 148
QY 122 YFPSEPGCIHYNIIMPQVETTSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 181
Db 149 YFPSEPGCIHYNIIMPQVETTSVLPSPALPLDLNNAITAFSTLEDLIRYLEPERW 208
QY 182 QLDLEDLYRPTWQLLGKAFVFGKSRVVDLNLLEEVRLYSCTPRNFSVIREELKRTDT 241
Db 209 QLDLEDLYRPTWQLLGKAFVFGKSRVVDLNLLEEVRLYSCTPRNFSVIREELKRTDT 268
QY 242 IFWPGCLLVKRCGGNCACCLHNCNECQVPSKVTKYKHYEVLQLRPKTVGRGLHSLTDVA 301
Db 269 IFWPGCLLVKRCGGNCACCLHNCNECQVPRKVTYKKYHEVLQLRPKTVGRGLHSLTDVA 328

QY 302 LEHHECDCVCRGSTGG 318
Db 329 LEHHECDCVCKGNSEG 345

RESULT 8
Q8K429 PRELIMINARY; PRT; 258 AA.
ID Q8K429
AC Q8K429;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Platelet-derived growth factor C (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
```

```

RC STRAIN=Sprague-Dawley; TISSUE=Skin;
RA Brown S.A., Coberly D.M., Rohrich R.R., Chao J.J.;
RT "Platelet Derived Growth Factor C (PDGF-C) Expression in Wound
RL Healing.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AF08348; AAM47265.1; -.
DR InterPro; IPR000859; CUB domain.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
FT NON TER 1 258
FT SEQUENCE 258 AA; 29255 MW; 88625B989FC3F8B CRC64;
SQ
Query Match 72.7%; Score 1260; DB 11; Length 258;
Best Local Similarity 85.6%; Pred. No. 1.1e-115;
Matches 220; Conservative 25; Mismatches 12; Indels 0; Gaps 0;
QY 15 QDPOHERITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVWVQLTDFRFGLEDPED 74
DB 1 QDPRHERVVTISGNSIHSPRPHTYPRNTVLVRLVAEENVWVQLTDFRFGLEDPED 60
QY 75 DICKYDFVEVEPEPDDGTTILGRWCGSGTVPGKQISKGNOIRIRFVSDYFPPSEPGFCIHYN 134
DB 61 DLCKYDFVEVEPEPDDGTVLGRWCGSGTVPGKQISKGNOIRIRFVSDYFPPSEPGFCIHY 120
QY 135 IVMQFTFAVSPVLPPSALPIDLLNNAITAFSTLEDLIRVLEPERWQDLEDLYRPTWQ 194
DB 121 IIMQVTEFTSPVLPSPSALPIDLLNNAITAFSTVEELIRLEPRWQIDLSLYKPTWP 180
QY 195 LLGKAFVGRKSRVVDNLLTVEVRLYSCTRNFVSVSIREELKRTDTIFWPGCLLVKRCG 254
DB 181 LLGKAFVGRKSKAVNLLNLLKEVKLYSCTRNFVSVSIREELKRTDTIFWPGCLLVKRCG 240
QY 255 GNCACCLHNCQCQVP 271
DB 241 GNCACCLHNCQCQVP 257
RESULT 9
Q9GZP0 PRELIMINARY; PRT; 370 AA.
ID Q9GZP0
AC Q9GZP0;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 23, Last sequence update)
DE SPINAL CORD-derived growth factor-B (MSTP036) (IRIS-expressed growth
DE factor long form) (platelet-derived growth factor D).
GN HSCDGF-B OR IEGF OR PDGFD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hamada T., Ui-Tei K., Inaki J., Miyata Y.;
RT "Molecular Cloning of SCDGF-B, a Novel Growth Factor Homologous to
RT SCDGF/PDGF-C/fallotenein.";
RL Biochem. Biophys. Res. Commun. 0:0-0(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RA Liu B., Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Liu S.,
RA Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J.,
RA Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q.,
RA Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Iris;

```

```

RA Wistow G.;
RT "Iris-expressed Growth Factor (IEGF).";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX PubMed=11331881;
RA Bergsten B., Eriksson U.;
RA Alitalo K., Ukkola M., Li X., Pietras K., Ostman A., Heldin C.H.,
RA "PDGF-D is a specific, protease-activated ligand for the PDGF beta-
RT receptor.";
RL Nat. Cell Biol. 3:512-516(2001).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=2123380; PubMed=11331882;
RA LaRoche W.J., Jeffers M., McDonald W.F., Chillakuru R.A.,
RA Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C.,
RA Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shinkets J.,
RA Shinkets R.A., Rothberg J.M., Lichtenstein H.S.;
RA "PDGF D, A Novel Protease-Activated Growth Factor.";
RL Nat. Cell Biol. 3:517-521(2001).
CC -I- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AB033832; BAB18903.1; -.
DR EMBL; AF113216; AAG39287.1; -.
DR EMBL; AY027517; AAK20081.1; -.
DR EMBL; AF336376; AAK56136.1; -.
DR EMBL; AF335584; AAK38840.1; -.
DR InterPro; IPR000859; CUB domain.
DR InterPro; IPR000072; PD_growth_factor.
DR InterPro; IPR000531; TonB_boxC.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF_2; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC 1; 1.
SQ SEQUENCE 370 AA; 42848 MW; D387F485E7BB7674 CRC64;
Query Match 42.7%; Score 741; DB 4; Length 370;
Best Local Similarity 46.6%; Pred. No. 2.2e-64;
Matches 153; Conservative 52; Mismatches 93; Indels 30; Gaps 9;
QY 10 EQNGVQD-PQHERITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVWVQLTDFRFG 68
DB 42 ESNHITDLYRRDETQVKGNGYVQSPFNLLTWRLLHS-QENTRIQLVFDNQFG 100
QY 69 LEDPDDICKYDFVEVEPEPDDGTT--ILGRWCGSGTVPGKQISKGNOIRIRFVSDYFPPSE 126
DB 101 LEEAENDICRVDYFVEVEDEISETSTIIRGWCCHKEVPPRIKSRWQIKITFKSDDYFVAK 160
QY 127 PFCIHYNIYVMPQFTEAV-----SPSVLPSPSALPIDLLNNAITAFS 167
DB 161 PGFKIYSL-LSDFPAAAASETNWSVTSSISGVSYNSPSVTDPT-LIADALDKIAED 218
QY 168 TLEDLIRVLEPERWQDLEDLYRPTWQLLGKAFVGRKSRVVDNLLTVEVRLYSCTRN 227
DB 219 TVEDLLKYFNPESWQEDLENMYLDFPRYGRSY-HDRKSK-VLDRLNDADKRYSCTRN 276
QY 228 FSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCQCQVPKSVTKKYHEVLQLRP- 286
DB 277 YSVNIREELKANVFFPRCLLVQRCGNGCGGTWNRSCTNSGKTVKKYHEVLQFEPG 336
QY 287 --KTGVRGLHKSITDVALEHHEECDCVC 312
DB 337 HIKRGRKTAVALVDIQLDHERCDDIC 364
RESULT 10
Q9BHW5 PRELIMINARY; PRT; 364 AA.
ID Q9BHW5
AC Q9BHW5;
DT 01-JUN-2001 (TREMELrel. 17, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)

```



DE	Iris-expressed growth factor short form (Spinal cord-derived growth factor-B).
GN	IEGF.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RN	SEQUENCE FROM N.A.
RP	TISSUE=Iris;
RC	TISSUE=Iris;
RA	Strausberg R.;
RL	Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AY027518; AAK20082.1; -.
DR	EMBL; BC030645; AAH30645.1; -.
DR	InterPro; IPR000859; CUB domain.
DR	InterPro; IPR00072; PD_growth_factor.
DR	InterPro; IPR00531; TonB_boxC.
DR	Pfam; PF00431; CUB; 1.
DR	PROSITE; PS01180; CUB; 1.
DR	PROSITE; PS0278; PDGF 2; 1.
DR	PROSITE; PS00430; TONB_DEPENDENT_REC 1; 1.
SQ	SEQUENCE 364 AA; 42166 MW; 245C53E8DDAE9EAC CRC64;
Query Match 42.6%; Score 739.5; DB 4; Length 364;	
Best Local Similarity 47.0%; Pred. No. 3.1e-64;	
Matches 150; Conservative 51; Mismatches 89; Indels 29; Gaps 8	
Qy	18 QHERIITVSTGSIHSPRPHTYPTVTLVRLVAEENVWTLQTFDERFGLDEPDDIC 77
Db	45 RRDETQVKGNGYVQSPFPFNSYPRNLLTWLHS-QENTRIQLVFDNQFGLAEANDIC 103
Qy	78 KYDFVEVEPSDGT--ILGRWCGSGTVPKQISKGNQIRIRFVSDEYPPSEPGFCIHVNI 135
Db	104 RYDFVEVEDISETSIIRGRWCGHKEVPPRIKSRTNQIKITPKSDDYFVAKPGFKIYSL 163
Qy	136 VMPOFTEAV-----SPSVLPSPALPLDLNNAITAFSTLEDLIRYL 176
Db	164 -LEDFOPAASATNWESVTSSIGSVNSPSTDEP-LIADALDKKIAEFDIVEDULKYF 221
Qy	177 EPESWQLDLEDYRPTWQLLQKAFVGRKSRVVDLNLTLTEEVRLYSCTPRNFVSIREEL 236
Db	222 NPESWQEDLNNYLDTPYRGESY-HDRKSK-VLDRLNDDAKRYSCTPRNSVNIRESL 279
Qy	237 KRTDTIFWPGCLLVKRCGNCACCLHNCCEQCVSKVTKKHYEVLQLRP---KTGVRGL 293
Db	280 KLANVVFPRCLLVQRCGNCOCGTWNRSCTNSGKTKVKYHEVLQFEPFGHKKRGRAK 339
Qy	294 HKSLTDVALEHHEECDCVC 312
Db	340 TMALVDIQLDHHRCDCIC 358
RESULT 11	
Q9EQT1	PRELIMINARY; PRT; 370 AA.
AC	Q9EQT1;
DT	01-MAR-'2001 (TREMBLrel. 16, Created)
DT	01-MAR-'2001 (TREMBLrel. 16, Last sequence update)
DT	01-MAR-'2003 (TREMBLrel. 23, Last annotation update)
DE	Spinal-cord derived growth factor-B.
GN	RSCDGF-B.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX	NCBI_TaxID=10116;
RN	[1]
RP	SEQUENCE FROM N.A.

RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,  
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,  
RA Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,  
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,  
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ono M.,  
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,  
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,  
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
RA Muramatsu M., Hayashizaki Y.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
[3]  
RN  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Body;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RA The RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
[4]  
RN  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Body;  
RX MEDLINE=21085660; PubMed=11217851;  
RA RIKEN FANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
[5]  
RN  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Body;  
RX MEDLINE=99279253; PubMed=10349636;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44(1999).  
[6]  
RN  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Body;  
RX MEDLINE=20499374; PubMed=11042159;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
[7]  
RN  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Body;  
RX MEDLINE=20530913; PubMed=11076861;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsumai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara B., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
CC -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
DR EMBL; AF355583; AAK38839.1; -.  
DR EMBL; AK003359; BAB2735.2; -.  
DR MGD; MGI:1919035; Pdgd.  
DR InterPro; IPR000859; CUB domain.  
DR InterPro; IPR000072; PD\_growth\_factor.  
DR Pfam; PF00431; CUB; 1.  
DR SMART; SM00042; CUB; 1.  
DR SMART; SM00141; PDGF; 1.  
DR PROSITE; PS01180; CUB; 1.  
DR PROSITE; PS02078; PDGF 2; 1.  
SQ SEQUENCE 370 AA; 42809 MW; 9E80B4CF6813BFBE CRC64;  
Query Match 42.4%; Score 736; DB 11; Length 370;  
Best Local Similarity 45.6%; Pred. No. 6.9e-64;

Matches 149; Conservative 56; Mismatches 94; Indels 28; Gaps 8;  
QY 10 EONGVQD-PQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVMQLTDFDRFG 68  
Db 42 ESNHLLTDLYQREENIQVTSNGHVQSPRPNSYPRNLLLTWMLRS-QBKTRIQLSFDHQFG 100  
QY 69 LEDPEDDICKYDFVEVEPSDGT--ILGRWCGSGTVPGKQISKGNOIRIRFVSDEYFPE 126  
Db 101 LEEAENDICRYDFVEVEVSESTVVRGRCWCGHKBEIPRITSRTNQIKITFKSDDYFVAK 160  
QY 127 PGFCIHYNIVMPQTEAV-----SPSVLPSPALPLDLLNNAITAFST 168  
Db 161 PGFKIYYSFVEDFQPEAASETNWSYSSFGVSHSFTDPT-LTADALDKTVAEDT 219  
QY 169 LEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLTEEVLYSCTPRNF 228  
Db 220 VEDLLKHFNFVSWQDDLENLYLDTPHYGRSY-HDRKSK-VDLRLNDDVKRYSCTPRNH 277  
QY 229 SVSTREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPSKVTKKHYEVLQLRP-- 286  
Db 278 SVNLREELKLTNAVFFPRCLLVQRCGNCGCGTVNWKSCCTCSSGKTVKKYHEVLKFEFGH 337  
QY 287 -KTGVRGLHKS LTDVALEHHEECDCVC 312  
Db 338 FRRGKAKNMALVDIQLDHERCDCIC 364  
RESULT 13  
Q8K2L3 PRELIMINARY; PRT; 261 AA.  
ID Q8K2L3  
AC Q8K2L3;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Similar to platelet-derived growth factor, D polypeptide.  
GN PDGFD.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
DR EMBL; BC030896; AAK30896.1; -.  
DR MGD; MGI:1919035; Pdgd.  
DR InterPro; IPR000859; CUB\_domain.  
DR Pfam; PF00431; CUB; 1.  
DR SMART; SM00042; CUB; 1.  
DR PROSITE; PS01180; CUB; 1.  
SQ SEQUENCE 261 AA; 30228 MW; 2ERC3F6373A52D09 CRC64;  
Query Match 25.0%; Score 434; DB 11; Length 261;  
Best Local Similarity 41.7%; Pred. No. 2.3e-34;  
Matches 93; Conservative 42; Mismatches 64; Indels 24; Gaps 6;  
QY 10 EONGVQD-PQHERIITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVMQLTDFDRFG 68  
Db 42 ESNHLLTDLYQREENIQVTSNGHVQSPRPNSYPRNLLLTWMLRS-QBKTRIQLSFDHQFG 100  
QY 69 LEDPEDDICKYDFVEVEPSDGT--ILGRWCGSGTVPGKQISKGNOIRIRFVSDEYFPE 126  
Db 101 LEEAENDICRYDFVEVEVSESTVVRGRCWCGHKBEIPRITSRTNQIKITFKSDDYFVAK 160  
QY 127 PGFCIHYNIVMPQTEAV-----SPSVLPSPALPLDLLNNAITAFST 168  
Db 161 PGFKIYYSFVEDFQPEAASETNWSYSSFGVSHSFTDPT-LTADALDKTVAEDT 219  
QY 169 LEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKRSRVVDL 211  
Db 220 VEDLLKHFNFVSWQDDLENLYLDTPHYGRSY-HDRKSKGIEV 261

Search completed: November 25, 2003, 21:04:34  
Job time : 29.0774 secs

```

RESULT 14
Q8QFX6 PRELIMINARY; PRT; 923 AA.
Q8QFX6;
AC Q8QFX6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 23, Last annotation update)
DE Neuprolin-1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=7955;
[1]
SEQUENCE FROM N.A.
RP Lee P., Gotschi K., Davidson A., Mannix R., Zon L., Klagesbrun M.;
RT "Neuprolin-1 is required for normal vascular development and is a
RL mediator of VEGF-dependent angiogenesis in zebrafish.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
DR EMBL; AY064213; AAL40862.1; -.
DR InterPro; IPR000859; CUB_domain.
DR InterPro; IPR000421; FA58_C.
DR InterPro; IPR000998; MAM_domain.
DR Pfam; PF00754; F5_F8_type_C; 2.
DR Pfam; PF00629; MAM; 1.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00231; FA58C; 2.
DR SMART; SM00137; MAM; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01285; FA58C_1; 1.
DR PROSITE; PS01286; FA58C_2; 2.
DR PROSITE; PS00740; MAM_1; 1.
DR PROSITE; PS0060; MAM_2; 1.
KW Glycoprotein; Receptor; Transmembrane.
SQ
SEQUENCE 923 AA; 102492 MW; 2ED84B129AA92B2D CRC64;

Query Match 10.6%; Score 184.5; DB 13; Length 923;
Best Local Similarity 30.9%; Pred. No. 4.4e-09;
Matches 60; Conservative 26; Mismatches 87; Indels 21; Gaps 7;

Qy 23 ITVSTNGSIHSRPHPHYPRNTVLVRLVAEENWVLTEDERFGLDEPDDEICKYDFV 82
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 29 IRTSANYLTSFGYFVSYPQSKCIWVITAFQPNQLINFNPHFDLEDE---CKDYV 85
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 83 EVEEPPSD--GVILGRWGSGVPGQISKGNOIRFVSDYVFSEPGFCIHYNVMP-- 138
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 86 EVROGVDENGGVGLGKICK--IAPFVVSNGQLPIKFVSD-YETHGAGFSRYELFKTGP 143
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 139 ---QFTEAVSPSLVPPSALEFLDNLINNAITAFSTLEDLIRYLEPFRWQDLEDLYRPTWQ 194
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 144 ECSRNFTS--SSGVIKSPGFPEKYPNNLDCFTFMIFAPQMSIVLEFSEFELEPDTPQ--- 198
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 195 LLGKAFVFGKRSRV 208
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 199 ---PAGVFCRYDRL 209
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 15
Q8AXP1 PRELIMINARY; PRT; 923 AA.
ID ID Q8AXP1
AC Q8AXP1
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Neuprolin-1.
OS Neop-1.
GN Neop-1.

```

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: November 25, 2003, 22:28:25 ; Search time 3642.09 Seconds  
(without alignments)  
16556.656 Million cell updates/sec

Title: US-09-852-209A-6  
Perfect score: 1474  
Sequence: 1 caccctggagacacagaag.....aatcacaaagcactgcacgc 1474

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481336 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:  
1: gb\_ba.\*  
2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*  
15: em\_ba.\*  
16: em\_fun.\*  
17: em\_hum.\*  
18: em\_in.\*  
19: em\_mu.\*  
20: em\_om.\*  
21: em\_or.\*  
22: em\_ov.\*  
23: em\_pat.\*  
24: em\_ph.\*  
25: em\_pl.\*  
26: em\_ro.\*  
27: em\_sts.\*  
28: em\_un.\*  
29: em\_vi.\*  
30: em\_htg\_hum.\*  
31: em\_htg\_inv.\*  
32: em\_htg\_other.\*  
33: em\_htg\_mus.\*  
34: em\_htg\_pln.\*  
35: em\_htg\_rod.\*  
36: em\_htg\_mam.\*  
37: em\_htg\_vrt.\*  
38: em\_sy.\*  
39: em\_htgo\_hum.\*  
40: em\_htgo\_mus.\*  
41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1444.8	98.0	2692	10	AF117608	AF117608 Mus muscu
2	1444.8	98.0	3512	10	AF266467	AF266467 Mus muscu
3	1444.8	98.0	3571	6	AR267281	AR267281 Sequence
4	1444.8	98.0	3571	6	AR282985	AR282985 Sequence
5	1444.8	98.0	3571	6	AX044520	AX044520 Sequence
6	1444.8	98.0	3571	6	AX118787	AX118787 Sequence
7	1435.2	97.4	2731	10	BC037696	BC037696 Mus muscu
8	1028.4	69.8	1038	10	AF286725	AF286725 Mus muscu
9	1020.8	69.3	1116	10	AB033830	AB033830 Rattus no
10	914.2	62.0	1817	9	AB033831	AB033831 Homo sapi
11	914.2	62.0	2825	6	AR210624	AR210624 Sequence
12	914.2	62.0	2825	6	AR232022	AR232022 Sequence
13	914.2	62.0	2849	6	AX047650	AX047650 Sequence
14	914.2	62.0	2849	6	AX391260	AX391260 Sequence
15	914.2	62.0	2849	6	AX464152	AX464152 Sequence
16	914.2	62.0	3007	6	AX234498	AX234498 Sequence
17	914.2	62.0	3007	9	AF091434	AF091434 Homo sapi
18	888.2	60.3	2152	9	AF244813	AF244813 Homo sapi
19	882	59.8	1804	6	AX739931	AX739931 Sequence
20	882	59.8	1804	9	AF260738	AF260738 Homo sapi
21	878.8	59.6	1760	6	AR267280	AR267280 Sequence
22	878.8	59.6	1760	6	AR282949	AR282949 Sequence
23	878.8	59.6	1760	6	AX044518	AX044518 Sequence
24	878.8	59.6	1760	6	AX118785	AX118785 Sequence
25	828.6	56.2	1328	6	BD004757	BD004757 Novel VEG
26	828.6	56.2	1328	6	BD168832	BD168832 Antibody
27	776.4	52.7	1035	6	AX027935	AX027935 Sequence
28	745.8	50.6	1035	6	AR282992	AR282992 Sequence
29	730.8	49.6	774	10	AF508348	AF508348 Rattus no
30	662.4	44.9	1675	5	AB033829	AB033829 Gallus ga
31	660.8	44.8	1035	6	AR282950	AR282950 Sequence
32	519	35.2	918	6	AX119274	AX119274 Sequence
33	355.4	24.1	218449	10	AC122835	AC122835 Mus muscu
34	355.4	24.1	253348	2	AC132143	AC132143 Mus muscu
35	344.8	23.4	504	6	AX027960	AX027960 Sequence
36	343	23.3	1711	10	BC006027	BC006027 Mus muscu
37	283	19.2	110000	2	AC128488	Continuation (3 of
38	283	19.2	250731	2	AC105473	AC105473 Rattus no
39	280.8	19.1	452	6	BD109268	BD109268 EST and e
40	239.4	16.2	213970	2	AC097765	AC097765 Rattus no
41	239.4	16.2	222528	2	AC107118	AC107118 Rattus no
42	221.8	15.0	130754	9	AC093325	AC093325 Homo sapi
43	221.8	15.0	152779	2	AC015837	AC015837 Homo sapi
44	216.6	14.7	279	6	AX027968	AX027968 Sequence
45	216.6	14.7	279	6	AX027989	AX027989 Sequence

ALIGNMENTS

RESULT 1  
AF117608  
LOCUS AF117608 2692 bp mRNA linear ROD 02-JAN-2000  
DEFINITION Mus musculus fallotein mRNA, complete cds.  
ACCESSION AF117608  
VERSION AF117608.1 GI:6652867  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 2692)  
REFERENCE  
AUTHORS Tsai, Y.-J., Lee, R.K.-K., Chen, Y.-H., Lin, S.-P. and Cheng, W.T.-K.  
TITLE cDNA cloning of fallotein from mouse ovary  
JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2692)  
 AUTHORS Tsai, J.-J., Lee, R. K.-K., Chen, Y.-H., Lin, S.-P. and Cheng, W. T.-K.  
 TITLE Direct Submission  
 JOURNAL Submitted (03-JAN-1999) Medical Research, Mackay Memorial Hospital,  
 45 Min Sheng Road, Tamsui, Taipei 25115, Taiwan

FEATURES  
 source  
 1..2692  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /sex="female"  
 /tissue\_type="ovary"  
 /dev\_stage="adult"  
 198..1235  
 /note="putative secretory protein"  
 /codon\_start=1  
 /evidence=not experimental  
 /product="fallotekin"  
 /protein\_id="AAF22516.1"  
 /db\_xref="GI:6652868"  
 /translation="MLLLGLLTSALAGORTCTRAESNLSSKLOLSSDKQEVDP  
 RHERVTISNGSIHSPKPHPTPRNVLVRLVAVDENVRIOLEDFERGLEPDD  
 ICKYDFVEEEDPSVLGWSGTVPGKQSGHNRIRFVSDSTFPBPFCYHY  
 SIIMPQVETSPVLPSPSLDLNNVAFSTLEELIRYLELRYLDRQVLDLSYK  
 TWOLGKAFYLSKVKVNLMLLKEVKLYSCTPRNFSVIRBELKRTDTIFWPGCLL  
 VKRCGNACCLHNCNEQCVPRKVTKKYHEVLQLRPKTKVGLKLSLTDVALEHHEE  
 CDCVCRGNAGG"  
 polyA signal  
 2662..2667  
 BASE COUNT 754 a 576 c 617 g 745 t  
 ORIGIN

Query Match 98.0%; Score 1444.8; DB 10; Length 2692;  
 Best Local Similarity 99.4%; Pred. No. 0;  
 Matches 1460; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 2 ACCTGGAGACACAGAGGGCTCTAGGAAAATTTGGATGGGATATGTGGAACCTA 61  
 DB 5 AACTGGAGACACAGAGGGCTCTAGGAAAATTTGGATGGGATATGTGGAACCTA 64  
 QY 62 CCCTGGATCTCTGCTGCCAGAGCCGGCCAGGCGCTTCCACCCGAGCGAGCTTTCCC 121  
 DB 65 CCCTGGATCTCTGCTGCCAGAGCCGGCCAGGCGCTTCCACCCGAGCGAGCTTTCCC 124  
 QY 122 CGGCTGGCTGAGCTTGGAGTCTGCTCTCCAGTGCCTCCGCGGAGTGAGCCCTCG 181  
 DB 125 C-GGCTGGCTGAGCTTGGAGTCTGCTCTCCAGTGCCTCCGCGGAGTGAGCCCTCG 183  
 QY 182 CCCAGTCAGCAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCTCGGCGGCC 241  
 DB 184 CCCAGTCAGCAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCTCGGCGGCC 243  
 QY 242 AAGAACGGGACTCTGGCTCAGTCCACCTGAGCAGCAAGTTCAGCTCTCCAGCGACA 301  
 DB 244 AAGAACGGGACTCTGGCTCAGTCCACCTGAGCAGCAAGTTCAGCTCTCCAGCGACA 303  
 QY 302 AGGAACGAGACGAGTGCAAGATCCCGGCAATGAGAGTGTCACTATATCTGGTAATG 361  
 DB 304 AGGAACGAGACGAGTGCAAGATCCCGGCAATGAGAGTGTCACTATATCTGGTAATG 363  
 QY 362 GGAGCATCCAGCCCGAGTTTCTCATAGTACCCAGAAATATGCTGCTGGTGGGA 421  
 DB 364 GGAGCATCCAGCCCGAGTTTCTCATAGTACCCAGAAATATGCTGCTGGTGGGA 423  
 QY 422 GATTAGTTCAGTAGATAAATGTGCGGATCCAGCTGACATTTGATGAGAGATTTGGGC 481  
 DB 424 GATTAGTTCAGTAGATAAATGTGCGGATCCAGCTGACATTTGATGAGAGATTTGGGC 483  
 QY 482 TGGAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAGTTCAGGAGCCCAAGT 541  
 DB 484 TGGAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAGTTCAGGAGCCCAAGT 543  
 QY 542 ATGGAAGTGTTTAGGACGCTGGTGTGTTCTGGGACTGTGGCAAGACAGACTTCTA 601

544 ATGGAAGCGTTTTAGGACGCTGGTGGTCTGGGACTGTGGCAGGAAACAGACTTCTA 603  
 QY 602 AAGGAATCATATCAGATAAGATTGTATCTGATGAGTATTTTCCATCTGAACCCGGAT 661  
 DB 604 AAGGAATCATATCAGATAAGATTGTATCTGATGAGTATTTTCCATCTGAACCCGGAT 663  
 QY 662 TCTGCACTCACAAGTATCATGCCACAAGTCAAGAAACCAAGAGTCTTCTGGTGT 721  
 DB 664 TCTGCACTCACAAGTATCATGCCACAAGTCAAGAAACCAAGAGTCTTCTGGTGT 723  
 QY 722 TGGCCCTTCACTTTGTCTGATGAGCTCTGCAACATGCTGTGACTGCCTTCACTACCT 781  
 DB 724 TGGCCCTTCACTTTGTCTGATGAGCTCTGCAACATGCTGTGACTGCCTTCACTACCT 783  
 QY 782 TGAAGAGCTGATTTCGTAACCTAGAGCCAGATCGATGGCAGGTGGACTTGGACAGCTCT 841  
 DB 784 TGAAGAGCTGATTTCGTAACCTAGAGCCAGATCGATGGCAGGTGGACTTGGACAGCTCT 843  
 QY 842 ACAAGCCACATCGGAGCTTTTGGCAAGGCTTTCCTGTATGGGAAAAAAGCAAGTGG 901  
 DB 844 ACAAGCCACATCGGAGCTTTTGGCAAGGCTTTCCTGTATGGGAAAAAAGCAAGTGG 903  
 QY 902 TGAATCTGAATCTCTCAAGGAGAGGTAAACCTCTACAGCTGCACACCCCGGAATCTCT 961  
 DB 904 TGAATCTGAATCTCTCAAGGAGAGGTAAACCTCTACAGCTGCACACCCCGGAATCTCT 963  
 QY 962 CAGTGTCCATACCGGAAGAGCTAAAGAGGACAGATACCATATTTCTGGCCAGGTGTCTCC 1021  
 DB 964 CAGTGTCCATACCGGAAGAGCTAAAGAGGACAGATACCATATTTCTGGCCAGGTGTCTCC 1023  
 QY 1022 TGGTCAAGCGCTGTGGAGGAAAATTTGCTCTGTTGCTCTCCATATTTGCAATGAATGTCA 1081  
 DB 1024 TGGTCAAGCGCTGTGGAGGAAAATTTGCTCTGTTGCTCTCCATATTTGCAATGAATGTCA 1083  
 QY 1082 GTGTCCACCTGAAAGTTTACAAAAAGTACCATGAGTCTTTCAGTTGAGACCAAAAACCTG 1141  
 DB 1084 GTGTCCACCTGAAAGTTTACAAAAAGTACCATGAGTCTTTCAGTTGAGACCAAAAACCTG 1143  
 QY 1142 GAGTCAAGGATTTGCAATGCTCACTCACTGATGCTGTGGAAACACCAAGGAATGTG 1201  
 DB 1144 GAGTCAAGGATTTGCAATGCTCACTCACTGATGCTGTGGAAACACCAAGGAATGTG 1203  
 QY 1202 ACTGTGTGTAGAGGAAACGAGGAGGTAACTGTCAGCTTCTGAGCAGTGTAGCAGCAGTGTAG 1261  
 DB 1204 ACTGTGTGTAGAGGAAACGAGGAGGTAACTGTCAGCTTCTGAGCAGTGTAGCAGCAGTGTAG 1263  
 QY 1262 CACTGGCATTTGCTGTACCCCAAGCAACCTTTCATCCCAAGCAAGTGTGGCCGAGGG 1321  
 DB 1264 CACTGGCATTTGCTGTACCCCAAGCAACCTTTCATCCCAAGCAAGTGTGGCCGAGGG 1323  
 QY 1322 CTCTCAGCTGCTGATGCTGGCTATGTTAAGATCTTACTGCTCTCCAAACCAATTTCTCAG 1381  
 DB 1324 CTCTCAGCTGCTGATGCTGGCTATGTTAAGATCTTACTGCTCTCCAAACCAATTTCTCAG 1383  
 QY 1382 TTGTTTCTCAATAGCTTCTCCCTGAGGACTTCAAGTGTCTTCTAAGAGCAGGAGGC 1441  
 DB 1384 TTGTTTCTCAATAGCTTCTCCCTGAGGACTTCAAGTGTCTTCTAAGAGCAGGAGGC 1443  
 QY 1442 ACCAAGGAGTCAATCAAGAGCACTGC 1470  
 DB 1444 ACCAAGGAGTCAATCAAGAGCACTGC 1472

## RESULT 2

AF266467

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AF266467 3512 bp mRNA linear ROD 02-JUN-2001

Mus musculus platelet-derived growth factor C (Pdgfr) mRNA,

complete cds.

AF266467

AF266467.1 GI:14279331

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 3512)

REFERENCE AUTHORS Gao,Z., Hart,C., Piddington,C., Sheppard,P., Shoemaker,K., Gilbertson,D., West,J. and O'Hara,P.J. Platelet-derived growth factor C (PDGF-C), a novel growth factor that binds to PDGF alpha receptor

TITLE Unpublished

JOURNAL 2 (bases 1 to 3512)

REFERENCE AUTHORS Gao,Z., Hart,C., Piddington,C., Sheppard,P., Shoemaker,K., Gilbertson,D., West,J. and O'Hara,P.J. Direct Submission

TITLE Submitted (10-MAY-2000) Biomedical Informatics, ZymoGenetics, Inc., 1201 Eastlake Avenue East, Seattle, WA 98102, USA

JOURNAL Location/Qualifiers

FEATURES source 1..3512 /organism="Mus musculus" /mol\_type="mRNA" /strain="C57BL/6J" /db\_xref="taxon:10090" 1..3512 /gene="Pdgfc" 1022..2059 /gene="Pdgfc" /note="PDGF-C/ZVEGF3" /codon\_start=1 /product="platelet-derived growth factor C" /protein\_id="AAK58566.1" /db\_xref="GI:14279332" /translation="MLILGLLLLSALAGQRTGRASNLSSKLQLSDKEQGVQDP RHERVVISNGSIHSFKPHYTPNNMVLVRLVAVDENVRQITFDERGLEPEDD ICKDFVEBEPDSGLRWGSGTVPKGTSGNHRIRFVSDYFPSPGFCIH SIIMPOVETTSPLVPPSLSLDLLNNAVTAFLBELIRLYPEPDRWQDLDSLKP TWOLGKAFLYGKSKVNNLLKEVKLYSCTPRNFSVSIRELKRTDTTFWPGCLL VKRCGNCAACCLHNCQCQVPRVTKYHVEVLQRLPKTVGYKLHLSLTDVALEHHE CDCVCRGNAGG"

BASE COUNT 850 a 920 c 861 g 881 t

ORIGIN

Query Match 98.0%; Score 1444.8; DB 10; Length 3512; Best Local Similarity 99.4%; Pred. No. 0; Matches 1460; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 2 ACCTGGACACACAGAGAGGCTCTAGGAAAATTTGGATGGGATTAATGTGGAACCTA 61

DB 829 AACTGGACACACAGAGAGGCTCTAGGAAAATTTGGATGGGATTAATGTGGAACCTA 888

QY 62 CCCTGCGATTCTCTGCGACAGCGCGCAGCGCTTCCACCGCAGCGACCTTCC 121

DB 889 CCCTGCGATTCTCTGCGACAGCGCGCAGCGCTTCCACCGCAGCGACCTTCC 948

QY 122 CGGCTGGGCTGAGCTTGGAGTGTCTGCTTCCCGAGTGGCGCGAGTGGAGCCCTCG 181

DB 949 C-GGCTGGGCTGAGCTTGGAGTGTCTGCTTCCCGAGTGGCGCGAGTGGAGCCCTCG 1007

QY 182 CCCCAGTCAGCAAAATGCTCTCTCGGCTCTCTGCTGACATCTGCTGCGCGCGCC 241

DB 1008 CCCCAGTCAGCAAAATGCTCTCTCGGCTCTCTGCTGACATCTGCTGCGCGCGCC 1067

QY 242 AAAGAACGGGACTCGGGCTGAGTCCAACTGAGCGAGTGGAGTGGAGTCTCCAGGACA 301

DB 1068 AAAGAACGGGACTCGGGCTGAGTCCAACTGAGCGAGTGGAGTGGAGTCTCCAGGACA 1127

QY 302 AGGAACAGAACGGAGTGAAGATCCCGGCATGAGAGTGTCTCACTATCTGGTAATG 361

DB 1128 AGGAACAGAACGGAGTGAAGATCCCGGCATGAGAGTGTCTCACTATCTGGTAATG 1187

QY 362 GGAGCATCCACAGCCGAAATTTCTCTATCATGTAACCAAGAAATATGGTGGTGTGA 421

DB 1188 GGAGCATCCACAGCCGAAATTTCTCTATCATATACCAAGAAATATGGTGGTGTGA 1247

QY 422 GATTAGTTCAGTAGAATAATGTGGGATCGAGTCACTTGTATGAGAGATTGGGC 481

1248 GATTAGTTCAGTAGATAAAATGTGGGATCAGCTGACATTTGATGAGAGATTGGGC 1307

QY 482 TGAAGATCCAGAGACGATATATGCAAGTATGATTTGTAGAGTTGAGAGCCCGAGT 541

DB 1308 TGAAGATCCAGAGACGATATATGCAAGTATGATTTGTAGAGTTGAGAGCCCGAGT 1367

QY 542 ATGGAAGTGTTTAGAGCGCTGGTGGTCTGGGACTGTGCCAGGAAAGCAGACTTCTA 601

DB 1368 ATGGAAGTGTTTAGAGCGCTGGTGGTCTGGGACTGTGCCAGGAAAGCAGACTTCTA 1427

QY 602 AAGGAATCATATCAGGATAAGATTTGTATCTGATGAGTATTTTCCATCTCAACCCGAT 661

DB 1428 AAGGAATCATATCAGGATAAGATTTGTATCTGATGAGTATTTTCCATCTCAACCCGAT 1487

QY 662 TCTGCATCCACTACAGTATTTATCATGCCAAGTCAAGAGTCAAGAAACACAGTCTCTCGGTGT 721

DB 1488 TCTGCATCCACTACAGTATTTATCATGCCAAGTCAAGAGTCAAGAAACACAGTCTCTCGGTGT 1547

QY 722 TGCCCCCTTCATCTTTGTCAATTGGACCTGCTCAACATGCTGACCTGACCTTCAGTACT 781

DB 1548 TGCCCCCTTCATCTTTGTCAATTGGACCTGCTCAACATGCTGACCTGACCTTCAGTACT 1607

QY 782 TGAAGAGCTGATTTCGGTACCTAGAGCCAGATCGATGGCAGGTGGAATTTGGACAGCTCT 841

DB 1608 TGAAGAGCTGATTTCGGTACCTAGAGCCAGATCGATGGCAGGTGGAATTTGGACAGCTCT 1667

QY 842 ACAAAGCAACATGCGAGCTTTGGGCAAGGCTTCTGTATGGGAAAAAAGCAAGTGG 901

DB 1668 ACAAAGCAACATGCGAGCTTTGGGCAAGGCTTCTGTATGGGAAAAAAGCAAGTGG 1727

QY 902 TGAATCTGAATCTCTCAAGAGAGAGTAAACTCTACAGTGCACACCCCGAACTTCT 961

DB 1728 TGAATCTGAATCTCTCAAGAGAGAGTAAACTCTACAGTGCACACCCCGAACTTCT 1787

QY 962 CAGTGTCCATACCGGAGAGCTAAAGAGACAGATACCATATTTCTGGCAGGTTGTCTCC 1021

DB 1788 CAGTGTCCATACCGGAGAGCTAAAGAGACAGATACCATATTTCTGGCAGGTTGTCTCC 1847

QY 1022 TGGTCAAGCGCTGTGGAGAAATTTGTGCTTCCATTAATTTGCAATGTAATGTCACT 1081

DB 1848 TGGTCAAGCGCTGTGGAGAAATTTGTGCTTCTCCATAATTTGCAATGTAATGTCACT 1907

QY 1082 GTGTCCCAAGTAAAGTTACAAAAGTACCATGAGTCTTTCAGTTGAGACCAAAAACGT 1141

DB 1908 GTGTCCCAAGTAAAGTTACAAAAGTACCATGAGTCTTTCAGTTGAGACCAAAAACGT 1967

QY 1142 GAGTCAAGGGATTGCATAAGTCACTCACTGATGTGGCTCTGGAAACACACGAGGAATGTG 1201

DB 1968 GAGTCAAGGGATTGCATAAGTCACTCACTGATGTGGCTCTGGAAACACACGAGGAATGTG 2027

QY 1202 ACTGTGTGTAGAGGAAAACGAGAGGTAATCTGACGCTTTCGTAGCAGCACTGTGAG 1261

DB 2028 ACTGTGTGTAGAGGAAAACGAGAGGTAATCTGACGCTTTCGTAGCAGCACTGTGAG 2087

QY 1262 CACTGGCATCTGTGTACCCCAAGCAACCTTCACTCCCAAGCAGGTTGGCCGAGG 1321

DB 2088 CACTGGCATCTGTGTACCCCAAGCAACCTTCACTCCCAAGCAGGTTGGCCGAGG 2147

QY 1322 CTCTCAGTGTCTGATGTGGCTATGTGAAGATCTTACTCTGCTCCCAACCAAAATCTCAG 1381

DB 2148 CTCTCAGTGTCTGATGTGGCTATGTGAAGATCTTACTCTGCTCCCAACCAAAATCTCAG 2207

QY 1382 TTGTTTGTCTCAATAGCCCTTCCCTGCGAGACTTCAAGTGTCTTCTTAAAGACAGAGC 1441

DB 2208 TTGTTTGTCTCAATAGCCCTTCCCTGCGAGACTTCAAGTGTCTTCTTAAAGACAGAGC 2267

QY 1442 ACCAAGAGGATCAATCAAAAGCACTGC 1470

DB 2268 ACCAAGAGGATCAATCAAAAGCACTGC 2296

LOCUS AR267281 3571 bp DNA linear PAT 10-APR-2003  
DEFINITION Sequence 34 from patent US 6495668.  
ACCESSION AR267281  
VERSION AR267281.1 GI:29697284  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 3571)  
AUTHORS Gilbert, T., Hart, C.E., Sheppard, P.O. and Gilbertson, D.G.  
TITLE Growth factor homolog ZVEGF4  
JOURNAL Patent: US 6495668-A 34 17-DEC-2002;  
FEATURES Location/Qualifiers  
source 1..3571  
/organism="unknown"  
BASE COUNT 876 a 935 c 875 g 885 t  
ORIGIN  
Query Match 98.0%; Score 1444.8; DB 6; Length 3571;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 1460; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  
QY 2 ACCTGGAGACACAGAGAGGGCTCTAGGAAAAATTTGGATGGGGATTATGTGGAACCTA 61  
Db 856 AACTGGAGACACAGAGAGGGCTCTAGGAAAAATTTGGATGGGGATTATGTGGAACCTA 915  
QY 62 CCCTGGGATCTCTGCTCCAGAGCGCGCCAGGCGCTTCCACCGCAGCGAGCCCTTTCCC 121  
Db 916 CCCTGGGATCTCTGCTCCAGAGCGCGCCAGGCGCTTCCACCGCAGCGAGCCCTTTCCC 975  
QY 122 CGGCTGGGCTGAGCCTTGGAGTCGTCTTCCAGTGCCTCCCGCCGCGAGTGAGCCCTCG 181  
Db 976 C-GGCTGGGCTGAGCCTTGGAGTCGTCTTCCAGTGCCTCCCGCCGCGAGTGAGCCCTCG 1034  
QY 182 CCCAGTCAGCCAAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCTCGGCGGCG 241  
Db 1035 CCCCAGTCAGCCAAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCTCGGCGGCGG 1094  
QY 242 AAAGAACGGGACTCGGCTGAGTCAACCTGAGCAGCAAGTTGCGAGCTCTCCACGACA 301  
Db 1095 AAAGAACGGGACTCGGCTGAGTCAACCTGAGCAGCAAGTTGCGAGCTCTCCACGACA 1154  
QY 302 AGGAACAGAACGGAGTCAAGATCCCGGCATCGAGAGTTCTCTATATCTGTAATG 361  
Db 1155 AGGAACAGAACGGAGTCAAGATCCCGGCATCGAGAGTTCTCTATATCTGTAATG 1214  
QY 362 GGAGCATCAAGCCGAGTTCTCTATACATGACCAAGAAATATGGTGGTGGGA 421  
Db 1215 GGAGCATCAAGCCGAGTTCTCTATACATGACCAAGAAATATGGTGGTGGGA 1274  
QY 422 GATTAGTTCAGTAGATGAAAATGTGCGGATCCAGCTGACATTTGATGAGAGATTGGGC 481  
Db 1275 GATTAGTTCAGTAGATGAAAATGTGCGGATCCAGCTGACATTTGATGAGAGATTGGGC 1334  
QY 482 TGGAGATCCAGAACGATATATGCAATATGATTTTGAAGTTGAGAGTGGAGCCAGTG 541  
Db 1335 TGGAGATCCAGAACGATATATGCAATATGATTTTGAAGTTGAGAGTGGAGCCAGTG 1394  
QY 542 ATGGAGTCTTTTAGGACGCTGTGTGTTCTGGGACTGTGCGAGAAAGCAGACTTCTA 601  
Db 1395 ATGGAGTCTTTTAGGACGCTGTGTGTTCTGGGACTGTGCGAGAAAGCAGACTTCTA 1454  
QY 602 AAGGAAATCATATCAGGATAAGATTGTATCTGATGAGTATTTTCCATCTGAACCCGGAT 661  
Db 1455 AAGGAAATCATATCAGGATAAGATTGTATCTGATGAGTATTTTCCATCTGAACCCGGAT 1514  
QY 662 TCTGCATCCACTACATATATCATGCCCAAGTCAAGAACCCAGAGTCCCTTCGGTGT 721  
Db 1515 TCTGCATCCACTACATATATCATGCCCAAGTCAAGAACCCAGAGTCCCTTCGGTGT 1574  
QY 722 TGGCCCTTCATCTTTGTCTATTCGACCTGCTCAACATGCTGATGCTGCTTCAGTACCT 781  
Db 1575 TGGCCCTTCATCTTTGTCTATTCGACCTGCTCAACATGCTGATGCTGCTTCAGTACCT 1634

QY 782 TGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGGACTTGGACAGCCTCT 841  
Db 1635 TGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGGACTTGGACAGCCTCT 1694  
QY 842 ACAAGCCAAATGCGCAGCTTTTGGGCAAGGCTTTCCCTGTATGGGAAAAAAGCAAGTGG 901  
Db 1695 ACAAGCCAAATGCGCAGCTTTTGGGCAAGGCTTTCCCTGTATGGGAAAAAAGCAAGTGG 1754  
QY 902 TGAATCTGAATCTCTCAAGGAAGAGTAAACTCTACAGCTGCACACCCCGGAACCTTCT 961  
Db 1755 TGAATCTGAATCTCTCAAGGAAGAGTAAACTCTACAGCTGCACACCCCGGAACCTTCT 1814  
QY 962 CAGTGTCCATACCGGAAGAGCTAAAGAGGACAGATACATATCTGGCAGGTTGTCTCC 1021  
Db 1815 CAGTGTCCATACCGGAAGAGCTAAAGAGGACAGATACATATCTGGCAGGTTGTCTCC 1874  
QY 1022 TGGTCAAGCGCTGTGGAGGAAATTTGGCTGTCTCTCCATAATGCAATGAATGTCAGT 1081  
Db 1875 TGGTCAAGCGCTGTGGAGGAAATTTGGCTGTCTCTCCATAATGCAATGAATGTCAGT 1934  
QY 1082 GTGTCCCAAGTAAAGTTTACAAAAAGTACCATGAGGTCCTTCAGTTGAGACCAAAAACTG 1141  
Db 1935 GTGTCCCAAGTAAAGTTTACAAAAAGTACCATGAGGTCCTTCAGTTGAGACCAAAAACTG 1994  
QY 1142 GAGTCAAGGGATTGCATAAGTCACTACTGATGTGGCTCTGGAACACACGAGGAAATGTG 1201  
Db 1995 GAGTCAAGGGATTGCATAAGTCACTACTGATGTGGCTCTGGAACACACGAGGAAATGTG 2054  
QY 1202 ACTGTGTGTAGAGGAACCGCAGGAGGTAACCTGCAGCCTTCGTAGCAGCACAGTGGAG 1261  
Db 2055 ACTGTGTGTAGAGGAACCGCAGGAGGTAACCTGCAGCCTTCGTAGCAGCACAGTGGAG 2114  
QY 1262 CACTGGCAATCTGTGTATCCCCCAAGCAACCTTCATCCCAACAGCGTTGGCCCGCAGGG 1321  
Db 2115 CACTGGCAATCTGTGTATCCCCCAAGCAACCTTCATCCCAACAGCGTTGGCCCGCAGGG 2174  
QY 1322 CTCTCAGCTGTGATGTGGCTATGATTAAGATCTTACTGTCTCAACCAAAATTTCTCAG 1381  
Db 2175 CTCTCAGCTGTGATGTGGCTATGATTAAGATCTTACTGTCTCAACCAAAATTTCTCAG 2234  
QY 1382 TTGTTTGTCTCAATAGCCTTCCCTGCGAGGCTTCAAGTGTCTTCTAAAGACCCAGAGGC 1441  
Db 2235 TTGTTTGTCTCAATAGCCTTCCCTGCGAGGCTTCAAGTGTCTTCTAAAGACCCAGAGGC 2294  
QY 1442 ACCAANAGAGTCAATCAAGACACTGC 1470  
Db 2295 ACCAANAGAGTCAATCAAGACACTGC 2323

RESULT 4  
LOCUS AR282985 3571 bp DNA linear PAT 10-APR-2003  
DEFINITION Sequence 42 from patent US 6528050.  
ACCESSION AR282985  
VERSION AR282985.1 GI:29719806  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 3571)  
AUTHORS Gao, Z., Hart, C.E., Piddington, C.S., Sheppard, P.O., Shoemaker, K.E.,  
Gilbertson, D.G. and West, J.W.  
TITLE Growth factor homolog zvegf3  
JOURNAL Patent: US 6528050-A 42 04-MAR-2003;  
FEATURES Location/Qualifiers  
source 1..3571  
/organism="unknown"  
BASE COUNT 876 a 935 c 875 g 885 t  
ORIGIN  
Query Match 98.0%; Score 1444.8; DB 6; Length 3571;  
Best Local Similarity 99.4%; Pred. No. 0;

Matches 1460; Conservative 0; Mismatches 8; Indels 1; Gaps 1;									
Qy	2	ACCTGGAGACACAGAGGGCTCTAGGAAAAATTTTGGATGGGATTAATGTGGAACCTA	61						
Db	856	AACCTGGAGACACAGAGGGCTCTAGGAAAAATTTTGGATGGGATTAATGTGGAACCTA	915						
Qy	62	CCCTGCGATTCTCTGCTGCCAGAGCCGGCCAGGCGCTTCCACCGCAGCGCAGCCCTTCCC	121						
Db	916	CCCTGCGATTCTCTGCTGCCAGAGCCGGCCAGGCGCTTCCACCGCAGCGCAGCCCTTCCC	975						
Qy	122	CGGCTGGGCTGAGCTTGGAGTGGTGGCTTCCCGAGTCCCGCGCGCGAGTGAGCCCTCG	181						
Db	976	C-GGCTGGGCTGAGCTTGGAGTGGTGGCTTCCCGAGTCCCGCGCGCGAGTGAGCCCTCG	1034						
Qy	182	CCCAGTCCAGCAAAATGCTCTCTCGCGCTCTCTCTGTGACATCTGCGCTGGCGCGGCC	241						
Db	1035	CCCAGTCCAGCAAAATGCTCTCTCGCGCTCTCTCTGTGACATCTGCGCTGGCGCGGCC	1094						
Qy	242	AAAGAACCGGAGCTCGGCTGAGTCCAACTGAGCAGCAAGTTGAGCTCTCCAGCGACA	301						
Db	1095	AAAGAACCGGAGCTCGGCTGAGTCCAACTGAGCAGCAAGTTGAGCTCTCCAGCGACA	1154						
Qy	302	AGGAACAGAACGGAGTCAAGATCCCGCATGAGAGGTTGTCACTATCTCTGTTAATG	361						
Db	1155	AGGAACAGAACGGAGTCAAGATCCCGCATGAGAGGTTGTCACTATCTCTGTTAATG	1214						
Qy	362	GGAGCATCCACAGCCGGAATTTCTCTACATGTAACCAAGAAATATGGTGTGTGGA	421						
Db	1215	GGAGCATCCACAGCCGGAATTTCTCTACATGTAACCAAGAAATATGGTGTGTGGA	1274						
Qy	422	GATTAGTTGCACTAGATGAATAATGTGCGGATCCAGCTGACATTTGATGAGAGATTGGGC	481						
Db	1275	GATTAGTTGCACTAGATGAATAATGTGCGGATCCAGCTGACATTTGATGAGAGATTGGGC	1334						
Qy	482	TGGAAGATCCAGACGATATATCAAGTATGATTTTGTAGAGTTGAGGAGCCGAGT	541						
Db	1335	TGGAAGATCCAGACGATATATCAAGTATGATTTTGTAGAGTTGAGGAGCCGAGT	1394						
Qy	542	ATGGAAGTGTGTTTAGGACGCTGGTGTGTTCTGGACTGTGCCAGAAAGCAGACTTCTA	601						
Db	1395	ATGGAAGTGTGTTTAGGACGCTGGTGTGTTCTGGACTGTGCCAGAAAGCAGACTTCTA	1454						
Qy	602	AAGGAAATCATATCAGGATAAGATTGTTATCTGATGAGTATTTTCATCTGAACCCGGAT	661						
Db	1455	AAGGAAATCATATCAGGATAAGATTGTTATCTGATGAGTATTTTCATCTGAACCCGGAT	1514						
Qy	662	TCGTGATCCACTACAGTATATCATGCCAAGTCAAGAACCAAGTCTCTCGGTCT	721						
Db	1515	TCGTGATCCACTACAGTATATCATGCCAAGTCAAGAACCAAGTCTCTCGGTCT	1574						
Qy	722	TGCCCCCTTCATCTTTGTCATTTGACCTGCTCAACAAATCTGTGACTGCTTCAGTACCT	781						
Db	1575	TGCCCCCTTCATCTTTGTCATTTGACCTGCTCAACAAATCTGTGACTGCTTCAGTACCT	1634						
Qy	782	TGGAAGAGCTGATTCGGTACCTAGACGACATCGATGGCAGGTGACTTGGACGCTCT	841						
Db	1635	TGGAAGAGCTGATTCGGTACCTAGACGACATCGATGGCAGGTGACTTGGACGCTCT	1694						
Qy	842	ACAAGCCAAATCGGACGCTTTTGGGCAAGGCTTCTCTGTATGGAAAAAAGCAAGTGG	901						
Db	1695	ACAAGCCAAATCGGACGCTTTTGGGCAAGGCTTCTCTGTATGGAAAAAAGCAAGTGG	1754						
Qy	902	TGAATCTGAATCTCTCAAGGAAGAGGTAAATCTACAGCTGCACACCCCGGAATCTCT	961						
Db	1755	TGAATCTGAATCTCTCAAGGAAGAGGTAAATCTACAGCTGCACACCCCGGAATCTCT	1814						
Qy	962	CAGTGTCCATACGGGAGAGCTAAAGAGGACAGATACCATATTTCTGGCCAGGTTGTCTCC	1021						
Db	1815	CAGTGTCCATACGGGAGAGCTAAAGAGGACAGATACCATATTTCTGGCCAGGTTGTCTCC	1874						
Qy	1022	TGCTCAAGCGCTGTGAGGAAATTTGTGCTGTTGTCTCCATAATTTGCAATGAATGTCACT	1081						
Db	1875	TGCTCAAGCGCTGTGAGGAAATTTGTGCTGTTGTCTCCATAATTTGCAATGAATGTCACT	1934						

QY	1082	GTGTCCCACTAAAGTTACAAAAAGTACCATGAGGTCTCTCAGTTGAGACCAAAAACTG	1141																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
----	------	--	------	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--



QY	62	CCCTGCGATTCTCTGCTGCCAGAGCGCGCAGCGCTTCCACCGCAGCGCAGCCTTTCC	121
Db	916	CCCTGCGATTCTCTGCTGCCAGAGCGCGCAGCGCTTCCACCGCAGCGCAGCCTTTCC	975
QY	122	CGGCTGGGCTGAGCCTTGGAGTCTGCTTCCCGAGTCCCGCGCGAGTGAGCCCTGG	181
Db	976	C-GGCTGGGCTGAGCCTTGGAGTCTGCTTCCCGAGTCCCGCGCGAGTGAGCCCTCG	1034
QY	182	CCCAGTCAAGCAAAATGCTCTCTTGGGCTCTCTCTGCTGACATCTGCCCTGGCGGCG	241
Db	1035	CCCAGTCAAGCAAAATGCTCTCTTGGGCTCTCTCTGCTGACATCTGCCCTGGCGGCG	1094
QY	242	AAAGAAACGGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCAGCTCTCCAGCGACA	301
Db	1095	AAAGAAACGGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCAGCTCTCCAGCGACA	1154
QY	302	AGGAACAGAACGGAGTCAAGATCCCGGCAATGAGAGAGTTGTCACTATATCTGTAATG	361
Db	1155	AGGAACAGAACGGAGTCAAGATCCCGGCAATGAGAGAGTTGTCACTATATCTGTAATG	1214
QY	362	GGAGCATCCACAGCCGAGTTTCCTCATAGCTACCCAGAAATATGGTCTGGTGTGA	421
Db	1215	GGAGCATCCACAGCCGAGTTTCCTCATAGCTACCCAGAAATATGGTCTGGTGTGA	1274
QY	422	GATTAGTTGCAGTAGAGTAAATGTGGGATCCAGCTGACATTTGATGAGAGATTTGGGC	481
Db	1275	GATTAGTTGCAGTAGAGTAAATGTGGGATCCAGCTGACATTTGATGAGAGATTTGGGC	1334
QY	482	TGGAAGATCCAGAGACGATATATGCAAGTATGATTTGTAGAGTTGAGGCCAGATG	541
Db	1335	TGGAAGATCCAGAGACGATATATGCAAGTATGATTTGTAGAGTTGAGGCCAGATG	1394
QY	542	ATGGAAGTGTTTTAGGACGCTGGTGTGGTCTCGGAGTGTGCCAGGAAAGCAGACTTCTA	601
Db	1395	ATGGAAGTGTTTTAGGACGCTGGTGTGGTCTCGGAGTGTGCCAGGAAAGCAGACTTCTA	1454
QY	602	AAGGAAATCATATCAGGAATAAGATTTGTATCTGATGAGTATTTTCCATCTGAACCCGGAT	661
Db	1455	AAGGAAATCATATCAGGAATAAGATTTGTATCTGATGAGTATTTTCCATCTGAACCCGGAT	1514
QY	662	TCTGCATCCATACAGTATTATCATGCCAAGTCACAGAACCAACAGTCCCTTCGGTGT	721
Db	1515	TCTGCATCCATACAGTATTATCATGCCAAGTCACAGAACCAACAGTCCCTTCGGTGT	1574
QY	722	TGCCCCCTTCATCTTTGTTCATTTGGACCTGCTCAACAATGCTGTGACTGCGCTTCAGTACCT	781
Db	1575	TGCCCCCTTCATCTTTGTTCATTTGGACCTGCTCAACAATGCTGTGACTGCGCTTCAGTACCT	1634
QY	782	TGGAAGACTGATTCGGTACCTAGAGCCAGATTCGATGSCAGTGGACTTGGACAGCCCTCT	841
Db	1635	TGGAAGACTGATTCGGTACCTAGAGCCAGATTCGATGSCAGTGGACTTGGACAGCCCTCT	1694
QY	842	ACAAGCCAACATGCGAGCTTTTGGCAAGGCTTTCTGTATGGGAAAAAAGCAAGTGG	901
Db	1695	ACAAGCCAACATGCGAGCTTTTGGCAAGGCTTTCTGTATGGGAAAAAAGCAAGTGG	1754
QY	902	TGAATCTGAATCTCCTCAAGGAAGAGGTAAACTCTACAGTGCACACCCCGGAACCTTCT	961
Db	1755	TGAATCTGAATCTCCTCAAGGAAGAGGTAAACTCTACAGTGCACACCCCGGAACCTTCT	1814
QY	962	CAGTGTCCATACGGGAAGGCTAAAGAGGACAGATACCATAATCTTGGCAGGTTGTCTCC	1021
Db	1815	CAGTGTCCATACGGGAAGGCTAAAGAGGACAGATACCATAATCTTGGCAGGTTGTCTCC	1874
QY	1022	TGGTCAAGCGCTGTGGAGGAAATTTGTCCTGTGTCTCCATAATGCAATGAATGTCAGT	1081
Db	1875	TGGTCAAGCGCTGTGGAGGAAATTTGTCCTGTGTCTCCATAATGCAATGAATGTCAGT	1934
QY	1082	GTGTCCCAAGTAAGTTACAAAAATGATCCATGAGGTCCTTCAGTTGAGACCAAAAATG	1141
Db	1935	GTGTCCCAAGTAAGTTACAAAAATGATCCATGAGGTCCTTCAGTTGAGACCAAAAATG	1994

Qy	1142	GAGTC	AAGGATTCGAT	TAAGTCACTC	ACTGATGTGGCTCT	GGNACACACGAGG	ATATGG	1201
Db	1995	GAGTC	AAGGATTCGAT	TAAGTCACTC	ACTGATGTGGCTCT	GGNACACACGAGG	ATATGG	2054
Qy	1202	ACTGT	GTGTGTCAG	AGAAACG	CAGGAGGGTAACT	GCAGGCTTCGT	AGCAGCACACGTGAG	1261
Db	2055	ACTGT	GTGTGTCAG	AGAAACG	CAGGAGGGTAACT	GCAGGCTTCGT	AGCAGCACACGTGAG	2114
Qy	1262	CAC	TGGCAATTC	TGTGTAC	CCCCCAACG	CACTTCATATCCCA	CACGAGTTGGCCGAGGG	1321
Db	2115	CAC	TGGCAATTC	TGTGTAC	CCCCCAACG	CACTTCATATCCCA	CACGAGTTGGCCGAGGG	2174
Qy	1322	CTC	TCACTGCTGAT	GTCTGCTAT	TGTAAGATCTT	ACTCGTCTCCAA	CCAAATTCCTCAG	1381
Db	2175	CTC	TCACTGCTGAT	GTCTGCTAT	TGTAAGATCTT	ACTCGTCTCCAA	CCAAATTCCTCAG	2234
Qy	1382	TTG	TTTGCTTCAAT	TAGCTCTT	CCCCCTGCAGG	ACTTCAAGTGTCTT	CTTAAAGACACGAGGC	1441
Db	2235	TTG	TTTGCTTCAAT	TAGCTCTT	CCCCCTGCAGG	ACTTCAAGTGTCTT	CTTAAAGACACGAGGC	2294
Qy	1442	ACCA	ANAGGAGTCAAT	CACAAG	CACATGC	1470		
Db	2295	ACCA	ANAGGAGTCAAT	CACAAG	CACATGC	2323		
RESULT 6								
AX118787								
LOCUS								
DEFINITION								
ACCESSION								
VERSION								
KEYWORDS								
SOURCE								
ORGANISM								
REFERENCE								
AUTHORS								
TITLE								
JOURNAL								
FEATURES								
source								
CDS								
BASE COUNT								
ORIGIN								
Query Match								
Best Local Similarity								
Matches 1460; Conservative								
Qy	2	ACCT	GGACACAG	AAGAGGCGTCT	AGAAAAATTTTGGAT	GGGATATGCGAACTA	61	
Db	856	AACT	GGAGACA	CAGAAAGAGGCGTCT	AGAAAAATTTTGGAT	GGGATATGCGAACTA	915	
Qy	62	CCCT	GGATTCTCT	GCTGCCAG	CCGCGCGCGCTTCC	ACCGCAGCGACGCTTTCCC	121	
Db	916	CCCT	GGATTCTCT	GCTGCCAG	CCGCGCGCGCTTCC	ACCGCAGCGACGCTTTCCC	975	

QY 122 CGGGCTGGGCTGAGCCCTTGGAGTCGTCTGCTTCCCCAGTGCCTGGCCGCGAGTGAGCCCTCG 181  
Db 976 C-GGCTGGGCTGAGCCCTTGGAGTCGTCTGCTTCCCCAGTGCCTGGCCGCGAGTGAGCCCTCG 1034  
QY 182 CCCAGTCAGGCAAAATGCTCTCTCTGGGCTCTCTCTGCTGACATCTGCTCCCTGGCCGCGCC 241  
Db 1035 CCCAGTCAGGCAAAATGCTCTCTCTGGGCTCTCTCTGCTGACATCTGCTCCCTGGCCGCGCC 1094  
QY 242 AANGAAGCGGAGCTCGGCTGAGTCCAACTGAGCAGCAAGTGTGAGCTCTCCAGCGACA 301  
Db 1095 AAGAAGCGGAGCTCGGCTGAGTCCAACTGAGCAGCAAGTGTGAGCTCTCCAGCGACA 1154  
QY 302 AGGAACAGAACCGGAGTGCAGAGTCCCGGCGATGAGAGAGTGTCTCAATATCTGTAATG 361  
Db 1155 AGGAACAGAACCGGAGTGCAGAGTCCCGGCGATGAGAGAGTGTCTCAATATCTGTAATG 1214  
QY 362 GGAGCATCCAGCCGGAATTTCTCTCATGTAAGTCCCAAGAAATATGCTGCTGGTGTGA 421  
Db 1215 GGAGCATCCAGCCGGAATTTCTCTCATGTAAGTCCCAAGAAATATGCTGCTGGTGTGA 1274  
QY 422 GATTAGTTCAGTATGAAATGTGCGGATCCAGCTGAGTATTTGATGAGATTTGGGC 481  
Db 1275 GATTAGTTCAGTATGAAATGTGCGGATCCAGCTGAGTATTTGATGAGATTTGGGC 1334  
QY 482 TGAAGATCCAGAACGATATATGCAAGTATGATTTTGTAGAAGTTGAGGAGCCCGAGT 541  
Db 1335 TGAAGATCCAGAACGATATATGCAAGTATGATTTTGTAGAAGTTGAGGAGCCCGAGT 1394  
QY 542 ATGGAAGTGTTTAGAACGCTGTGTGTTCTGGGACTGTGCGAGATGTCAGAAAGCAGACTTCTA 601  
Db 1395 ATGGAAGTGTTTAGAACGCTGTGTGTTCTGGGACTGTGCGAGATGTCAGAAAGCAGACTTCTA 1454  
QY 602 AAGGAATCATATCAGATAAGATTTGATCTGATGAGTATTTCCATCTGAACCCGGAT 661  
Db 1455 AAGGAATCATATCAGATAAGATTTGATCTGATGAGTATTTCCATCTGAACCCGGAT 1514  
QY 662 TCTGCATCCACTACAGTATATCATGCCACAGTCAAGAACCAAGTGTGCTTGGTGT 721  
Db 1515 TCTGCATCCACTACAGTATATCATGCCACAGTCAAGAACCAAGTGTGCTTGGTGT 1574  
QY 722 TGGCCCTTCATCTTGTCTATGGACCTGCTCAAGATGCTGATGCTGATGCTTCACTACCT 781  
Db 1575 TGGCCCTTCATCTTGTCTATGGACCTGCTCAAGATGCTGATGCTTCACTACCT 1634  
QY 782 TGAAGAGCTGATTCGGTACTAGACAGATCGATGGCAGGTGGACTTGGACAGCCTCT 841  
Db 1635 TGAAGAGCTGATTCGGTACTAGACAGATCGATGGCAGGTGGACTTGGACAGCCTCT 1694  
QY 842 ACAAGCCACATGGCAGCTTTGGGCAAGCTTCTCTGTATGGGAAAAAAGCAAGTGG 901  
Db 1695 ACAAGCCACATGGCAGCTTTGGGCAAGCTTCTCTGTATGGGAAAAAAGCAAGTGG 1754  
QY 902 TGAATCTGAATCTCTCAAGAGAGAGTAAACTCTACAGCTGCACACCCCGAATCTCT 961  
Db 1755 TGAATCTGAATCTCTCAAGAGAGAGTAAACTCTACAGCTGCACACCCCGAATCTCT 1814  
QY 962 CAGTGTCCATACGGGAGAGCTAAAGAGGACAGATACCATATTTCTGGCCAGGTTGTCTCC 1021  
Db 1815 CAGTGTCCATACGGGAGAGCTAAAGAGGACAGATACCATATTTCTGGCCAGGTTGTCTCC 1874  
QY 1022 TGTCAAGCCTGTGGAGGAAATGTGCTGCTTGTCTCCATTAATGCAATGATGTCAGT 1081  
Db 1875 TGTCAAGCCTGTGGAGGAAATGTGCTGCTTGTCTCCATTAATGCAATGATGTCAGT 1934  
QY 1082 GTCTCCACGTAAGTTACAAAAGTACCATGAGGTCTCTCAGTTGAGACCAAAACTG 1141  
Db 1935 GTCTCCACGTAAGTTACAAAAGTACCATGAGGTCTCTCAGTTGAGACCAAAACTG 1994  
QY 1142 GAGTCAAGGATGCAATAAGTCACTCACTGATGTGGCTCTGGAAACCAAGAGGATGTG 1201  
Db 1995 GAGTCAAGGATGCAATAAGTCACTCACTGATGTGGCTCTGGAAACCAAGAGGATGTG 2054  
QY 1202 ACTGTGTGTAGAGGAAACGAGGAGGGTAACTGACGCTTCTGTAGCAGACACAGTGTGAG 1261

Db 2055 ACTGTGTGTAGAGGAAACGAGGAGGTAACTGACGCTTCTGTAGCAGCAGCAGCTGTAG 2114  
QY 1262 CACTGGCAATTCGTGTATCCCCCAAGCAACCTTCATCCCAACAGCGTTGGCCGAGGG 1321  
Db 2115 CACTGGCAATTCGTGTATCCCCCAAGCAACCTTCATCCCAACAGCGTTGGCCGAGGG 2174  
QY 1322 CTCTCAGCTGCTGATGCTGGCTATGTTAAGATCTTACTCTCTCAACCAAAATTCCTAG 1381  
Db 2175 CTCTCAGCTGCTGATGCTGGCTATGTTAAGATCTTACTCTCTCAACCAAAATTCCTAG 2234  
QY 1382 TTGTTTGTCTCAATAGCTTCCCTCGCAGGACTTCAAGTGTCTTCTAAAGACCAAGGC 1441  
Db 2235 TTGTTTGTCTCAATAGCTTCCCTCGCAGGACTTCAAGTGTCTTCTAAAGACCAAGGC 2294  
QY 1442 ACCAAGAGGAGTCAATCAAAAGCACTGC 1470  
Db 2295 ACCAAGAGGAGTCAATCAAAAGCACTGC 2323

## RESULT 7

BC037696 2731 bp mRNA linear ROD 16-APR-2003  
LOCUS BC037696  
DEFINITION Mus musculus platelet-derived growth factor, C polypeptide, mRNA  
(cDNA clone MGC:46836 IMAGE:408749), complete cds.

ACCESSION BC037696

VERSION BC037696.1 GI:22902442

KEYWORDS MGC.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 2731)

AUTHORS

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
Altshuler, S.F., Zesberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
Schetz, T.E., Brownstein, M.J., Udwin, T.B., Toshiyuki, S.,  
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,  
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,  
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.W.,  
Worley, K.C., Hale, S.J., Garcia, A.M., Gay, L.J., Hulyk, S.W.,  
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,  
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,  
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,  
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
Butterfield, Y.S., Krzywinski, M.I., Skalski, U., Smallos, D.E.,  
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

REFERENCE 2 (bases 1 to 2731)

Strausberg, R.

Direct Submission

Submitted (13-SEP-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT MGC help desk

Email: [cgabs-t@mail.nih.gov](mailto:cgabs-t@mail.nih.gov)

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>

Contact: misc_mgc@nhgri.nih.gov	
Akhter,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B.,	
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,	
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,	
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,	
Maduro,Q.L., Mastello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,	
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,	
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,	
Young,A., Zhang,L.-H. and Green,E.D.	
Clone distribution: MGC clone distribution information can be found	
through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a>	
Series: IRAC Plate: 80 Row: f Column: 13	
This clone was selected for full length sequencing because it	
passed the following selection criteria: matched mRNA gi: 10242384.	
FEATURES	
source	Location/Qualifiers
1..2731	/organism="Mus musculus"
	/mol_type="mRNA"
	/strain="CZECH II"
	/db_xref="taxon:10090"
	/clone="MGC:46836 IMAGE:4008749"
	/tissue types="Mammary tumor metastasized to lung."
	MMTV-LTR/Wnt1 model. Expression driven by an MMTV-LTR
	enhancer."
	/clone_lib="NCI CGAP_Lu30"
	/lab_host="DH10B"
	/notes="Vector: pCMV-SPORT6"
1..2731	
	/genes="PdGfc"
	/note="synonym: 1110064L01Rik"
	/db_xref="LocusID:54635"
	/db_xref="MGI:1859631"
209..1246	
	/codon_start=1
	/product="platelet-derived growth factor, C polypeptide"
	/protein_id="AAH37696.1"
	/db_xref="GI:22902443"
	/db_xref="LocusID:54635"
	/translation="MLLLGLLLLSALAGQRTGTRAESNLSKQLQSSDKRQNGVQDP
	RHRVTVISNGSIHSPKFPHTYPRNMLVRLVAVNDENVRIQLTDFRFLGDEPD
	LCKYDFVEBPDSGLVGRWCGSTVPGKTSKGNHRIKRVSDYFSPSPGFCIHY
	SLIMPOVTEITSPSLVPLSLDLNNAVTFSTBELIRYLEPDRWQVLDLSLYKP
	TWOLLGAFIYKSKVYNLKLKEVKLYSCTPRNFSVIRBELKRTDITFWPGCLL
	VKRCGNACCLLHCNQCQVPRKVTYKXHYEVLQRPKTVKGLHLSLTDVALBHEE
	CDCVCRGNAGG"
BASE COUNT	786 a 582 c 620 g 743 t
ORIGIN	
Query Match 97.4%; Score 1435.2; DB 10; Length 2731;	
Best Local Similarity 99.0%; Pred. No. 0;	
Matches 1454; Conservative 0; Mismatches 14; Indels 1; Gaps 1;	
QY	2 ACCTGGAGACACAGAGGGCTCTAGGAAAAATTTGGATGGGATTAATGTGAAACTA 61
Db	16 AACTGGAGACACAGAGGGCTCTAGGAAAAATTTGGATGGGATTAATGTGAAACTA 75
QY	62 CCCTGGGATTTCTGTCGCGAGCGCGCGAGCGCTTCCACCGCAGCGAGCTTTCCC 121
Db	76 CCCTGGGATTTCTGTCGCGAGCGCGCGAGCGCTTCCACCGCAGCGAGCTTTCCC 135
QY	122 CGGCTGGGCTGAGCTTGGAGTCTGCTTCCCGAGTCCCGCGCGAGTGAGCCCTCG 181
Db	136 C-GGCTGGGCTGAGCTTGGAGTCTGCTTCCCGAGTCCCGCGCGAGTGAGCCCTCG 194
QY	182 CCCAGTCAGCCAAATGCTCTCTCGGCTCTCTCTGTCGACATCTGCCCTGGCGGCC 241
Db	195 CCCAGTCAGCCAAATGCTCTCTCTCGGCTCTCTCTGTCGACATCTGCCCTGGCGGCC 254
QY	242 AAGAACCGGGAGCTCGGGCTGAGTCCACCTGAGCAGCAAGTTGAGCTCTCCAGGACA 301
Db	255 AAGAACCGGGAGCTCGGGCTGAGTCCACCTGAGCAGCAAGTTGAGCTCTCCAGGACA 314

QY	302 AGGAACAGAACGGAGTCGAAGATCCCGGCATFGAGAGAGTTGCTCACTATATCTGTTAATG 361
Db	315 AGGAGCAGAACGGAGTCGAAGATCCCGGCATFGAGAGAGTTGCTCACTATATCTGTTAATG 374
QY	362 GGAGCATCCACAGCCCGAAGTTTCTCATACCTACCCAGAAATATGCTGCTGGA 421
Db	375 GGAGCATCCACAGCCCGAAGTTTCTCATACCTACCCAGAAATATGCTGCTGGA 434
QY	422 GATTAGTTCAGTACAGTAAATGTGCGGATCCAGCTGACATTTGATGAGAGATTTGGGC 481
Db	435 GATTAGTTCAGTACAGTAAATGTGCGGATCCAGCTGACATTTGATGAGAGATTTGGGC 494
QY	482 TGGAGATCCAGAGACGATATATCAAGTATGATTTTGTAGAGTTGAGGAGCCAGTG 541
Db	495 TGGAGATCCAGAGACGATATATCAAGTATGATTTTGTAGAGTTGAGGAGCCAGTG 554
QY	542 ATGGAAGTGTGTTAGACGCTGTTGTTCTGGGACTGTGCGAGAAACGACACTCTA 601
Db	555 ATGGAAGTGTGTTAGACGCTGTTGTTCTGGGACTGTGCGAGAAACGACACTCTA 614
QY	602 AAGGAATCATATCAGATAAGATTTGTATCTGATGATGATTTTCCATCTGAACCCGGAT 661
Db	615 AAGGAATCATATCAGATAAGATTTGTATCTGATGATGATTTTCCATCTGAACCCGGAT 674
QY	662 TCTGCATCCACTACAGTATATCATGCCACAAGTCACAGAAACCAAGTCCTTCGGTGT 721
Db	675 TCTGCATCCACTACAGTATATCATGCCACAAGTCACAGAAACCAAGTCCTTCGGTGT 734
QY	722 TGGCCCTTCATCTTTGTCATTCGACCTGCTCAACATGCTGTGACTGCCTTCAGTACCT 781
Db	735 TGGCCCTTCATCTTTGTCATTCGACCTGCTCAACATGCTGTGACTGCCTTCAGTACCT 794
QY	782 TGGAGAGCTGATTTGGTACCTAGAGCCAGATCGATGGCAGGTGGACTTGGACAGCCTCT 841
Db	795 TGGAGAGCTGATTTGGTACCTAGAGCCAGATCGATGGCAGGTGGACTTGGACAGCCTCT 854
QY	842 ACAAGCCAAACATGGCAGCTTTTGGGCAAGCTTTCCTGTATGGAAAAAAGCAAGTGG 901
Db	855 ACAAGCCAAACATGGCAGCTTTTGGGCAAGCTTTCCTGTATGGAAAAAAGCAAGTGG 914
QY	902 TGAATCTGAATCTCTCAAGGAGAGGTAAACTCTACAGCTGCACACCCCGGAATCTCT 961
Db	915 TGAATCTGAATCTCTCAAGGAGAGGTAAACTCTACAGCTGCACACCCCGGAATCTCT 974
QY	962 CAGTGTCCATACGGAAGAGCTAAAGAGGACAGATACCATATTTCTGGCAGGTGTCTCC 1021
Db	975 CAGTGTCCATACGGAAGAGCTAAAGAGGACAGATACCATATTTCTGGCAGGTGTCTCC 1034
QY	1022 TGGTCAAGCGCTGTGGAGGAAATTTGTGCTGTTGCTCCATAATTCGATGAATGTCACT 1081
Db	1035 TGGTCAAGCGCTGTGGAGGAAATTTGTGCTGTTGCTCCATAATTCGATGAATGTCACT 1094
QY	1082 GTGTCCCAAGTAAAGTTTACAAAAAGTACCAATGAGTCTCTCAGTTGAGACCAAAAACTG 1141
Db	1095 GTGTCCCAAGTAAAGTTTACAAAAAGTACCAATGAGTCTCTCAGTTGAGACCAAAAACTG 1154
QY	1142 GAGTCAAGGGATTGCAATAAGTCACTCACTGATGTGGCTCTGGAAACACCAAGGAATGTG 1201
Db	1155 GAGTCAAGGGATTGCAATAAGTCACTCACTGATGTGGCTCTGGAAACACCAAGGAATGTG 1214
QY	1202 ACTGTGTGTAGAGGAAACCGAGAGGTTAACTGACGCTTCTGAGCAGCAGCAGTGAG 1261
Db	1215 ACTGTGTGTAGAGGAAACCGAGAGGTTAACTGACGCTTCTGAGCAGCAGCAGTGAG 1274
QY	1262 CACTGGCATTTCTGTATCCCCCAAGCAACTTTCATCCCCCAGCAGCTTGGCCGAGGG 1321
Db	1275 CACTGGCATTTCTGTATCCCCCAAGCAACTTTCATCCCCCAGCAGCTTGGCCGAGGG 1334
QY	1322 CTCTCAGCTGCTGATGCTGGCTATGGTAAAGATCTTACTCGTCTCCAAACCAATTTCTCAG 1381
Db	1335 CTCTCAGCTGCTGATGCTGGCTATGGTAAAGATCTTACTCGTCTCCAAACCAATTTCTCAG 1394
QY	1382 TTGTTTGTCTCAATAGACCTTCCCCTGAGGACTTCAAGTGTCTTCTTAAAGACGAGGC 1441

Db	1395	TTGTTTGCTTCAATAGCTTCCTCCCTCAGACCTTCAGGTGCTCTCTATAAAGACCGAGGC	1455
QY	1442	ACCAANAGGAGTCAATCACAAAGCACTGC	1470
Db	1455	ACCAAGAGGAGTCAATCACAAAGCACTGC	1483
RESULT 8			
AF286725		1038 bp	linear
LOCUS			ROD 23-AUG-2000
DEFINITION			Mus musculus platelet-derived growth factor C (Pdgfc) mRNA, complete cds.
ACCESSION			AF286725
VERSION			AF286725.1
KEYWORDS			GI:9652343
SOURCE			Mus musculus (house mouse)
ORGANISM			Mus musculus
REFERENCE			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; 1 (bases 1 to 1038)
AUTHORS			Ding, H., Wu, X., Kim, I., Tam, P. P., Koh, G. Y. and Nagy, A.
TITLE			The mouse Pdgfc gene: dynamic expression in embryonic tissues during organogenesis
JOURNAL			Mech. Dev. 96 (2), 209-213 (2000)
MEDLINE			20417814
PUBMED			10960785
REFERENCE			2 (bases 1 to 1038)
AUTHORS			Ding, H., Wu, X., Tam, P. P. L. and Nagy, A.
TITLE			Direct Submission
JOURNAL			Submitted (12-JUL-2000) Samuel Lunenfeld Research Institute, Mount Sinai Hospital, 600 University Avenue, Toronto, Ontario M5G 1X5, Canada
FEATURES			Location/Qualifiers
source			1..1038
			/organism="Mus musculus"
			/mol_type="mRNA"
			/strain="Swiss-Webster/NIH"
			/db_xref="taxon:10090"
gene			1..1038
			/gene="pdgfc"
CDS			1..1038
			/gene="Pdgfc"
			/note="PDGFC; similar to PDGF/VEGF"
			/codon_start=1
			/product="platelet-derived growth factor C"
			/protein_id="AAF91483.1"
			/db_xref="GI:9652344"
			/translation="MLLGLLLLTSLALAQRTGTRAEENLSKLQISDKEONGVDDI RHERVVTISGSHSPKPHPTPRNVLVRLVADENVRTQITFDERFLEDEDED ICKDFVBPVSDGSLGRWCGSETPGKTSKGNHIRIFVSDPEYFPSEFGFCH SIIMPOVTEITSPVLPTSSLDLNNNAFTSLLELIRYLEPDRWQVDLDSLYK TWQLLGLKAFLYVKKSKVYNILLLKEVKLYSCTPRNFVSIRIELKRTDTRFWPGL VARCGNCACCLHNCNEQCQPRKTKKKVHEVLQLRPKTGVKGLHSLTDVALEHHE CDCVCRGNAGG"
BASE COUNT	287 a	230 c	274 g 247 t
ORIGIN			
Query Match			69.8%; Score 1028.4; DB 10; Length 1038;
Best Local Similarity			99.4%; Pred. No. 2.8e-288;
Matches 1032; Conservative			0; Mismatches 6; Indels 0; Gaps 0
QY	196	ATGCTCTCTCGGCCCTCTCTCTGTGTGACATCTGCCCTGCGCGCCAAAGAACGGGACT	255
Db	1	ATGCTCTCTCGGCCCTCTCTCTGTGTGACATCTGCCCTGCGCGCCAAAGAACGGGACT	60
QY	256	CGGGCTGAGTCCAACTGACGACCAAGTTGACGCTTCCAGCGACAAAGAACGGA	315
Db	61	CGGGCTGAGTCCAACTGACGACCAAGTTGACGCTTCCAGCGACAAAGAACGGA	120
QY	316	GTGCAAGATCCCGGATGAGAGAGTTGTCACTATATCTGGTAATGGGACATCCACGC	375
Db	121	GTGCAAGATCCCGGATGAGAGAGTTGTCACTATATCTGGTAATGGGATCCACGC	180

AB033831	1817 bp	mRNA	linear	PRI 26-JUL-2000			
LOCUS	Homo sapiens hSCDGF mRNA for spinal cord-derived growth factor, complete cds.						
DEFINITION	Homo sapiens hSCDGF mRNA for spinal cord-derived growth factor, complete cds.						
ACCESSION	AB033831						
VERSION	AB033831.1	GI:9392293					
KEYWORDS	spinal cord-derived growth factor; scdGF gene.						
SOURCE	Homo sapiens (human)						
ORGANISM	Homo sapiens						
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
AUTHORS	1 (sites) Hamada, T., Ui-Tei, K. and Miyata, Y.						
TITLE	A novel gene derived from developing spinal cords, SCDGF, is a unique member of the PDGF/VSGF family						
JOURNAL	FEBS Lett. 475 (2), 97-102 (2000)						
MEDLINE	20317014						
PUBMED	10858496						
REFERENCE	2 (bases 1 to 1817)						
AUTHORS	Hamada, T., Ui-Tei, K. and Miyata, Y.						
TITLE	Direct Submission						
JOURNAL	Submitted (25-OCT-1999) Tsuyoshi Hamada, Nippon Medical School,						

Department of Pharmacology; 1-1-5, Sendagi, Bunkyo-ku, Tokyo  
113-8602, Japan (E-mail: t-hamada@nms.ac.jp,  
Tel: 81-3-3822-2131 (ex. 5277), Fax: 81-3-5814-1684)

FEATURES

source  
Location/Qualifiers  
1. .1817  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="brain"  
/dev\_stage="embryo"  
1. .1817  
/gene="hSCDGF"  
327. .1364  
/gene="hSCDGF"  
/codon\_start=1  
/product="spinal cord-derived growth factor"  
/protein\_id="BAB03266.1"  
/db\_xref="GI:9392294"  
/translation="MSLFGLLLTALAGQGTQAEINLSKQFNSKQNGVQDP  
QHERIITVSTNGSIHSPRPHYPTNTVLVRLVAEENVMIOQLTDFRFLGLEDPD  
ICKYDFVEBPSSDGLILGRWCGSTVFKQISKNQIRIRFVSEYFSPFGCIHY  
NIVMPOETAEVSPVLPSPALDILNNATFASLEDLIRYLEPRLQLELDLYRP  
TWOLLKAFVGRKSERVDLNLITVEVRLYSCTPNSFVSIREELKRDITTFWPCCLL  
VRCGCGNACCLHNCBQCVPKSKYKXVHEVLQLRPKTVGRGLHLSLTDVALEHES  
CDCVCRGSTGG"  
BASE COUNT 501 a 412 c 424 g 477 t 3 others  
ORIGIN  
Query Match 62.0%; Score 914.2; DB 9; Length 1817;  
Best Local Similarity 83.5%; Pred. No. 6.4e-255;  
Matches 1050; Conservative 0; Mismatches 203; Indels 4; Gaps 1;  
QY 2 ACCTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTAATGGAAACTA 61  
Db 129 AACTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTAATGGAAACTA 188  
QY 62 CCCTGGATTCTCTGTCAGAGCGCGCGAGCGCTTCCACCGCAGCGAGCGCTTTCCC 121  
Db 189 CCCTGGATTCTCTGTCAGAGCGCGCGAGCGCTTCCACCGCAGCGAGCGCTTTCCC 248  
QY 122 CGG----GCTGGGCTGAGCTTGGAGTCTGCTTCCCGAGTCCCGCGCGAGTCAAGC 177  
Db 249 TGGCGGTGTGAAAGAGATCGGGAGTCGTCTTCCAAAGTCCCGCGCGAGTCAAGC 308  
QY 178 CTCGCCCGAGTCAGCCAAATGCTCTCTCGGCTCTCTGCTGACATCTGCGCTGGCC 237  
Db 309 CTCACCCCGAGTCAGCCAAATGAGCTCTCTCGGCTCTCTGCTGACATCTGCGCTGGCC 368  
QY 238 GGCCTAAGAACGGGAGCTCGGCTGAGTCCCACTGAGCAGCAAGTTGAGCTCTCCAGC 297  
Db 369 GGCCTAAGAACGGGAGCTCGGCTGAGTCCCACTGAGTAAATTCACAGTTTCCAGC 428  
QY 298 GACAGGACACAGAGAGTCAAGATCCCGCATGAGAGAGTGTCTACTATCTGGT 357  
Db 429 AACAGGACACAGAGAGTCAAGATCCCTGACATGAGAGATTAATCTGTCTACT 488  
QY 358 AATGGGAGATCCACAGCCCGAAGTTTCTCTATACGTACCCAGAAATATGGTGGTG 417  
Db 489 AATGGAGATTACAGCCCAAGTTTCTCTATCTATCTATCAAGAAATACGGTCTGGTA 548  
QY 418 TGAGATTAGTTCAGTAGATGAATGTCCGATCCAGTCCAGTGCATTTGATGAGATTT 477  
Db 549 TGGAGATTAGTTCAGTAGAGGAAATGTATGATGATCAACTTACGTTTGTATGAAGATTT 608  
QY 478 GGCCTGAAGATCCAGAGACGATATATCAAGTATGATTTTGTAGAAATTTGAGGAGCCC 537  
Db 609 GGCCTGAAGATCCAGAGAGTATGATATGATGATGATTTTGTAGAGTTGAGGAGCCC 668  
QY 538 AGTGATGGAAGTGTATAGGACGCTGGTGTGGTCTGGGACTGTGCCAGGAAAGAGACT 597  
Db 669 AGTGATGGAAGTATATAGGCGCTGGTGTGGTCTGGTACTGTGACAGGAAAGAGATT 728  
QY 598 TCTAAGGAAATCATATCAGGATGAAGATTTGTATCTGATGAGTATTTTCCATCTGAACCC 657

Db 729 TCTAAGGAAATCAATTTAGGATAGATTTGTATCTGATGATATTTTCTCTCTGAACCA 788  
QY 658 GGATTCTGCATCCACTACAGATTATATGCAACAGTCAAGTCAAGAAACCAAGTCTCTCG 717  
Db 789 GGGTTCTGCATCCACTACCAATTGTCTGACCAATTCACAGAAAGCTGTGAGTCTCTCA 848  
QY 718 GTGTTGCCCTTCTATCTTTGTCTGATGACCTGCTCAACAAATGCTGTGATGCTCTCACT 777  
Db 849 GTGCTACCCCTTCTGAGCTTTGCCACTGACCTGCTTAAATATGCTATTAATGCTCTTGT 908  
QY 778 ACCTTGAAGAGCTGATTTCGGTACCTAGAGCAGATCGATGCGAGTGTGACTTTGACAGC 837  
Db 909 ACCTTGAAGAGCTTATTCGATATCTTGAACCGAGAGATGCGAGTTGACCTTAGAGAT 968  
QY 838 CTCTAAGGCCAACATGCGAGCTTTTGGCAAGGCTTCTCTATGCGGAAAAAAGCAAA 897  
Db 969 CTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTTTTGGAAAGAAATCCAGA 1028  
QY 898 GTGGTGAATCTGAATCTCTCAAGAGAGGTAAAACTCTAGAGCTGCAACCCCGGAAC 957  
Db 1029 GTGGTGGATCTGAACCTTCTTAAACGAGGAGGTAAAGATTATACAGCTGCAACCTCTGTAAC 1088  
QY 958 TTCTCAGTGTCCATACGCGAAGAGCTTAAAGAGAGCAGATACCATATTTCTGGCCAGTTGT 1017  
Db 1089 TTCTCAGTGTCCATTAAGGAGAGAACTTAAGAGAACCGATACCATTTTCTGGCCAGTTGT 1148  
QY 1018 CTCCTGGTCAAGCGCTGTGGAGAAATTTGCTGCTGTGTCTCTCATTAATTTGCAATGATGT 1077  
Db 1149 CTCCTGGTTAAACGCTGTGTTGGAACTGTGCTGTGTGTCTCCCAATTTGCAATGATGT 1208  
QY 1078 CAGTGTGCTCCAGTTAAAGTTACAAAAAGTACCAAGTACCTGAGTCTCTGAGTTCAGCAACAAA 1137  
Db 1209 CAATGTGTCTCCAGCAAGATTACTAAAAAATACCAAGTCTCTGAGTTCAGTTCAGCAACAAAG 1268  
QY 1138 ACTGGAGTCAAGGATTGCTAAGTCACTCACTGATGTGCTCTGAGTTCAGTTCAGCAACAAAG 1197  
Db 1269 ACGGTGTCAAGGATTGCAAAATCACTCCAGCGTGGCTTGGAGCAACATGAGGAG 1328  
QY 1198 TGTGACTGTGTGTAGAGAAACGAGAGGGTAACTGAGCGCTTCGTGATGAGGACAC 1254  
Db 1329 TGTGACTGTGTGTAGAGAGGAGCAGAGGAGTAGCGCATCACCAACGAGCAGCTC 1385  
RESULT 11  
AR210624  
LOCUS Sequence 1 from patent US 6391311. linear PAT 20-JUN-2002  
DEFINITION  
ACCESSION AR210624  
VERSION AR210624.1 GI:21513401  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 2825)  
TITLES Ferrara,N. and Kuo,S.S.  
JOURNAL Polypeptides having homology to vascular endothelial cell growth  
FEATURES factor and bone morphogenetic protein 1  
Patent: US 6391311-A 1 21-MAY-2002;  
source Location/Qualifiers  
1. .2825  
/organism="unknown"  
BASE COUNT 849 a 522 c 605 g 848 t 1 others  
ORIGIN  
Query Match 62.0%; Score 914.2; DB 6; Length 2825;  
Best Local Similarity 83.5%; Pred. No. 7e-255;  
Matches 1050; Conservative 0; Mismatches 203; Indels 4; Gaps 1;  
QY 2 ACCTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTAATGGAAACTA 61  
Db 61 AACTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTAATGGAAACTA 120









||||| 1107 CTCCTGGTAAACGCTGTGGTGGGACCTGCTCTGTGTCTCCAAATTCGAATGAT 1166  
QY 1078 CAGTGTGCCACGCTAAAGTTTACAAAAGTACCATAGAGTCTCTTCAAGTTGAGACCAAAA 1137  
Db 1167 CAATGTGTCCCAAGCAAAAGTTTACTAAAAAATACCACGAGTCTCTTCAAGTTGAGACCAAAAG 1226  
QY 1138 ACTGAGTCAAGGATTCGATTAAGTCACTCACTGATGTGGCTCTGGAACACACGAGGAA 1197  
Db 1227 ACCGTGTGAGGGGATTCGCAAAATCACTCACCGACGTGGCCCTGGAGCACCATGAGGAG 1286  
QY 1198 TGTGACTGTGTGTAGAGGAAACGAGGAGGTAACTGACGCTTCTGAGCAGCAC 1254  
Db 1287 TGTGACTGTGTGTGACAGGGAGCACAGGAGGATAGCCGCATCACACCAGCAGCTC 1343  
  
RESULT 14  
AX391260 2849 bp DNA linear PAT 23-MAR-2002  
LOCUS Sequence 3 from Patent WO0073445.  
ACCESSION AX391260  
VERSION AX391260.1 GI:19699933  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
Ferrara,N., Williams,P.M., Baker,K.P., Ashkenazi,A.J., Goddard,A.,  
Godowski,P.J., Gurney,A.L., Kuo,S.S., Mark,M.R., Marsters,S.A.,  
Pitti,R.M., Wood,W.I., Gerber,H., Gerritsen,M.E., Paoni,N.F. and  
Watanabe,C.K.  
TITLE Promotion or inhibition of angiogenesis and cardiovascularization  
JOURNAL Patent: WO 0073445-A 3 07-DEC-2000;  
Genentech Inc. (US)  
FEATURES  
Location/Qualifiers  
1..2849  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 851 a 528 c 619 g 850 t 1 others  
ORIGIN  
  
Query Match 62.0%; Score 914.2; DB 6; Length 2849;  
Best Local Similarity 83.5%; Pred. No. 7e-255;  
Matches 1050; Conservative 0; Mismatches 203; Indels 4; Gaps 1;  
  
QY 2 ACCTGAGACACAGAGGGCTCTAGGAAAATTTTGGATGGGATTTATGTGGAACATA 61  
Db 87 AACTGGAGACACAGAGGGCTCTAGGAAAATTTTGGATGGGATTTATGTGGAACATA 146  
QY 62 CCTCGGATTCCTGCTGCCAGAGCGGCGCTTCCACCGCAGCGAGCTTTTCCC 121  
Db 147 CCTCGGATTCCTGCTGCCAGAGCGGCTTCCACCGCAGCGAGCTTTTCCC 206  
QY 122 CGG----GCTGGGCTGAGCCTTGAGTGTGCTTCCCGAGTGCCTCCCGCGAGTGTGAGCC 177  
Db 207 TGGCGGTGTGAAAGACTCGGGAGTGTGCTTCCAAAGTCCCGCGCTGAGTGTGAGCT 266  
QY 178 CTGCGCCCGTACGCAAAATGCTCTCTCGGCTCTCTGCTGATGCTGATGCTGCGCC 237  
Db 267 CTACCCCGTACGCAAAATGAGGCTCTTCCGGCTTCTCTGCTGATGCTGCTGCGCC 326  
QY 238 GGCCAAAGACGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCGAGCTTCCAGC 297  
Db 327 GGCCAGAGACGGGACTCAGCGGGAATCCAACTGAGTAGTAATTCAGATTTCAGC 386  
QY 298 GACAAGAAACAGACGAGGTGCAAGATCCCGCGCATGAGAGAGTTGTCACTATCTGGT 357  
Db 387 AACAAAGAAACAGACGAGGTGCAAGATCCCTCAGCATGAGAGAAATTTACTGTGTCTACT 446  
QY 358 AATGGAGCATCCACAGCCCGAGTTTCTCTATACGTACCCAGAAATATGTTGCTGTG 417  
|||||

Db 447 AATGGAAGTATTCACAGCCCAAGGTTTCTCATATCTTATCCAAAGAAATACGGTCTTGGTA 506  
QY 418 TGGAGATTAGTTGCTAGTAGATGAAAATGTGCGGATCCAGCTGACATTTTATGAGAGATT 477  
Db 507 TGAAGATTAGTAGCAGTAGAGGAAAATGTATGATACAACTTACGTTTATGAAAGATT 566  
QY 478 GGGCTGGAAGATCCAGAGAAGATATATGCAAGTATGATTTTGTAGAAATTCAGGAGGCC 537  
Db 567 GGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTTGTAGAAATTCAGGAGGCC 626  
QY 538 AGTATGGAAGTGTGTTTAGGACGCTGTGTGCTCTTGGACCTGTGCCAGGAAAGCAGACT 597  
Db 627 AGTATGGAAGTATATATAGGCGCTGTGTGCTCTTGGTACTGTACAGGAAAGAGATT 686  
QY 598 TCTAAAGGAAATCATATCAGGATAAGATTGTATCTGTAGTATTTTCCATCTGAAACCC 657  
Db 687 TCTAAAGGAAATCAAAATTAGGATAGATTGTATCTGTATGATATTTTCTCTGAACCA 746  
QY 658 GGATTCGTGATCCATCAGTATTTATCATGCGACAAAGTACAGAAACCCAGGATCTCTCG 717  
Db 747 GGGTTCTGCATCCACTACAACTTGTCAATGCGCACAAATTCACAGAGCTGTGAGTCTTCA 806  
QY 718 GTGTTGCCCTTCTCATCTTTGTCTTGGACCTGCTCAACAATGCTGTGACTGCTTCACT 777  
Db 807 GTGCTACCCCTTCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 866  
QY 778 ACCTTGGAAAGAGCTGATTCGCTACCTAGAGCAGATCGATGGCAGGTGGAATTTGGACG 837  
Db 867 ACCTTGGAAAGAGCTTATTCGATATCTTGAACAGAGAGATGGCAGTTGAGATTTAGA 926  
QY 838 CTCACAGCCCAACATGCGAGCTTTTGGCAGGCTTCTCTGTATGGGAAAAAAGCAAA 897  
Db 927 CTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTGTTTGGAAAGAAATCCAG 986  
QY 898 GTGGTGAATCTGAATCTCTCAAGGAGAGGTAAATCTACAGCTGCACACCCCGGAAC 957  
Db 987 GTGGTGAATCTGAATCTCTCAAGGAGAGGTAAATCTACAGCTGCACACCCCGGAAC 1046  
QY 958 TTCTCAGTGTCCATACGGGAAGCTTAAAGAGGACAGATACCAATTTCTGGCCAGGTTGT 1017  
Db 1047 TTCTCAGTGTCCATACGGGAAGCTTAAAGAGGACCGATACCAATTTCTGGCCAGGTTGT 1106  
QY 1018 CTCCTGGTCAAGCGCTGTGAGGAAATTTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1077  
Db 1107 CTCCTGGTCAAGCGCTGTGAGGAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1166  
QY 1078 CAGTGTGTCCCGTAAAGTTTCAAAAAGTACCATGAGTCTCTCAGTTGAGACCAAAA 1137  
Db 1167 CAGTGTGTCCCGTAAAGTTTCAAAAAGTACCATGAGTCTCTCAGTTGAGACCAAAA 1226  
QY 1138 ACTGAGTCAAGGATTCGATTAAGTCACTCACTGATGTGGCTCTGGAACACCCAGAGAA 1197  
Db 1227 ACCGTGTGAGGGGATTCGCAAAATCACTCACCGAGCTGGGCTTGGAGCACTGAGGAG 1286  
QY 1198 TGTGACTGTGTGTAGAGGAAACGAGGAGGTAACTGAGCTTCTGAGCAGCAC 1254  
Db 1287 TGTGACTGTGTGTGACAGGGAGCACAGGAGGATAGCCGCATCACACCAGCAGCTC 1343  
  
RESULT 15  
AX464152 2849 bp DNA linear PAT 16-JUL-2002  
LOCUS Sequence 285 from Patent WO0140466.  
ACCESSION AX464152  
VERSION AX464152.1 GI:21899092  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
Baker,K.P., Beresini,M., Deforge,L., Desnoyers,L., Filvaroff,E.,  
Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L.,

Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K.,  
Wood, W.L. and Zhang, Z.  
Secreted and transmembrane polypeptides and nucleic acids encoding  
same

JOURNAL Patent: WO 0140466-A 285 07-JUN-2001;  
Genentech Inc. (US)

FEATURES Location/Qualifiers

1..2849  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 851 a 528 c 619 g 850 t 1 others

Query Match	62.0%;	Score 914.2;	DB 6;	Length 2849;
Best Local Similarity	83.5%;	Pred. No. 7e-255;		
Matches 1050;	Conservative	0;	Mismatches 203;	Indels 4; Gaps 1;
QY	2	ACCTGGAGACACAGAGAGGGCTCTAGGAAATTTTGGATGGGATTATGTGGAACTA	61	
Db	87	AACCTGGAGACACAGAGAGGGCTCTAGGAAATTTTGGATGGGATTATGTGGAACTA	146	
QY	62	CCCTGGATTCTGTGTCAGAGCCGCGCAGCGCTTCACCGCAGCGCAGCTTCC	121	
Db	147	CCCTGGATTCTGTGTCAGAGCGGCTCGCGCTTCACCGCAGCGCAGCTTCC	206	
QY	122	CGS---GCTGGGCTGAGCTTGGAGTCTGCTGCCAGTCCCGCGCGAGTGAGCC	177	
Db	207	TGGCGGTGTGAAGAGACTCGGGAGTCTGCTTCCAAAGTCCCGCGCGTGGTGGCT	266	
QY	178	CTCGCCCACTCAGCCAAATGCTCTCTCGGCTCTCTGCTGACATCTGCTGGCC	237	
Db	267	CTCACCCAGTCAGCCAAATGAGCCTCTCGGCTCTCTGCTGACATCTGCTGGCC	326	
QY	238	GGCCHAAAGACGGGACTCGGCTGAGTCCAGCTCAGCAGCAGTTCAGCTCTCAGC	297	
Db	327	GGCCAGACAGCGGACTCAGCGGAAATCCAACTCAGTAGTAATATTCAGTTTCCAGC	386	
QY	298	GACAGGAACAGAACGGAGTGCAGATCCCGCATGAGAGTGTCTACTATATCTGGT	357	
Db	387	AACAGGAACAGAACGGAGTGCAGATCTCAGCTCAGCAGCAGTTCAGCTCTCAGC	446	
QY	358	AATGGAGCATCCACAGCCCGAAGTTTCTCATACGTACCCAGAAATATGGTGGTG	417	
Db	447	AATGGAGTATTCACAGCCCAAGTTTCTCATACGTATCCAAAGAAATACGGTCTTGGTA	506	
QY	418	TGGAGATTAGTTGACGTAGATGAATATGCGGATCCAGCTGACATTTGATGAGATTT	477	
Db	507	TGGAGATTAGTACGTAGAGGAAATATGATGATACAACTTACGTTTGTATGAAGATTT	566	
QY	478	GGGCTGGAAGATCCAGAACGATATATGCAAGTATGATTTGTAGAAGTTGAGGAGCCC	537	
Db	567	GGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTGTAGAAGTTGAGGAGCCC	626	
QY	538	AGTGATGGAAGTGTATTTAGGACGCTGGTGGTTCGGGACTGTGCCAGGAAAGCAGCT	597	
Db	627	AGTGATGGAAGTGTATTTAGGAGCGCTGGTGGTTCGGGACTGTGCCAGGAAAGCAGTT	686	
QY	598	TCTAAGGAATCATATCAGGATAAGATTTGTATCTGTAGTATTTCCATCTGAACCC	657	
Db	687	TCTAAGGAATCATATCAGGATAAGATTTGTATCTGTAGTATTTCCATCTGAACCA	746	
QY	658	GGATTCTGCATCCACTACAGTATTTATCCCAAGTACAGAAACCAAGTCTCTTCG	717	
Db	747	GGGTTCTGCATCCACTACAGTATTTATCCCAAGTACAGAAACCAAGTCTCTTC	806	
QY	718	GTGTTGCCCTTTCATCTTTGTCATTTGAGCTGCTGCTCAACATGCTGTGACTGCTTCAGT	777	
Db	807	GTGCTACCCCTTTCAGCTTTGCCACTGAGCTGCTTAAATGCTATTAAGTCTTGTAGT	866	
QY	778	ACCTTGGAGAGCTGATTCGGTACCTAGACCGAGATCGATGGCAGGTGGACTTGGACGC	837	
Db	867	ACCTTGGAGAGCTTATTCGATATCTTTGAACACAGAGAGATGGCAGGTGGACTTGAAGAT	926	

QY	838	CTCTACAGCCCAACATGCGAGCTTTTGGCAAGGCTTTCTGTATCGGAAAAAAGCAAA	897	
Db	927	CTATATAGCCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTGTTTGGAAAGAAATCCAGA	986	
QY	898	GTGGTGAATCTGAATCTCTCAAGGAGAGGTAATACTCTACAGCTGCACACCCCGAAC	957	
Db	987	GTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAAC	1046	
QY	958	TTCTCAGTGTCCATACCGGAGAGGCTTAAAGAGGACAGATACCATATTTCTGGCCAGTTGT	1017	
Db	1047	TTCTCAGTGTCCATACCGGAGAGGCTTAAAGAGGACAGATACCATATTTCTGGCCAGTTGT	1106	
QY	1018	CTCTGGTCAAGCGCTGTGGAGGAAATTTGCTGTGTGCTCCATATTTGCAATGAATGT	1077	
Db	1107	CTCTGGTCAAGCGCTGTGGTGGAACTCTGCTGTGTGCTCCCAATTTGCAATGAATGT	1166	
QY	1078	CAGTGTGTCCCACTGAATTTACAAAAAGTACCATGAGTCTCTCAGTTGAGACCAAAA	1137	
Db	1167	CAATGTGTCCCAAGCAAAAGTTACTAAAAAATACCAAGAGTCTCTCAGTTGAGACCAAG	1226	
QY	1138	ACTGGAGTCAAGGAGTTGCATTAAGTCACTCACTGATGTGCTCTGGAACACACACGAGAA	1197	
Db	1227	ACCGTGTCAAGGAGTTGCATTAAGTCACTCACTGATGTGCTCTGGAACACACACGAGAA	1286	
QY	1198	TGTGACTGTGTGTAGAGGAAACCGAGGAGGTAACCTGAGGCTTTCTGTAGCAGCAC	1254	
Db	1287	TGTGACTGTGTGTAGAGGAGCAACAGGAGGATAGCCGATCACCACGAGCAGCTC	1343	

Search completed: November 26, 2003, 03:42:42  
Job time : 3647.09 secs



PR 03-DEC-1998; 98US-0110749.  
PR 18-DEC-1998; 98US-0113002.  
PR 21-MAY-1999; 99US-0135426.  
PR 15-JUL-1999; 99US-0144022.  
XX (LUDW-) LUDWIG INST CANCER RES.  
PA (UYHE-) UNIV HELSINKI LICENSING LTD.  
XX Eriksson U, Aase K, Lee X, Ponten A, Uutela M, Alitalo K;  
PI Oestman A, Heldin C, Betsholtz C;  
PI WPI, 2000-292954/25.  
DR P-PSDB; AAY84559.  
XX Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation,  
PT differentiation, growth and motility of cells expressing the PDGF-C  
PT receptor -  
XX Claim 7; Fig 5; 135pp; English.  
XX The present sequence encodes murine platelet-derived growth factor C  
CC (PDGF-C) (formally designated VEGF-F). PDGF-C polypeptides have the  
CC ability to stimulate and enhance proliferation or differentiation,  
CC and/or growth or motility of cells expressing a PDGF-C receptor.  
CC PDGF-C polypeptides can be used in pharmaceuticals for promoting cell  
CC proliferation, preferably in combination with one other growth factor  
CC and heparin. Pharmaceuticals comprising PDGF-C polypeptides can also  
CC be used for stimulating connective tissue or wound healing. The  
CC truncated form of PDGF-C and used to regulate the receptor-binding  
CC specificity of PDGF-C. PDGF-C can also be used to promote fibroblast  
CC mitogenesis in a mammal and to induce PDGF alpha receptor activation.  
CC PDGF-C antagonists can be used to inhibit tumour growth of a tumour  
CC expressing PDGF-C in a mammal. Specific types of human tumours, e.g.  
CC choriocarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma  
CC and erythroleukemia, can be identified by testing for expression of  
CC PDGF-C. PDGF-C antagonists can also be used to inhibit tissue  
CC remodelling during invasion of tumour cells into a normal population of  
CC cells. Antagonists can also be used to treat fibrotic conditions,  
CC especially found in the lung, kidney or liver.  
XX Sequence 1474 BP; 381 A; 368 C; 384 G; 340 T; 1 other;

Db 361 GGGAGCATCCACAGCCCGAAGTTTCCTCATAGTACCAAGAAATATGCTGCTGTGG 420  
Qy 421 AGATTAGTTGAGTAGATAAAATGTGCGGATCCAGCTGACATTTGATGAGAGATTGGG 480  
Db 421 AGATTAGTTGAGTAGATAAAATGTGCGGATCCAGCTGACATTTGATGAGAGATTGGG 480  
Qy 481 CTGGAAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAAAGTTGAGAGCCAGT 540  
Db 481 CTGGAAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAAAGTTGAGAGCCAGT 540  
Qy 541 GATGGAAGTGTGTTAGGACGCTGTGTTCTGGACTGTGCCAGGAAGCAGACTTCT 600  
Db 541 GATGGAAGTGTGTTAGGACGCTGTGTTCTGGACTGTGCCAGGAAGCAGACTTCT 600  
Qy 601 AAAGGAATCATATCAGGATAAGATTTCATCTGATGAGTATTTTCCATCTGAACCCGGA 660  
Db 601 AAAGGAATCATATCAGGATAAGATTTCATCTGATGAGTATTTTCCATCTGAACCCGGA 660  
Qy 661 TTCTGCATCCACTACAGTATTATCATGCCAACAGTTCACAGAAACCCAGAGTCTTGGGTG 720  
Db 661 TTCTGCATCCACTACAGTATTATCATGCCAACAGTTCACAGAAACCCAGAGTCTTGGGTG 720  
Qy 721 TTGCCCCCTTCATCTTTCTGTCATTTGACCTGCTCAACAATGCTGCTCACTCCCTTCAGTACC 780  
Db 721 TTGCCCCCTTCATCTTTCTGTCATTTGACCTGCTCAACAATGCTGCTCACTCCCTTCAGTACC 780  
Qy 781 TTGGAAGAGCTGATTTCGGTACCTAGAGCCAGATCCAGTGGAGTGGACTTGGACAGCCTC 840  
Db 781 TTGGAAGAGCTGATTTCGGTACCTAGAGCCAGATCCAGTGGAGTGGACTTGGACAGCCTC 840  
Qy 841 TACAAGCCAAACATGCGAGCTTTTGGGCAAGGCTTTCTGTTATGGGAAAAAGCAAGTG 900  
Db 841 TACAAGCCAAACATGCGAGCTTTTGGGCAAGGCTTTCTGTTATGGGAAAAAGCAAGTG 900  
Qy 901 GTGAATCTGAATCTCTCTCAAGAGAGGTAACCTCTACAGCTGCACACCCCGGAATTC 960  
Db 901 GTGAATCTGAATCTCTCTCAAGAGAGGTAACCTCTACAGCTGCACACCCCGGAATTC 960  
Qy 961 TCAGTGTCCATACGGGAGAGCTAAAGAGGACAGATACCATATTTCTGCGCAGGTTGCTC 1020  
Db 961 TCAGTGTCCATACGGGAGAGCTAAAGAGGACAGATACCATATTTCTGCGCAGGTTGCTC 1020  
Qy 1021 CTGGTCAAGCGCTGTGGAGAAATTTGCTGCTGTGCTCCATATTTGCAATGATGTCAG 1080  
Db 1021 CTGGTCAAGCGCTGTGGAGAAATTTGCTGCTGTGCTCCATATTTGCAATGATGTCAG 1080  
Qy 1081 TGTGTCACCAAGTAAAGTTACAAAAGTAGTACCATGAGTCTCTCAGTTGAGACCAAAACT 1140  
Db 1081 TGTGTCACCAAGTAAAGTTACAAAAGTAGTACCATGAGTCTCTCAGTTGAGACCAAAACT 1140  
Qy 1141 GGAGTCAAGGGATTGCAATAGTCACTCACTGATGTGGCTCTGGAAACCAACGAGGAATGT 1200  
Db 1141 GGAGTCAAGGGATTGCAATAGTCACTCACTGATGTGGCTCTGGAAACCAACGAGGAATGT 1200  
Qy 1201 GACTGTGTGTAGAGAAACGAGAGGGTAACCTGACGCTTCGTAGACGACACGTGA 1260  
Db 1201 GACTGTGTGTAGAGAAACGAGAGGGTAACCTGACGCTTCGTAGACGACACGTGA 1260  
Qy 1261 GCACTGGCAATCTGTGTACCCCAAGCAACCTTCATCCCAACGAGCTGTGCGCGAGG 1320  
Db 1261 GCACTGGCAATCTGTGTACCCCAAGCAACCTTCATCCCAACGAGCTGTGCGCGAGG 1320  
Qy 1321 GCTCTCAGCTGTGATGCTGGCTATGTAAGATCTTACTCGTCTCCAAACCAATTCCTCA 1380  
Db 1321 GCTCTCAGCTGTGATGCTGGCTATGTAAGATCTTACTCGTCTCCAAACCAATTCCTCA 1380  
Qy 1381 GTTGTGTTGTTCAATAGCTTCCCTGCGAGGATTCAGTGTCTTCTAAAGACCGAGG 1440  
Db 1381 GTTGTGTTGTTCAATAGCTTCCCTGCGAGGATTCAGTGTCTTCTAAAGACCGAGG 1440  
Qy 1441 CACCAANAGAGTCAATCAAAAGCACTGCACCG 1474  
Db 1441 CACCAANAGAGTCAATCAAAAGCACTGCACCG 1474

XX	SQ	Sequence	3571 BP; 876 A; 935 C; 875 G; 885 T; 0 other;	Query Match	98.0%; Score 1444.8; DB 21; Length 3571;
				Best Local Similarity	99.4%; Pred. No. 0;
				Matches 1460; Conservative	0; Mismatches 8; Indels 1; Gaps 1;
QY	2	ACTTGGAGACACAGAGAGGGCTCTAGGAAAAATTTGGATGGGATTATGTGGAAACTA	61		
DB	856	AAC TGGAGACACAGAGAGGGCTCTAGGAAAAATTTGGATGGGATTATGTGGAAACTA	915		
QY	62	CCCTGCCATTCTCTGCTGCACAGACCGCGCCAGGCGCTTCCACGCGCAGCGCTTTCCC	121		
DB	916	CCCTGCCATTCTCTGCTGCACAGACCGCGCGCTTCCACGCGCAGCGCTTTCCC	975		
QY	122	CGGGCTGGGCTGAGCCTTGGAGTGTGCGTTCCCGTCCCGCGCGAGTGAGCCCTCG	181		
DB	976	C-GGCTGGGCTGAGCCTTGGAGTGTGCGTTCCCGTCCCGCGCGAGTGAGCCCTCG	1034		
QY	182	CCCAGTGCAGCAATGCTCTCTCTGGGCTCTCTGCTGCTGACATCTGCCCTGGCGGGC	241		
DB	1035	CCCAGTGCAGCAATGCTCTCTCTGGGCTCTCTGCTGCTGACATCTGCCCTGGCGGGC	1094		
QY	242	AAAGAA CGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCGAGCTCTCCAGCGACA	301		
DB	1095	AAAGAA CGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCGAGCTCTCCAGCGACA	1154		
QY	302	AGGAACAGAACCGAGTGCAGATCCC CGGCATGAGAGAGTTGTCACTATATCTCGTAA TG	361		
DB	1155	AGGAACAGAACCGAGTGCAGATCCC CGGCATGAGAGAGTTGTCACTATATCTCGTAA TG	1214		
QY	362	GGAGATCCACAGCCGGAAGTTTCTCATAGCTACCGAAGAAATATGGTGTGTTGGGA	421		
DB	1215	GGAGATCCACAGCCGGAAGTTTCTCATATACATACCAAGAAATATGGTGTGTTGGGA	1274		
QY	422	GATTAGTTCAGTGTAGTGAATAATGTGGGATCCAGCTGACATTTGATGAGAGATTGGGC	481		
DB	1275	GATTAGTTCAGTGTAGTGAATAATGTGGGATCCAGCTGACATTTGATGAGAGATTGGGC	1334		
QY	482	TGGAAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAAAGTTGAGGAGCCAGTG	541		
DB	1335	TGGAAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAAAGTTGAGGAGCCAGTG	1399		
QY	542	ATGGAAGTGTTTTAGGACGCTGGTGTGTTCTGGGACTGTGCGAGGAAAGCAGACTTCTA	601		
DB	1395	ATGGAAGTGTTTTAGGACGCTGGTGTGTTCTGGGACTGTGCGAGGAAAGCAGACTTCTA	1455		
QY	602	AAGGAAATCATATCAGGATAGATTTGTATCTGATGAGTATTTTCCATCTGAACCCGAT	661		
DB	1455	AAGGAAATCATATCAGGATAGATTTGTATCTGATGAGTATTTTCCATCTGAACCCGAT	1511		
QY	662	TCCTGATCCACTACAGTATTTATCATGCCACAAGTCA CAGAAACCA CGAGTCCCTCGGTGT	721		
DB	1515	TCCTGATCCACTACAGTATTTATCATGCCACAAGTCA CAGAAACCA CGAGTCCCTCGGTGT	1579		
QY	722	TGCCCCCTTCATCTTTGTCA TTGGACCTGCTCAACAATGCTGTGATCGCTTCAGTACT	781		
DB	1575	TGCCCCCTTCATCTTTGTCA TTGGACCTGCTCAACAATGCTGTGATCGCTTCAGTACT	1633		
QY	782	TGGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGCACTTGGACAGCCTCT	841		
DB	1635	TGGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGCACTTGGACAGCCTCT	1699		
QY	842	ACAAGCCAACTGGCAGCTTTTGGGCAAGGCTTTCTCTGTATGGGAAAAAAGCAAGTGG	901		
DB	1695	ACAAGCCAACTGGCAGCTTTTGGGCAAGGCTTTCTCTGTATGGGAAAAAAGCAAGTGG	1759		
QY	902	TGAATCTGAATCTCTCTCAAGGAAGAGGTAAACTCTACAGCTGCACACCCCGGAATCTCT	961		
DB	1755	TGAATCTGAATCTCTCTCAAGGAAGAGGTAAACTCTACAGCTGCACACCCCGGAATCTCT	1814		
QY	962	CAGTGTCCATACGGGAAGCTTAAAGAGGACAGATACCATATTTCTGGCCAGGTGTCTCC	1021		

Db 1815 CAGTGTCCATACGGGAAGAGCTAAGAGGACAGATACATATTTCTGGCCAGTTGTCTCC 1874

Qy 1022 TGGTCAAGCGCTGTGGAGAAATTTGGCTTTGTCTTCCATAATGCAATGATGTCAGT 1081

Db 1875 TGGTCAAGCGCTGTGGAGAAATTTGTGCTTGTCTTCCATAATGCAATGATGTCAGT 1934

Qy 1082 GTGTCCCAAGTAAATTTACAAAAAGTACCATGAGGTCTTTCAGTTGAGACCAAAAACTG 1141

Db 1935 GTGTCCCAAGTAAATTTACAAAAAGTACCATGAGGTCTTTCAGTTGAGACCAAAAACTG 1994

Qy 1142 GAGTCAAGGATTCATAAGTCACTCACTGATGTGGCTTCTGGAAACACACAGGAATGTG 1201

Db 1995 GAGTCAAGGATTCATAAGTCACTCACTGATGTGGCTTCTGGAAACACACAGGAATGTG 2054

Qy 1202 ACTGTGTGTAGAGGAACGAGAGGTAACCTGACGCTTCTGTAGCAGCACAGTGTAG 1261

Db 2055 ACTGTGTGTAGAGGAACGAGAGGTAACCTGACGCTTCTGTAGCAGCACAGTGTAG 2114

Qy 1262 CACTGGCAATCTGTGTACCCCAAGCAACCTTCATCCCAACAGCGTTGGCCGACGGG 1321

Db 2115 CACTGGCAATCTGTGTACCCCAAGCAACCTTCATCCCAACAGCGTTGGCCGACGGG 2174

Qy 1322 CTCTCAGCTGCTGATGTGGCTATGTTAAAGATCTTACTGTCTCCAAACCAAAATCTCAG 1381

Db 2175 CTCTCAGCTGCTGATGTGGCTATGTTAAAGATCTTACTGTCTCCAAACCAAAATCTCAG 2234

Qy 1382 TGTGTTGTTCAATAGCTTCCCTGCGAGGCTTCAAGTGCTTCTTAAAGACCAAGAGGC 1441

Db 2235 TGTGTTGTTCAATAGCTTCCCTGCGAGGCTTCAAGTGCTTCTTAAAGACCAAGAGGC 2294

Qy 1442 ACCAAGAGGATCAATCAAGACACTGC 1470

Db 2295 ACCAAGAGGATCAATCAAGACACTGC 2323

RESULT 3

AAA51527

ID AAA51527 standard; cDNA; 3571 BP.

XX AC AAA51527;

XX DT 26-SEP-2000 (first entry)

DE Murine vascular endothelial growth factor homologue, ZVEGF3 DNA.

XX Vascular endothelial growth factor; homologue; zveg3; CUB domain;  
KW Cysteine knot; platelet-derived growth factor; PDGF; neuropilin;  
KW chromosome 4q28.3; cytostatic; anti-psoriatic; anti-inflammatory;  
KW anti-diabetic; ophthalmological; anti-rheumatic; anti-arthritis;  
KW vulnery; ss.

XX OS Mus musculus.

XX FH Key Location/Qualifiers  
XX CDS 1049..2086  
XX FT /\*tag= a  
XX PT /product= ZVEGF3

XX PN W0200034474-A2.

XX PD 15-JUN-2000.

XX PF 07-DEC-1999; 99WO-US28968.

XX PR 07-DEC-1998; 98US-0207120.

XX PR 06-JUL-1999; 99US-0142576.

XX PR 21-OCT-1999; 99US-0161653.

XX PR 12-NOV-1999; 99US-0165255.

XX (ZYMO ) ZYMOGENETICS INC.

XX Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;

PI Gilbertson DG, West JW;

XX WPI; 2000-423420/36.  
DR P-PSDB; AAY96861.  
XX Novel zveg3 polypeptides and nucleotides encoding them useful for  
PT stimulating growth of smooth muscle cells and fibroblasts comprising an  
PT epitope bearing portion of a specific amino acid sequence  
XX Claim 30; Page 166-169; 173pp; English.  
XX This DNA encodes murine ZVEGF3 a novel vascular endothelial growth  
CC factor homologue. Polypeptides comprising an epitope-bearing portion  
CC human or murine ZVEGF3 are claimed. The growth factors comprise a growth  
CC factor domain and a CUB domain (generic sequence motifs are shown in  
CC AAY96859 and AAY96860). The growth factor domain is characterized by an  
CC arrangement of cysteine residues and beta-strands that is characteristic  
CC of the "cysteine knot" structure of the platelet-derived growth factor  
CC (PDGF) family. The CUB domain shows homology to CUB domains in  
CC neuropilins, human bone morphogenetic protein-1, porcine seminal plasma  
CC protein, bovine acidic seminal fluid protein and Xenopus laevis  
CC tolloid-like protein. Structural analysis and homology predict that  
CC ZVEGF3 polypeptides complex with a second polypeptide to form multimeric  
CC proteins. The human zveg3 gene has been mapped to chromosome 4q28.3.  
CC ZVEGF3 is useful for stimulating the growth of fibroblasts or smooth  
CC muscle cells, for activating cell surface PDGF-alpha receptor and for  
CC inhibiting PDGF-alpha receptor mediated cellular processes. ZVEGF3 is  
CC useful for regulating (post-development) organ growth, regeneration and  
CC maintenance, as well as tissue maintenance and repair processes. ZVEGF3  
CC antagonists are useful for treating cancer, rheumatoid arthritis,  
CC diabetic retinopathy, ischemic limb disease, peripheral vascular  
CC disease, myocardial ischemia, vascular intimal hyperplasia,  
CC atherosclerosis, wound healing, chronic liver disease and haemangioma  
CC formation. ZVEGF3 can also be used to modulate neurite growth and  
CC development of the nervous system, and for treating neurodegenerative  
CC diseases.

XX SQ Sequence 3571 BP; 876 A; 935 C; 875 G; 885 T; 0 other;

Query Match 98.0%; Score 1444.8; DB 21; Length 3571;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 1460; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

Qy 2 ACCTGGAGACACAGAGGGCTCTAGGAAAATTTTGGATGGGGATTATGGAACATA 61

Db 856 AACTGGAGACACAGAGGGCTCTAGGAAAATTTTGGATGGGGATTATGGAACATA 915

Qy 62 CCTCGGATTCCTGCTGCCAGCGCGCCAGCGCTTCCACCGCAGCGCAGCTTTCCC 121

Db 916 CCTCGGATTCCTGCTGCCAGCGCGCCAGCGCTTCCACCGCAGCGCAGCTTTCCC 975

Qy 122 CGGGCTGGGCTGAGCCTTGGAGTCGTCTTCCCAAGTCCCGCCCGAGTGAGCCCTCG 181

Db 976 C-GGCTGGGCTGAGCCTTGGAGTCGTCTTCCCAAGTCCCGCCCGAGTGAGCCCTCG 1034

Qy 182 CCCCAGTCAGCCAAATGCTTCTCGGCTCTCTCTGTCGACATCTGCCCTGGCCGCC 241

Db 1035 CCCCAGTCAGCCAAATGCTTCTCTCGGCTCTCTCTGTCGACATCTGCCCTGGCCGCC 1094

Qy 242 AAAGACGGGACTCGGGCTGAGTCCAACTCAGCAGCAAGTTGTCAGCTCTCCAGCGACA 301

Db 1095 AAAGACGGGACTCGGGCTGAGTCCAACTCAGCAGCAAGTTGTCAGCTCTCCAGCGACA 1154

Qy 302 AGGAACAGAACGGAGTGCAGATATCCCGGCATGAGAGAGTTGTCACTATATCTGGTAATG 361

Db 1155 AGGAACAGAACGGAGTGCAGATATCCCGGCATGAGAGAGTTGTCACTATATCTGGTAATG 1214

Qy 362 GGAGCATCCACAGCCCGGAATGTTCTCATACGTACCAAGAAATATGGTGTGTGGA 421

Db 1215 GGAGCATCCACAGCCCGGAATGTTCTCATACGTACCAAGAAATATGGTGTGTGGA 1274

Qy 422 GATTAGTTCAGTGTAGTGAATGTCGGATCCAGCTCCAGTTCATTTGATGAGAGATTTGGGC 481

Db 1275 GATTAGTTCAGTGTAGTGAATGTCGGATCCAGTTCATTTGATGAGAGATTTGGGC 1334

QY 482 TGGAGATCCAGAACGATATATGCAAGTAGTATGATTTTGTAGAGCTTGAGAGCCAGTG 541  
Db 1335 TGGAGATCCAGAACGATATATGCAAGTAGTATGATTTTGTAGAGCTTGAGAGCCAGTG 1394  
QY 542 ATGGAAGTGTATTTAGGACGCTGGTGTGTTCTGGGACTGTGCGAGGAAAGCAGACTTCTA 601  
Db 1395 ATGGAAGTGTATTTAGGACGCTGGTGTGTTCTGGGACTGTGCGAGGAAAGCAGACTTCTA 1454  
QY 602 AAGGAATCATATCAGGATAGATTTGTATCTGATGAGTATTTTCCATCTGAACCGGAT 661  
Db 1455 AAGGAATCATATCAGGATAGATTTGTATCTGATGAGTATTTTCCATCTGAACCGGAT 1514  
QY 662 TCTGCATCCATACAGTATTTATCATGCCCAAGTACAGAGTACAGAAACCCAGAGTCTCTGGGT 721  
Db 1515 TCTGCATCCATACAGTATTTATCATGCCCAAGTACAGAGTACAGAAACCCAGAGTCTCTGGGT 1574  
QY 722 TGCCTCCCTTCATCTTTGTGATTTGGACCTGCTCAACAATCTGTGACTGCTTCAGTACT 781  
Db 1575 TGCCTCCCTTCATCTTTGTGATTTGGACCTGCTCAACAATCTGTGACTGCTTCAGTACT 1634  
QY 782 TGGAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGGACTTTGGACAGCTCT 841  
Db 1635 TGGAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGGACTTTGGACAGCTCT 1694  
QY 842 ACAAGCCACATGGCAGCTTTTGGGCAAGCTTTTCTGTATGGGAAAAAAGCAAGTGG 901  
Db 1695 ACAAGCCACATGGCAGCTTTTGGGCAAGCTTTTCTGTATGGGAAAAAAGCAAGTGG 1754  
QY 902 TGAATCTGAATCTCTCAAGGAAGAGTAAACTCTACAGCTGCACACCCCGAATCTCT 961  
Db 1755 TGAATCTGAATCTCTCAAGGAAGAGTAAACTCTACAGCTGCACACCCCGAATCTCT 1814  
QY 962 CAGTGTCATACGGGAAGAGCTAAAGAGACAGATACCATATTTCTGGCCAGGTTGTCTCC 1021  
Db 1815 CAGTGTCATACGGGAAGAGCTAAAGAGACAGATACCATATTTCTGGCCAGGTTGTCTCC 1074  
QY 1022 TGGTCAAGCGCTGTGAGGAAATTTGTCCTGTTGTCTCCATAATTCGAATGAATGTCAGT 1081  
Db 1875 TGGTCAAGCGCTGTGAGGAAATTTGTCCTGTTGTCTCCATAATTCGAATGAATGTCAGT 1934  
QY 1082 GTGTCCCACTGAAGTTACAAAAGTACCATGAGTCTCTTCAAGTTGAGACCAAAAGTCTG 1141  
Db 1935 GTGTCCCACTGAAGTTACAAAAGTACCATGAGTCTCTTCAAGTTGAGACCAAAAGTCTG 1994  
QY 1142 GAGTCAAGGATTTGCATAGTCACTCACTGATGCTCTGGAACACCCAGAGGAATGTG 1201  
Db 1995 GAGTCAAGGATTTGCATAGTCACTCACTGATGCTCTGGAACACCCAGAGGAATGTG 2054  
QY 1202 ACTGTGTGTAGAGGAAACGCGAGGAGGTPAATGCGAGCTTCTGTAGCAGCACACGTGAG 1261  
Db 2055 ACTGTGTGTAGAGGAAACGCGAGGAGGTPAATGCGAGCTTCTGTAGCAGCACACGTGAG 2114  
QY 1262 CACTGCACTCTGTATACCCCAACAGACCTTCACTCCACAGGTTGGCCGAGGG 1321  
Db 2115 CACTGCACTCTGTATACCCCAACAGACCTTCACTCCACAGGTTGGCCGAGGG 2174  
QY 1322 CTCTCAGCTGCTGATGCTGCTATGTAAGATCTTACTGCTCTCAACCAAAATTTCTCAG 1381  
Db 2175 CTCTCAGCTGCTGATGCTGCTATGTAAGATCTTACTGCTCTCAACCAAAATTTCTCAG 2234  
QY 1382 TTGTTTGTCTCAATAGCTTCCCTCGCAGACTTCAAGTGTCTTCTTAAAGACAGAGGC 1441  
Db 2235 TTGTTTGTCTCAATAGCTTCCCTCGCAGACTTCAAGTGTCTTCTTAAAGACAGAGGC 2294  
QY 1442 ACCAAGAGGATCAATCACAAGCACTGC 1470  
Db 2295 ACCAAGAGGATCAATCACAAGCACTGC 2323

RESULT 4  
AAD04650  
ID AAD04650 standard; DNA; 3571 BP.

XX AAD04650;  
XX AC  
XX DT 04-JUL-2001 (first entry)  
XX Mouse Zvegf3 DNA.  
DE  
XX Mouse; Zvegf3 antagonist; cell proliferation; stellate cell activation;  
KW extracellular matrix production; fibrosis; VEGF-R; PDGF-C;  
KW platelet-derived growth factor; PDGF; vascular endothelial growth factor;  
KW VEGF; mitogenic effect; therapy; keloid; scleroderma; fibrotic disorder;  
KW chronic active hepatitis; fulminant viral hepatitis; amyloidosis;  
KW diabetic nephropathy; alpha-1-antitrypsin deficiency; silicosis;  
KW asbestosis; renal arteriosclerosis; post necrotic cirrhosis;  
KW diabetic glomerulosclerosis; focal glomerulosclerosis; hyperostosis;  
KW pulmonary hypertension; idiopathic pulmonary fibrosis; osteopetrosis;  
KW bronchiolitis obliterans-organising pneumonia; transplant vasculopathy;  
KW fibroproliferative disorder; ds.  
OS  
XX Mus musculus.  
XX  
XX Key Location/Qualifiers  
XX CDS 1049..2086  
XX /tag= a  
XX /product= "Mouse Zvegf3 protein"  
XX WO200128586-A1.  
XX  
XX 26-APR-2001.  
XX  
XX 23-OCT-2000; 2000WO-US29270.  
XX  
XX 21-OCT-1999; 99US-0161653.  
XX 12-NOV-1999; 99US-0165255.  
XX 01-AUG-2000; 2000US-0222223.  
XX  
XX (ZYMO ) ZYMOGENETICS INC.  
XX  
XX Gilbertson DG;  
XX  
XX WPI; 2001-300278/31.  
XX P-PSDB; AAE00998.  
XX  
XX Use of zvegf3 antagonist for reducing fibroproliferative disorder of  
XX kidney, liver and bone, reducing extracellular matrix production, -  
XX treating fibrosis or reducing stellate cell activation in mammal -  
XX Example 2; Page 58-61; 70pp; English.  
XX  
XX The patent discloses materials and methods for reducing cell  
XX proliferation or extracellular matrix production, treating fibrosis and  
XX reducing stellate cell activation in a mammal. The method comprises  
XX administering a composition containing a Zvegf3 antagonist in combination  
XX with a delivery vehicle. The Zvegf3 is a protein that is structurally  
XX related to platelet-derived growth factor (PDGF) and the vascular  
XX endothelial growth factors (VEGF). The Zvegf3 protein is also designated  
XX as "VEGF-R" and "PDGF-C". The Zvegf3 antagonist is useful to block the  
XX mitogenic effects of zvegf3 and thereby to inhibit or prevent and treat  
XX keloids, scleroderma, fibrotic disorders of liver such as chronic active  
XX hepatitis, fulminant viral hepatitis, post necrotic cirrhosis and  
XX alpha-1-antitrypsin deficiency, fibrotic disorders of the kidney such as  
XX diabetic glomerulosclerosis, focal glomerulosclerosis, diabetic  
XX nephropathy, amyloidosis and renal arteriosclerosis, fibrotic disorders  
XX of the lung such as silicosis, asbestosis, idiopathic pulmonary fibrosis,  
XX bronchiolitis obliterans-organising pneumonia and pulmonary hypertension,  
XX fibrotic disorders of pancreas, fibroproliferative disorders of the  
XX vasculature such as transplant vasculopathy and hyperostosis.  
XX The present sequence is mouse Zvegf3 DNA.  
SQ Sequence 3571 BP; 876 A; 935 C; 875 G; 885 T; 0 other;

Query Match 98.0%; Score 1444.8; DB 22; Length 3571;



Best Local Similarity 99.4%; Pred. No. 0;					Matches 1460; Conservative 0; Mismatches 8; Indels 1; Gaps 1;				
QY	2	ACCTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATATATGTGGAACCTA	61						
Db	856	AACTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATATATGTGGAACCTA	915						
QY	62	CCCTGGATTCTCTCTGTCAGAGCGGCGCCAGCGCTTCCACCGAGCGAGCCCTTTCC	121						
Db	916	CCCTGGATTCTCTCTGTCAGAGCGGCGCCAGCGCTTCCACCGAGCGAGCCCTTTCC	975						
QY	122	CGGGCTGGGCTGAGCCCTTGGAGTCGTCCTTCCAGTCCCGCCGCGAGTCAGCCCTCG	181						
Db	976	C-GGCTGGGCTGAGCCCTTGGAGTCGTCCTTCCAGTCCCGCCGCGAGTCAGCCCTCG	1034						
QY	182	CCCCAGTCAGCAAAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCCCTGGCGGCC	241						
Db	1035	CCCCAGTCAGCAAAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCCCTGGCGGCC	1094						
QY	242	AAAGAACGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCACTCTCCAGCGACA	301						
Db	1095	AAAGAACGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCACTCTCCAGCGACA	1154						
QY	302	AGGAAACAGAACCGAGTGCAGATCCCGGCATGAGAGAGTTGTCATATATCTGTGAATG	361						
Db	1155	AGGAAACAGAACCGAGTGCAGATCCCGGCATGAGAGAGTTGTCATATATCTGTGAATG	1214						
QY	362	GGAGCATCCACAGCCGAGTTTCCTCATACGTACCCAGAAATATGGTGGTGGGA	421						
Db	1215	GGAGCATCCACAGCCGAGTTTCCTCATACGTACCCAGAAATATGGTGGTGGGA	1274						
QY	422	GATTAGTTCAGTAGATGAAATGTGCGGATCCAGCTGACATTTGATGAGAGATTTGGGC	481						
Db	1275	GATTAGTTCAGTAGATGAAATGTGCGGATCCAGCTGACATTTGATGAGAGATTTGGGC	1334						
QY	482	TGGAAGATCCAGAACGATATATGCAAGTATGATTTGTAGAGTTGAGAGCCAGTG	541						
Db	1335	TGGAAGATCCAGAACGATATATGCAAGTATGATTTGTAGAGTTGAGAGCCAGTG	1394						
QY	542	ATGGAAGTGTTTAGAGCGCTGTGTGTTCTGGGACTGTGCCAGAAAGCAGACTTCTA	601						
Db	1395	ATGGAAGTGTTTAGAGCGCTGTGTGTTCTGGGACTGTGCCAGAAAGCAGACTTCTA	1454						
QY	602	AAGGAATCATATCAGGATAAGATTTGTATCTGATGAGTATTTTCCATCTGAACCCGGAT	661						
Db	1455	AAGGAATCATATCAGGATAAGATTTGTATCTGATGAGTATTTTCCATCTGAACCCGGAT	1514						
QY	662	TCTGCAATCAGTATATCATGCCACAGTACAGAAACCAAGTCCTTCGGTGT	721						
Db	1515	TCTGCAATCAGTATATCATGCCACAGTACAGAAACCAAGTCCTTCGGTGT	1574						
QY	722	TGCCCCCTTCATCTTTGTCAATGGAACCTGCTCAACATGCTGACTGCCTTCAGTACCT	781						
Db	1575	TGCCCCCTTCATCTTTGTCAATGGAACCTGCTCAACATGCTGACTGCCTTCAGTACCT	1634						
QY	782	TGGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGGAATTCGACAGCCTCT	841						
Db	1635	TGGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGGAATTCGACAGCCTCT	1694						
QY	842	ACAAGCCACATGGCAGCTTTTGGGCAAGCTTTCTGATGGGAAAAAAGCAAGTGG	901						
Db	1695	ACAAGCCACATGGCAGCTTTTGGGCAAGCTTTCTGATGGGAAAAAAGCAAGTGG	1754						
QY	902	TGAATCTGAATCTCTCAAGGAAGAGGTAAATCTTACAGTCGACACCCCGGAATCTCT	961						
Db	1755	TGAATCTGAATCTCTCAAGGAAGAGGTAAATCTTACAGTCGACACCCCGGAATCTCT	1814						
QY	962	CAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACATATTTCTGCCAGGTGTCTCC	1021						
Db	1815	CAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACATATTTCTGCCAGGTGTCTCC	1874						
QY	1022	TGGTCAAGCGCTGTGGAGGAAATGTGCTGTGTTCTTCCATATTTGCAATGATGTCAGT	1081						

Db	1875	TGTCCAAGCGCTGTGGAGGAAATTTGCTGCTGTTGCTCTCCATTAATTTGCAATGATGTCACT	1934
QY	1082	GTGTCCTCCACGTAAAGCTTACAAAAAAGTACCATGAGGTCTCTCAGTTGAGACCAAAAACTG	1141
Db	1935	GTGTCCTCCACGTAAAGCTTACAAAAAAGTACCATGAGGTCTCTCAGTTGAGACCAAAAACTG	1994
QY	1142	GAGTCAAGGGATTTGCATTAAGTCACTCACTGATGTGGCTCTGGAAACACCCAGGAGATGTG	1201
Db	1995	GAGTCAAGGGATTTGCATTAAGTCACTCACTGATGTGGCTCTGGAAACACCCAGGAGATGTG	2054
QY	1202	ACTGTGTGTGTAGAGAAACGAGGAGGTAACTGCAGCTCTTCTGAGCAGCACACGTGAG	1261
Db	2055	ACTGTGTGTGTAGAGAAACGAGGAGGTAACTGCAGCTCTTCTGAGCAGCACACGTGAG	2114
QY	1262	CACCTGGCATTTCTGTGTACCCCCCAAGCAACCTTATCCCCACAGCGTTGCGCGCAGGG	1321
Db	2115	CACCTGGCATTTCTGTGTACCCCCCAAGCAACCTTATCCCCACAGCGTTGCGCGCAGGG	2174
QY	1322	CTCTCAGCTGTGATGCTGGCTATGTTAAAGATCTTACTCGTCTCCAAACCAATTTCTCAG	1381
Db	2175	CTCTCAGCTGTGATGCTGGCTATGTTAAAGATCTTACTCGTCTCCAAACCAATTTCTCAG	2234
QY	1382	TTGTTTGTCTTCAATAGCCCTTCCCTGCGAGACTTCAAGTGTCTTCTAAAGACCCAGAGGC	1441
Db	2235	TTGTTTGTCTTCAATAGCCCTTCCCTGCGAGACTTCAAGTGTCTTCTAAAGACCCAGAGGC	2294
QY	1442	ACCAANAGGAGTCAATCAAAAACACTGC	1470
Db	2295	ACCAANAGGAGTCAATCAAAAACACTGC	2323
RESULT 5			
ID	ABS68648	standard; cDNA; 3571 BP.	
AC	ABS68648;		
XX	19-NOV-2002 (first entry)		
DT	Mouse cDNA encoding VEGF-like protein zvegf 3.		
DE	ss; gene; VEGF; vascular endothelial growth factor; zvegf 3;		
XX	chromosome 3; cell proliferation; differentiation; metabolism;		
KW	migration; revascularisation; solid tumour; diabetic retinopathy;		
KW	psoriasis; rheumatoid arthritis; cancer; autoimmune disease;		
KW	inflammation; myocardial ischaemia; scleroderma; fibrosis; mouse;		
KW	glomerulosclerosis; atherosclerosis; skin wound; ulcer; burn;		
KW	skin grafting; female reproductive tract disorder; chronic liver disease;		
KW	circulatory disorder; heart failure; neurodegenerative disease;		
KW	multiple sclerosis; Parkinson's disease; Alzheimer's disease; stroke;		
KW	neurite outgrowth.		
OS	Mus musculus.		
XX	US6432673-B1.		
XX	13-AUG-2002.		
XX	07-DEC-1999; 99US-0457066.		
XX	07-DEC-1998; 98US-111173P.		
PR	06-JUL-1999; 99US-142576P.		
PR	21-OCT-1999; 99US-161653P.		
PR	12-NOV-1999; 99US-165255P.		
XX	(ZYMO ) ZYMOGENETICS INC.		
XX	Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KB;		
PI	Gilbertson DG, West JW;		
XX	WPI; 2002-689759/74.		
DR	P-PSDB; ABG92894.		
XX			



PT Novel polypeptide, designated zvegf3 useful for treating skin wounds,  
PT ulcers, burns, skin grafting, female reproductive tract disorders,  
PT Parkinson's disease, and Alzheimer's disease -  
XX Example 4; Column 97-104; 68pp; English.  
PS  
XX The invention relates to an isolated polypeptide, designated zvegf3  
CC (a vascular endothelial growth factor-like protein) of 111-136 amino acid  
CC residues in length and comprises the sequence appearing as ABG92889  
CC from amino acid residues 235-345. Also included are an isolated  
CC protein comprising a first polypeptide disulphide bonded to a second  
CC polypeptide, where each of the first and second polypeptides is from  
CC zvegf 3, and where the protein modulates cell proliferation,  
CC differentiation, metabolism or migration, the zvegf 3 encoding  
CC polynucleotides and zvegf 3 expression vectors and host cells.  
CC Zvegf 3 is useful as additives in tissue adhesives for promoting  
CC revascularisation of the healing tissue, for designing molecules that  
CC antagonise semaphorin-stimulated activities, including neurite growth,  
CC cardiovascular development, cartilage and limb development, and T and  
CC B-cell function, and for imaging tumours or other sites of abnormal cell  
CC proliferation and in gene therapy applications. The proteins are useful  
CC therapeutically to stimulate tissue development or repair, or cellular  
CC differentiation or proliferation, for stimulating the growth of  
CC fibroblast or smooth muscle cells, as molecular weight standards, as  
CC reagents in assays for determining circulatory level of the protein or as  
CC standards in the analysis of cell phenotype, for identifying inhibitors  
CC of their activity which are useful for reducing the growth of solid  
CC tumours, for treating diabetic retinopathy, psoriasis, rheumatoid  
CC arthritis, various forms of cancers, autoimmune disease, inflammation,  
CC myocardial ischaemia, scleroderma, and reducing fibrosis, including scar  
CC formation, keloids, liver fibrosis, lung fibrosis (e.g. silicosis,  
CC asbestosis), kidney fibrosis (including diabetic nephropathy),  
CC glomerulosclerosis, atherosclerosis, skin wounds, ulcers, burns, skin  
CC grafting, and female reproductive tract disorders, chronic liver disease  
CC (hepatitis), cirrhosis, Reye's syndrome, Wilson's disease, circulatory  
CC disorders e.g. heart failure, hepatic or portal vein thrombosis, cardiac  
CC sclerosis, neurodegenerative diseases such as multiple sclerosis,  
CC Parkinson's disease, Alzheimer's disease, and for regenerating neurite  
CC outgrowths following strokes. The gene for mouse zvegf3 is located on  
CC chromosome 3. The present sequence encodes zvegf 3.  
XX  
SQ Sequence 3571 BP; 876 A; 935 C; 875 G; 885 T; 0 other;  
Query Match 98.0%; Score 1444.8; DB 24; Length 3571;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 1460; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  
2 ACCTGGAGACACAGAGGGCTCTAGGAAAAATTTGGATGGGATTTATGTGAAACTA 61  
856 AACTGGAGACACAGAGGGCTCTAGGAAAAATTTGGATGGGATTTATGTGAAACTA 915  
62 CCCTGGCATCTCTGCTGCCAGAGCCGCGAGGCTTCCACCGCAGCGAGCTTTCCC 121  
916 CCCTGGCATCTCTGCTGCCAGAGCCGCGAGGCTTCCACCGCAGCGAGCTTTCCC 975  
122 CGGGCTGGGCTGAGCTTTGGAGTGTGCTTTCCCGAGTCCCGCGGAGTGAGCCCTCG 181  
976 C-GGCTGGGCTGAGCTTTGGAGTGTGCTTTCCCGAGTCCCGCGGAGTGAGCCCTCG 1034  
182 CCCAGTCAGGCAATGTCTCTCTGCGCTCTCTCTGCTGACATCTGCTGCGCGGCC 241  
1035 CCCAGTCAGGCAATGTCTCTCTGCGCTCTCTCTGCTGACATCTGCTGCGCGGCC 1094  
242 AAGAACGGGACTCGGGCTGAGTCCACCTGAGCAGCAAGTTGAGCTCTCCAGCGACA 301  
1095 AAGAACGGGACTCGGGCTGAGTCCACCTGAGCAGCAAGTTGAGCTCTCCAGCGACA 1154  
302 AGGAACAGACGGAGTGAAGATCCCGCGCATGAGAGAGTTGTCACTATATCTGGTAATG 361  
1155 AGGAACAGACGGAGTGAAGATCCCGCGCATGAGAGAGTTGTCACTATATCTGGTAATG 1214  
362 GGAGCATCCACAGCCGAGTTTCTCTATACGTACCCAGAAATATGGTGTGTGTGGA 421

Db 1215 GGAGCATCCACAGCCCGAAGTTTCTCTCATACATACCCAGAAATATGGTCTGTGTGGA 1274  
Qy 422 GATTAGTTGCAGTAGATGAAATGTGCGGATCCAGCTGCATTTGATGAGAGATTTGGGC 481  
Db 1275 GATTAGTTGCAGTAGATGAAATGTGCGGATCCAGCTGCATTTGATGAGAGATTTGGGC 1334  
Qy 482 TGAAGATCCAGAGACGATATATGCAAGTATGATTTCTAGAGTTGAGAGCCAGTG 541  
Db 1335 TGAAGATCCAGAGACGATATATGCAAGTATGATTTCTAGAGTTGAGAGCCAGTG 1394  
Qy 542 ATGGAAGTGTGTTAGGACGCTGTGTGTTCTGGACTGTGCCAGGAAACAGACTTCTA 601  
Db 1395 ATGGAAGTGTGTTAGGACGCTGTGTGTTCTGGACTGTGCCAGGAAACAGACTTCTA 1454  
Qy 602 AAGGAAATCATATCAGGATAAAGATTTGTATCTCATGAGTATTTTCACTGAAACCCGAT 661  
Db 1455 AAGGAAATCATATCAGGATAAAGATTTGTATCTCATGAGTATTTTCCATCTGAACCCGAT 1514  
Qy 662 TCTGCATCCACTACAGTATTTATCATGCCACAGTCAAGAACACAGAGTCCCTTCGGTGT 721  
Db 1515 TCTGCATCCACTACAGTATTTATCATGCCACAGTCAAGAACACAGAGTCCCTTCGGTGT 1574  
Qy 722 TSCCCCTTCTCATCTTTGTCTATTTGGACCTGCTCAACATGCTGTGACTGCCCTTCAGTACT 781  
Db 1575 TSCCCCTTCTCATCTTTGTCTATTTGGACTGCTCAACATGCTGTGACTGCCCTTCAGTACT 1634  
Qy 782 TGAAGAGCTGATTCGGTACTAGAGCCAGATGATGGAGGTGGAGCTTGAGAGCCCTCT 841  
Db 1635 TGAAGAGCTGATTCGGTACTAGAGCCAGATGATGGAGGTGGAGCTTGAGAGCCCTCT 1694  
Qy 842 ACAAGCCAAATGCGCAGCTTTTGGGCAAGCTTTTCCGTATGGGAAAAAGCAAGTGG 901  
Db 1695 ACAAGCCAAATGCGCAGCTTTTGGGCAAGCTTTTCCGTATGGGAAAAAGCAAGTGG 1754  
Qy 902 TGAATCTGAATCTCTCAAGAGAGAGTAAACTCTACAGCTGCACACCCCGGAATCTCT 961  
Db 1755 TGAATCTGAATCTCTCAAGAGAGAGTAAACTCTACAGCTGCACACCCCGGAATCTCT 1814  
Qy 962 CAGTGTCCATACCGGAAAGAGCTAAAGAGGACAGATACCATATCTGGCCAGGTGTCTCC 1021  
Db 1815 CAGTGTCCATACCGGAAAGAGCTAAAGAGGACAGATACCATATCTGGCCAGGTGTCTCC 1874  
Qy 1022 TGCTCAAGCGCTGTGGAGGAAATTTGCTGCTTCTCCATATTTGCAATGCAATGCTCAGT 1081  
Db 1875 TGCTCAAGCGCTGTGGAGGAAATTTGCTGCTTCTCCATATTTGCAATGCAATGCTCAGT 1934  
Qy 1082 GTGTCCACAGTAAAGTTTACAAAAAGTACCAGTGGTCTTTCAGTTGAGACCAAAACTG 1141  
Db 1935 GTGTCCACAGTAAAGTTTACAAAAAGTACCAGTGGTCTTTCAGTTGAGACCAAAACTG 1994  
Qy 1142 GAGTCAAGGGATTCATTAAGTCACTCACTGATGTGGCTCTGGAAACACACGAGGAATGTG 1201  
Db 1995 GAGTCAAGGGATTCATTAAGTCACTCACTGATGTGGCTCTGGAAACACACGAGGAATGTG 2054  
Qy 1202 ACTGTGTGTAGAGGAAACGAGGGTAACTGCGAGCTTTCGTTAGCAGCAGCAGTCAAG 1261  
Db 2055 ACTGTGTGTAGAGGAAACGAGGGTAACTGCGAGCTTTCGTTAGCAGCAGCAGTCAAG 2114  
Qy 1262 CACTGGCATTCGTGTATCCCCCAAGCAACCTTCATCCCCACAGCGTGTGGCCCGCAGGG 1321  
Db 2115 CACTGGCATTCGTGTATCCCCCAAGCAACCTTCATCCCCACAGCGTGTGGCCCGCAGGG 2174  
Qy 1322 CTCTCAGCTGTGATGTGGCTATGGTAAAGATCTTACTCGTCTCCAAACCAATTTCTCAG 1381  
Db 2175 CTCTCAGCTGTGATGTGGCTATGGTAAAGATCTTACTCGTCTCCAAACCAATTTCTCAG 2234  
Qy 1382 TTGTTTGTCTCAATAGCCTTCCCTGCGAGGACTTCAAGTGTCTTCTAAAGACCAAGGC 1441  
Db 2235 TTGTTTGTCTCAATAGCCTTCCCTGCGAGGACTTCAAGTGTCTTCTAAAGACCAAGGC 2294  
Qy 1442 ACCAAGAGGAGTCAATCAAAAGCACTGC 1470  
Db 2295 ACCAAGAGGAGTCAATCAAAAGCACTGC 2323

RESULT 6  
AAI72444  
ID AAI72444 standard; cDNA; 3571 BP.  
XX  
AC AAI72444;  
XX  
DT 16-MAY-2002 (first entry)  
XX  
DE Mouse zveg3 coding sequence.  
XX  
KW Gene; human; mouse; zveg3; zveg4; platelet derived growth factor;  
PDGF; homolog; growth; bone; ligament; cartilage; proliferation;  
osteoblast; chondrocyte; bony defect; fracture; bone graft;  
implant; periodontal pocket; osteoclast; bone marrow stem cell;  
osteoporosis; ss.  
XX  
OS Mus musculus.  
XX  
FH Key Location/Qualifiers  
CDS 1049..2086  
/\*tag= a  
/product= "zveg3"  
XX  
FN US200204225-A1.  
XX  
PD 10-JAN-2002.  
XX  
XX 29-MAR-2001; 2001US-0823033.  
XX  
PF 07-DEC-1998; 98US-111173P.  
XX  
PR 06-JUL-1999; 99US-142578P.  
XX  
PR 21-OCT-1999; 99US-161653P.  
XX  
PR 12-NOV-1999; 99US-165255P.  
XX  
PR 31-MAR-2000; 2000US-193723P.  
XX  
PR 07-DEC-1999; 99US-0457066.  
XX  
XX (HART/) HART C E.  
XX  
PA (GILB/) GILBERTSON D G.  
XX  
XX  
XX Hart CE, Gilbertson DG;  
XX  
XX WPI; 2002-171026/22.  
XX  
XX P-PSDB; AAB47890.  
XX  
XX Promoting growth of bone, ligament or cartilage in a mammal, involves  
XX administering to the mammal a protein which comprises growth factor  
XX domain of zveg3 protein, a homolog of platelet-derived growth factor  
XX  
XX  
XX Disclosure; Page 16-19; 31pp; English.  
XX  
XX The sequences given in AAI72443-44 encode human and mouse zveg3,  
XX respectively. zveg3 is a platelet derived growth factor (PDGF) homolog  
XX and it was used in the method of the invention for promoting growth of  
XX bone, ligament or cartilage and stimulating proliferation of osteoblasts  
XX or chondrocytes in a mammal. The proteins used were preferably a dimeric  
XX protein of residues 235-345 of human zveg3 or all of the mouse zveg3  
XX protein, with a delivery vehicle. The method of the invention is useful  
XX for promoting growth of bone, ligament or cartilage in a mammal, where  
XX the composition is administered at a site of a bony defect, preferably  
XX a fracture, bone graft site, implant site, or periodontal pocket, and  
XX for stimulating proliferation of osteoblasts or chondrocytes in a  
XX mammal. It is further useful for promoting proliferation of osteoblasts,  
XX osteoclasts, chondrocytes or bone marrow stem cells, where the bone  
XX marrow stem cells are harvested from a patient prior to culture. The  
XX method is therefore useful for treating osteoporosis.  
XX  
XX  
XX Sequence 3571 BP; 876 A; 935 C; 875 G; 885 T; 0 other;  
SQ  
Query Match 98.0%; Score 1444.8; DB 24; Length 3571;  
Best Local Similarity 99.4%; Pred. No. 0;

	Matches	1460;	Conservative	0;	Mismatches	8;	Indels	1;	Gaps	1;
QY	2	ACCTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATATATGTGAACTA	61							
DB	856	AACTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATATATGTGAACTA	915							
QY	62	CCCTGGATTCTCTGCTGCAGAGCGCGCGCTTCCACCGCAGCGCAGCTTTCC	121							
DB	916	CCCTGGATTCTCTGCTGCAGAGCGCGCGCTTCCACCGCAGCGCAGCTTTCC	975							
QY	122	CGGGCTGGGCTGAGCCTTGGAGTCGCTCCCGAGTCCCGCGAGTGGAGCCCTCG	181							
DB	976	C-GGCTGGGCTGAGCCTTGGAGTCGCTTCCCGAGTCCCGCGAGTGGAGCCCTCG	1034							
QY	182	CCCCAGTCAGCCAAATGCTCCTCTCGGCCCTCCTCTGTGACATCTGCGCCGCGCC	241							
DB	1035	CCCCAGTCAGCCAAATGCTCCTCTCGGCCCTCCTCTGTGACATCTGCGCCGCGCC	1094							
QY	242	AAAGAACGGGGACTCGGGCTGAGTCCAACTGAGCAGCAGATTGCGAGCTCTCCAGCGACA	301							
DB	1095	AAAGAACGGGGACTCGGGCTGAGTCCAACTGAGCAGCAGATTGCGAGCTCTCCAGCGACA	1154							
QY	302	AGGAACAGAACGGAGTGCAGATCCCGCGCATGAGAGATTGTCACTATATCTGTAATG	361							
DB	1155	AGGAACAGAACGGAGTGCAGATCCCGCGCATGAGAGATTGTCACTATATCTGTAATG	1214							
QY	362	GGAGCATCCACAGCCCGAAGTTTCTCTCATAGTACCAAGAAATATGGTGTGTGGGA	421							
DB	1215	GGAGCATCCACAGCCCGAAGTTTCTCTCATAGTACCAAGAAATATGGTGTGTGGGA	1274							
QY	422	GATTAGTTGAGTAGATGAAAAATGTGCGGATCCAGCTGACATTTGATGAGAGATTGGGC	481							
DB	1275	GATTAGTTGAGTAGATGAAAAATGTGCGGATCCAGCTGACATTTGATGAGAGATTGGGC	1334							
QY	482	TGGAGATCCAGAGACGATATATGCAAGTATGATTTGTAGAAAGTTGAGAGCCAGTG	541							
DB	1335	TGGAGATCCAGAGACGATATATGCAAGTATGATTTGTAGAAAGTTGAGAGCCAGTG	1394							
QY	542	ATGGAAGTGTTTTAGGACGCTGGTGTGGACTGTGCCAGAGAAAGCAGACTTCTA	601							
DB	1395	ATGGAAGTGTTTTAGGACGCTGGTGTGGACTGTGCCAGAGAAAGCAGACTTCTA	1454							
QY	602	AAGAAATCATATCAGGATTAAGATTGTATCTGATGAGTATTTTCCATCTCAACCCGAT	661							
DB	1455	AAGAAATCATATCAGGATTAAGATTGTATCTGATGAGTATTTTCCATCTCAACCCGAT	1514							
QY	662	TCTGCATCCACTACAGTATTATATGACCAAGTACAGAAACCAAGAGTCTTCGGTGT	721							
DB	1515	TCTGCATCCACTACAGTATTATATGACCAAGTACAGAAACCAAGAGTCTTCGGTGT	1574							
QY	722	TGCCCCCTTCATCTTTTGTTCATTTGGACCTGCTCAACAATGCTGTGACTTGCCTT	781							
DB	1575	TGCCCCCTTCATCTTTTGTTCATTTGGACCTGCTCAACAATGCTGTGACTTGCCTT	1634							
QY	782	TGGAAGACTGATTCGGTACCTAGAGCCAGATCCAGTGCAGTGTGACTTGGACAGCTCT	841							
DB	1635	TGGAAGACTGATTCGGTACCTAGAGCCAGATCCAGTGCAGTGTGACTTGGACAGCTCT	1694							
QY	842	ACAAGCCAACTAGGAGCTTTTGGCAAGGCTTTCCTGTATGGGAAAAAAGCAAGTGG	901							
DB	1695	ACAAGCCAACTAGGAGCTTTTGGCAAGGCTTTCCTGTATGGGAAAAAAGCAAGTGG	1754							
QY	902	TGAATCTGAATCTCTCAAGGAAGAGGTAAACTCTACAGCTGCACACCCCGGAATCTT	961							
DB	1755	TGAATCTGAATCTCTCAAGGAAGAGGTAAACTCTACAGCTGCACACCCCGGAATCTT	1814							
QY	962	CAGTGTCCATACGGAAGAGCTTAAGAGGACAGATACCATATCTTGGCCAGGTGTCTCC	1021							
DB	1815	CAGTGTCCATACGGAAGAGCTTAAGAGGACAGATACCATATCTTGGCCAGGTGTCTCC	1874							
QY	1022	TGGTCAAGCGCTGTGGAGAAATTTGCTGCTGTTGTCTCCATTAATGCAATGATGTCA	1081							
DB	1875	TGGTCAAGCGCTGTGGAGAAATTTGCTGCTGTTGTCTCCATTAATGCAATGATGTCA	1934							

QY 1082 GTGTCACGTAAGTTACAAAAGTACCAATGAGTCCCTTCAGTTCAGACCCAAAATCG 1141  
| | | | |  
Db 1935 GTGTCACGTAAGTTACAAAAGTACCAATGAGTCCCTTCAGTTCAGACCCAAAATCG 1994  
| | | | |  
QY 1142 GAGTCAAGGATTCATTAAGTCACTCACTGATGTGGCTCTGGAACACCCAGGAAATGTG 1201  
| | | | |  
Db 1995 GAGTCAAGGATTCATTAAGTCACTCACTGATGTGGCTCTGGAACACCCAGGAAATGTG 2054  
| | | | |  
QY 1202 ACTGTGTGTAGAGAAACGAGAGGGTAACTGACGCTTCGTAGCAGCACAGTGGAG 1261  
| | | | |  
Db 2055 ACTGTGTGTAGAGAAACGAGAGGGTAACTGACGCTTCGTAGCAGCACAGTGGAG 2114  
| | | | |  
QY 1262 CACTGGCAATTCGTGTACCCCAAGCAACCTTCATCCCAAGAGCGTTCGCGCCAGGG 1321  
| | | | |  
Db 2115 CACTGGCAATTCGTGTACCCCAAGCAACCTTCATCCCAAGAGCGTTCGCGCCAGGG 2174  
| | | | |  
QY 1322 CTCTCAGCTGTGATGCTGGCTATGTTAAAGATCTTACTCTCCTCAACCAAAATTCCTAG 1381  
| | | | |  
Db 2175 CTCTCAGCTGTGATGCTGGCTATGTTAAAGATCTTACTCTCCTCAACCAAAATTCCTAG 2234  
| | | | |  
QY 1382 TTGTTTGTCTCAATAGCTTCCTCTGACGACTTCAAGTGTCTTCTAAAGACCCAGAGGC 1441  
| | | | |  
Db 2235 TTGTTTGTCTCAATAGCTTCCTCTGACGACTTCAAGTGTCTTCTAAAGACCCAGAGGC 2294  
| | | | |  
QY 1442 ACCAAGAGGATCAATCAAGCACTGC 1470  
| | | | |  
Db 2295 ACCAAGAGGATCAATCAAGCACTGC 2323  
| | | | |

RESULT 7  
ABX93182  
ID ABX93182 standard; DNA; 3571 BP.  
AC  
AC ABX93182;  
DT 22-MAY-2003 (first entry)  
XX  
DE DNA encoding mouse growth factor homologue, zvegfg3.  
KW Mouse; growth factor homologue; zvegfg3; fibroblast; smooth muscle cell;  
KW cell-surface platelet-derived growth factor alpha receptor; PDGF;  
KW full-thickness skin wound; female reproductive tract; duodenal ulcer;  
KW prolonged bleeding; periodontal disease; tissue adhesive; liver damage;  
KW revascularisation; healing tissue; liver disease; CPC; CHN; cirrhosis;  
KW chronic active hepatitis; hepatic chronic passive congestion; stroke;  
KW central haemorrhagic necrosis; hepatic vein thrombosis; ischaemia;  
KW portal vein thrombosis; cardiac sclerosis; new vessel formation;  
KW endothelial precursor stem cell; neovascularisation; wound healing;  
KW organ transplant; tissue grafting; peripheral neuropathy; spinal cord;  
KW sensory neurite outgrowth; brain damage; head injury; paralysis;  
KW spinal injury; neurodegenerative disease; diabetic retinopathy;  
KW psoriasis; arthritis; scleroderma; keloid; liver fibrosis; psoriasis;  
KW lung fibrosis; kidney fibrosis; glomerulosclerosis; cancer;  
KW proliferative vascular disorder; ocular neovascularisation;  
KW inflammatory disorder; rheumatoid arthritis; vasculogenesis;  
KW angiogenesis; nervous system disorder; cytostatic; hepatotropic;  
KW vulvar; tranquiliser; cerebroprotective; neuroprotective; nootropic;  
KW ophthalmological; dermatological; coagulant; cardiant; chromosome 3;  
KW gene; ds.  
XX  
OS Mus musculus.  
XX  
FH Key Location/Qualifiers  
FT CDS 1049..2086  
FT /\*tag= a  
FT /product= "Zvegfg3"  
XX  
FT US2002177193-A1.  
XX  
PN 28-NOV-2002.  
XX  
PD 02-MAY-2002; 2002US-0139583.  
PF

XX 07-DEC-1998; 98US-111173P.  
PR 06-JUL-1999; 99US-142576P.  
PR 21-OCT-1999; 99US-161653P.  
PR 12-NOV-1999; 99US-165255P.  
PR 07-DEC-1999; 99US-0457066.  
XX  
PA (ZYMO ) ZYMOGENETICS INC.  
XX  
PI Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;  
PI Gilbertson DG, West JW;  
XX  
XX WPI; 2003-328485/31.  
DR P-PSDB; ABG76398.  
XX  
XX New isolated zvegfg3 polypeptide, useful for treating cancer,  
XX Alzheimer's disease, Parkinson's disease, chronic active hepatitis,  
XX hepatic vein thrombosis, comprises growth factor domain and CUB domain  
XX .  
PS Example 4; Page 53-55; 73pp; English.  
XX  
XX The present invention relates to the isolation of a growth factor  
XX homologue referred to as zvegfg3, and the polynucleotide sequence  
XX encoding it. The zvegfg3 polypeptide is useful for stimulating the  
XX growth of fibroblasts or smooth muscle cells, or for activating a  
XX cell-surface platelet-derived growth factor (PDGF) alpha receptor.  
XX The zvegfg3 polypeptide is useful as a PDGF alpha receptor agonist and  
XX thus is useful for treating full-thickness skin wounds, female  
XX reproductive tract and prolonged bleeding, periodontal disease,  
XX damaged liver tissue, and duodenal ulcers. The polypeptide is also  
XX useful as an additive in tissue adhesives for promoting  
XX revascularisation of healing tissue. The zvegfg3 polypeptide is also  
XX useful for treating liver damage including damage due to liver  
XX disease, chronic active hepatitis, hepatic chronic passive congestion  
XX (CPC), central haemorrhagic necrosis (CHN), hepatic vein thrombosis,  
XX portal vein thrombosis, cardiac sclerosis, and many types of cirrhosis.  
XX The polypeptide is useful for enhancing expansion and mobilisation of  
XX endothelial precursor stem cells, creating and stabilising new vessel  
XX formation in areas requiring neovascularisation, including areas of  
XX ischaemia, organ transplants, wound healing, and tissue grafting. It  
XX may be used for treating peripheral neuropathies by increasing spinal  
XX cord and sensory neurite outgrowth, and as part of therapeutic  
XX treatment for the regeneration of neurite outgrowths following strokes,  
XX brain damage caused by head injuries, and paralysis caused by spinal  
XX injuries. Application may also be made in treating neurodegenerative  
XX diseases (e.g. multiple sclerosis, Alzheimer's disease, Parkinson's  
XX disease), diabetic retinopathy, psoriasis, arthritis, scleroderma, and  
XX reducing fibrosis, keloids, liver fibrosis, lung fibrosis, kidney  
XX fibrosis, and glomerulosclerosis. An antibody that binds zvegfg3 is  
XX useful for blocking the mitogenic, chemotactic, or angiogenic effects  
XX of zvegfg3, and for treating proliferative vascular disorders, ocular  
XX neovascularisation, inflammatory disorders, rheumatoid arthritis,  
XX psoriasis, cancer, impaired or excessive vasculogenesis or angiogenesis,  
XX and diseases of the nervous system. The present sequence encodes  
XX mouse zvegfg3. The gene encoding mouse zvegfg3 maps to chromosome 3.  
SQ  
Sequence 3571 BP; 876 A; 935 C; 875 G; 885 T; 0 other;  
Query Match 98.0%; Score 1444.8; DB 25; Length 3571;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 1460; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  
QY 2 ACCTGGAGACACAGAGAGGGCTCTAGAAAAATTTTGGATGGGATTTATGTGAAACTA 61  
| | | | |  
Db 856 AACTGGAGACACAGAGAGGGCTCTAGAAAAATTTTGGATGGGATTTATGTGAAACTA 915  
| | | | |  
QY 62 CCCTGGCAATTCGTGTGCGAGAGCCGCGCGGCTTCACCCAGGAGCGCTTTCCC 121  
| | | | |  
Db 916 CCCTGGCAATTCGTGTGCGAGAGCCGCGCGGCTTCACCCAGGAGCGCTTTCCC 975  
| | | | |  
QY 122 CGGGCTGGCTGAGCCTTGGAGTGTCTTCCCACTCCCGCGGAGTGAGCCTTCG 181  
| | | | |



CC skin graft growth, tissue repair, proliferation of new blood vessels,  
CC tissue regeneration and organ repair by promoting angiogenic activity or  
CC vascularization. This sequence encodes the human VEGF-X protein isolated  
CC from clones 4 and 7 described in the method of the invention.  
XX  
SQ Sequence 1473 BP; 406 A; 321 C; 361 G; 385 T; 0 other;

Query Match 62.0%; Score 914.2; DB 21; Length 1473;  
Best Local Similarity 83.5%; Pred. No. 1.1e-267;  
Matches 1050; Conservative 0; Mismatches 203; Indels 4; Gaps 1;

QY 2 ACCTGGAGACACAGAGAGCGCTCTAGGAAAAATTTGGATGGGATATATGGAAACTA 61  
DB 59 AACTGGAGACACAGAGAGCGCTCTAGGAAAAATTTGGATGGGATATATGGAAACTA 118  
QY 62 CCTCGGATCTCTGCTGCAGAGCGCCAGCGCTTCCACCGCAGCGAGCTTTCCTC 121  
DB 119 CCTCGGATCTCTGCTGCAGAGCGCTTCCACCGCAGCGAGCTTTCCTCCTCC 178  
QY 122 CGG----GCTGGGCTGAGCCTTGGAGTCGTCTGCTTCCCGAGTCCCGCGAGTGAGCC 177  
DB 179 TGGCGTGTGAAGAGACTCGGGAGTCGTCTTCCAAAGTCCCGCGTGAAGCT 238  
QY 178 CTGCCCCAGTCAGCCAAATGCTCTCTCTCGGCTCTCTCTGTGACATCTGCCCTGGCC 237  
DB 239 CTCACCCAGTCAGCCAAATGAGCCTCTTCGGGCTCTCTCTGTGACATCTGCCCTGGCC 298  
QY 238 GGCCTGAAGACGGGAGCTCGGCTGAGTCCCACTGAGCAGCAGTTCAGCTCTCCAGC 297  
DB 299 GGCCTGAAGACGGGAGCTCGGCTGAGTTCCACTGAGTGAATTCCTGATTTCCAGT 358  
QY 298 GACAAGGAACAGACGAGGAGTCAGATCCCGGATGAGAGAGTGTCACTATATCTGGT 357  
DB 359 AACAGGAACAGACGAGGATACAGATCTCTCAGCATGAGAGATTTACTGTCTACT 418  
QY 358 AATGGAGAGATTCACAGCCGAGTTCCTCATACGTACCAAGAAATATGCTGCTGGTG 417  
DB 419 AATGGAGATTCACAGCCGAGTTCCTCATACGTATCCAGAAATACCGTCTTGTA 478  
QY 418 TGGAGATAGTTCAGTAGATGAATGTCGGATCCAGCTGACATTTGATGAGAGATTT 477  
DB 479 TGGAGATAGTTCAGTAGAGAAATGTATGGATACAACTTACGTTTGTATGAAGATTT 538  
QY 478 GGGCTGAAGATCCAGAGACGATATATGCAAGTATGATTTGTAGAAGTTGAGAGGCC 537  
DB 539 GGGCTTGAAGACCCAGAGAGATGACATATGCAAGTATGATTTGTAGAAGTTGAGAGGCC 598  
QY 538 AGTGATGGAAGTGTATGAGACGCTGTGTGGTCTGGGACTGTGCCGAGAAACGAGACT 597  
DB 599 AGTGATGGAACATATATAGGCGCTGTGTGGTCTGGTACTGTACCGAGGAAACAGATT 658  
QY 598 TCTAAGGAATCATATCAGGATGAAGTTTCTATCTGATGATATTTTCCATCTGAAGCC 657  
DB 659 TCTAAGGAATCAATATGAGATGAAGTTTCTATCTGATGATATTTTCTCTGAAGCA 718  
QY 658 GGATTTCTGCATCCACTACAGTATATCATGCCACAGTACAGAAACACAGAGTCTTCG 717  
DB 719 GGGTTCTGCATCCACTACCAATTTGTCTATGATGATATTTTCTCTGAAGCA 778  
QY 718 GTGTTGCCCTTCTCATCTTTGTGATGAGACCTGTCTCAACATGCTGTGACTGCTTCAGT 777  
DB 779 GTGTTGCCCTTCTCAGCTTTGCCACTGAGCCTGTCTTAATATGCTATTAATGCTTCAGT 838  
QY 778 ACCTTGGAAGAGCTGATTCGGTACCTAGAGCAGATCGATGCGAGTGCAGCTTGACAGC 837  
DB 839 ACCTTGGAAGACCTTATTCGATATCTTGAACAGAGATGCGATTCGATTCGATGAGAT 898  
QY 838 CTCTACAGCCAAACATGCGAGCTTTTGGCGAAGGCTTTTCTGTATGGGAAAAAAGCAAA 897  
DB 899 CTATATAGCCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTGTTTGGGAAAGAAATCCAGA 958  
QY 898 GTGTGAATCTGAATCTCTCTCAAGGAAGGATGAACCTCTCAGCTGCACACCCCGGAAC 957

DB 959 GTGGTGATCTGAACCTTTCTAAACAGAGGAGGTAAAGATTATACAGCTGCACACCTCGTAAC 1018  
QY 958 TTCTCAGTGTCCATACCGGGAAGAGCTAAAGAGGACAGATACCATATTTCTGGCCAGGTTGT 1017  
DB 1019 TTCTCAGTGTCCATAGGGAAGAACTAAAGAGAACCGATACCATATTTCTGGCCAGGTTGT 1078  
QY 1018 CTCTGTGTCAAGCGCTGTGGAGAAATTTGGCTGTGTCTTCCATATTTGCAATGAATGT 1077  
DB 1079 CTCTGTGTAAAGCGCTGTGGTGGAACTGTGCTGTGTCTTCCCAATTTGCAATGAATGT 1138  
QY 1078 CAGTGTGTCCACGTAAGTTACAAAAAGTTACCAATCAGCTTCCTTCACTTGTGAGACCAAAA 1137  
DB 1139 CAATGTGTCTCCAGCAAGTTACTAAAAAATACCCAGGTCCTTCAGTTGAGACCAAG 1198  
QY 1138 ACTGGAGTCAAGGATTGCTAAGTCACTCACTCATGTGGCTCTGGAAACACACGAGGAA 1197  
DB 1199 ACCGTTGTGAGGAGTTGCACAAATCACTCACGACGTGGCTGGAGCACCATGAGGAG 1258  
QY 1198 TGTGACTGTGTGTAGAGAAACGAGGAGGTAACTGACGCTTCTGTAGCAGCAC 1254  
DB 1259 TGTGACTGTGTGTGACAGGAGGACACAGGAGATAGCGCATCACCACGACGCTC 1315

RESULT 9  
ABQ81461  
ID ABQ81461 standard; cDNA; 2632 BP.  
XX AC ABQ81461;  
XX AC ABQ81461;  
DT 19-DEC-2002 (first entry)  
XX Human vascular endothelial growth factor-X cDNA.  
DE Vascular endothelial growth factor-X; VEGF-X;  
KW platelet-derived growth factor-C; PDGF-C; human; smooth muscle;  
KW cell proliferation; tissue repair; antiarteriosclerotic; vulnerary;  
KW vasotrophic; uropathic; gene therapy; chromosome 4q31-q32; gene; ss.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH CDS 257..1294  
FT /tag= a  
FT /product= "VEGF-X"  
FT sig\_peptide 257..322  
FT /tag= b  
FT mat\_peptide 323..1291  
FT /tag= c  
FT misc\_feature 363..364  
FT /tag= d  
FT /note= "location of predicted mRNA splicing event"  
FT misc\_feature 568..569  
FT /tag= e  
FT /note= "location of predicted mRNA splicing event"  
FT misc\_feature 703..704  
FT /tag= f  
FT /note= "cryptic splice donor/acceptor site"  
FT misc\_feature 744..745  
FT /tag= g  
FT /note= "location of predicted mRNA splicing event"  
FT misc\_feature 942..943  
FT /tag= h  
FT /note= "location of predicted mRNA splicing event"  
FT misc\_feature 979..980  
FT /tag= i  
FT /note= "cryptic splice donor/acceptor site"  
FT misc\_feature 1165..1166  
FT /tag= j  
FT /note= "location of predicted mRNA splicing event"  
XX WO200272127-A2.  
XX 19-SEP-2002.  
PD

XX 07-MAR-2002; 2002WO-EP02616.  
 XX 09-MAR-2001; 2001US-274901P.  
 XX (JANC ) JANSSEN PHARM NV.  
 XX Geesin JC, Gosiewska A, Xu J, Gordon R, Yon J, Dhanraj SN;  
 PI Harris I;  
 XX MPI: 2002-723297/78.  
 DR P-PSDB; ABB79984.  
 XX  
 XX Use of vascular endothelial growth factor polypeptides, its CUB domain  
 PT and polynucleotides, for manufacturing a medicament for treating or  
 PT preventing diseases associated with reduced smooth muscle cell  
 PT proliferation -  
 XX  
 PS Claim 1; Fig 1(a); 48pp; English.  
 XX  
 CC The present sequence is the cDNA sequence of human vascular  
 CC endothelial growth factor-X (VEGF-X), or platelet-derived growth  
 CC factor-C (PDGF-C), a novel member of the VEGF/PDGF family. The  
 CC cDNA was obtained from a search of expressed sequence tag  
 CC databases. Positions of mRNA splicing events were determined  
 CC either from direct sequencing on an isolated BAC clone or by  
 CC comparison of partial BAC database sequences. No information on  
 CC splicing events is available for the region from nucleotides  
 CC 900 to 957. Cryptic splice donor/acceptor sites were deduced from  
 CC variant sequences isolated by PCR. The VEGF-X gene was localised  
 CC to the long arm of human chromosome 4, region q31-q32. The VEGF-X  
 CC protein, and its CUB domain, exhibit a mitogenic activity on human  
 CC smooth muscle cell. Claimed methods of treating or preventing  
 CC a urethral dysfunction, bladder dysfunction, pelvic floor  
 CC reconstruction, sphincter dysfunction or a dysfunction associated  
 CC with aberrant endogenous VEGF-X activity comprise administering a  
 CC VEGF-X polypeptide (or its CUB domain), a nucleic acid molecule  
 CC encoding it, an expression vector comprising the nucleic acid  
 CC molecule, or a pharmaceutical composition comprising the nucleic  
 CC acid molecule or polypeptide. Claimed methods of treating or  
 CC preventing atherosclerosis, neointimal hyperplasia caused by artery  
 CC anastomosis or balloon catheter, post-angioplasty restenosis  
 CC caused by arterial stenting after percutaneous transluminal coronary  
 CC angioplasty, comprise administering neutralising VEGF-X antibodies,  
 CC antisense VEGF-X sequences or non-protein antagonists. Methods of  
 CC diagnosing a pathological condition, or a susceptibility to such a  
 CC condition, associated with smooth muscle cell proliferation, and  
 CC for identifying compounds that inhibit or enhance smooth muscle  
 CC cell proliferation, are also claimed.  
 XX  
 SQ Sequence 2632 BP; 772 A; 502 C; 557 G; 801 T; 0 other;  
 Query Match 62.0%; Score 914.2; DB 24; Length 2632;  
 Best Local Similarity 83.5%; Pred. No. 1.6e-267;  
 Matches 1050; Conservative 0; Mismatches 203; Indels 4; Gaps 1;  
 QY 2 ACCTGGAGACACAGAGGGGCTCTAGGAAAATTTTGGATGGGATTTATGTGAAACTA 61  
 DB 59 AACTGGAGACACAGAGGGGCTCTAGGAAAATTTTGGATGGGATTTATGTGAAACTA 118  
 QY 62 CCCTGGGATTTCTGTGCGAGCGCCAGCGGCTTCCACCGAGCGAGCCTTCC 121  
 DB 119 CCCTGGGATTTCTGTGCGAGCGGCTTCCACCGAGCGGCTTCCACCGAGCCTTCC 178  
 QY 122 CGG---GCTGGGCTGAGCCTTGGATCGTCGCTTCCCGAGTGGCGAGTGACC 177  
 DB 179 TGGCGGTGGTGAAGAGACTCGGAGTCGCTTCCAAAGTCCCGCGGTGAGAGCT 238  
 QY 178 CTCGCCCCAGTCAGCAAAATGCTCTCTCGGCGCTTCTCTGCTGACATCTGCCCTGGCC 237  
 DB 239 CTCACCCAGTCAGCCAAATGAGCCTCTTGGGCTTCTCTGCTGACATCTGCCCTGGCC 298  
 QY 238 GGCCAAAGACGGGAGCTCGGGCTGAGTCCAAACCTGAGCAGCAAGTTGCGAGCTCTCCAGC 297

299	GGCCACAGACAGGGGACTCAGGCGGAATCCAACTGAGTAGTAAATTTCCAGTTTCCAGC	358
298	GACAAGAAACAGAAACGAGTGCAGAGATCCCGCATGAGAGAGTTGTCACTATATCTGGT	357
359	AACAAGAAACAGAAACGAGTGCAGAGATCCCGCATGAGAGAGTTGTCACTATATCTGGT	418
358	AATGGGAGATCCACAGCCCGAAAGTTTCTCATACGTAACCCAGAAATATGGTGCTGGTG	417
419	AATGGAGATTTACAGCCCGAAAGTTTCTCATACGTAACCCAGAAATATGGTGCTGGTG	478
418	TGAGATTTAGTTCAGTAGATGAATTCGGATCCGATCCAGCTGACATTTGATGAGAGATT	477
479	TGAGATTTAGTTCAGTAGAGGAAATGTATGGATCAACTTACGTTTGTATGAAGAGATT	538
478	GGCTCGAAGATCCAGAAACGATATATGCAAGTATGATTTGTAGAAGTTGAGGAGCC	537
539	GGCTCGAAGATCCAGAAACGATATATGCAAGTATGATTTGTAGAAGTTGAGGAGCC	598
538	AGTATGGAGATTTTATAGGACGCTGGTGTGGTCTTGGGACTGTGCCAGAAAGCAGACT	597
599	AGTATGGAGATTTTATAGGACGCTGGTGTGGTCTTGGTACTGTACCAGGAAACAGATT	658
598	TCATAAGAAATCATATCAGGATAAGATTTGTATCTGATGAGTATTTCCATCTGAACCC	657
659	TCATAAGAAATCAATTAGGATAAGATTTGTATCTGATGAGTATTTCCATCTGAACCC	718
658	GGATTCGCATCCACTACAGTATTTATCATGCCCAAGTCACAGAAACCCAGAGTCTTTCG	717
719	GGGTTCGCATCCACTACAGTATTTATCATGCCCAAGTCACAGAAAGCTGTGAGTCTTCA	778
718	GTGTGCCCCCTTCATCTTTGTCAATGGACCTGCTCAACAATGTGTGACTGCCTTCAGT	777
779	GTGTGCCCCCTTCAGCTTTGCCACTGCACTGCTTAATAATGCTATAACTGCCTTTAGT	838
778	ACCTTGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGGAGGTGGACTTGCAGAC	837
839	ACCTTGAAGAGCTTATTCGATATCTTGAACCCAGAGAGATGGCAGTTTGAAGAT	898
838	CTCTACAAGCAACATCGGAGCTTTTGGGCAAGGCTTCTCTGTATGGGAAAAAAGCAAA	897
899	CTATATAGGCAACTTGGCACTTCTTGGCAAGGCTTTGTTTGGAGAAAAATCCAGA	958
898	GTGTGTAATCTGAATCTCTCAAGAAAGAGTAAACTCTACAGCTGCACACCCCGAAC	957
959	GTGTGTAATCTGAATCTCTCAAGAAAGAGTAAACTCTACAGCTGCACACCTCGTAAC	1018
958	TTCTCAGTGTCCATACGGGAGAGCTTAAAGAGGACAGATACCATATTTCTGCCAGTTGT	1017
1019	TTCTCAGTGTCCATACGGGAGAGCTTAAAGAGGAGACCATATTTCTGCCAGTTGT	1078
1018	CTCTGCTCAAGCGCTGTGGAGAAATTTGCGCTTGTGTCTCCCAATTTGCAATGAATGT	1077
1079	CTCTGCTTAAACGCTGTGGTGGAACTGTGCTTGTGTCTCCCAATTTGCAATGAATGT	1138
1078	CAGTGTGTCCACGTAAGTTTCAAAAAAGTACCATGAGGTCCTTTCAGTTGAGACCAAAA	1137
1139	CAATGTGTCCCAAGCAAGTTTCTAAAAAATACACGAGGTCCTTTCAGTTGAGACCAAG	1198
1138	ACTGAGTCAAGGATTCATAGTCACTCATGATGTGGCTCTGGACACACACGAGGAA	1197
1199	ACCGGTGTGAGGATTTGCAAAATCACTACCAGCGTGGCCCTTGGACACCATGAGAG	1258
1198	TGTGACTGTGTGTAGAGGAAACGAGGAGGTTAACTTGCAGCCTTCTGTAGCAGCAC	1254
1259	TGTGACTGTGTGTGACAGGGAGGACAGAGGAGTAGCGCATCACCCACGAGCAGCTC	1315

RESULT 10  
 AAA71990  
 ID AAA71990 standard; cdna; 2668 BP.  
 XX  
 AC AAA71990;









QY 958 TTCTCAGTCTCCATACGGGAAGAGCTAAAGAGGACAGATACCATATTCTGGCCAGGTGT 1017  
Db |||||  
QY 1021 TTCTCAGTCTCCATAGGAAGAGACTAAAGAGAACCGATACCATTTCTGGCCAGGTGT 1080  
Db |||||  
QY 1018 CTCCTGGTCAAGCGCTGTGGAGAAATGTGCTGTGTCTCATTAATTTGCAATGAATGT 1077  
Db |||||  
QY 1081 CTCCTGGTTAAACGGCTGTGGTGGAACTGTGCCCTGTGTGCTCCACAATTTGCAATGAATGT 1140  
QY 1078 CAGTGTGTCACGTTAAAGTTACAAAAAGTACCATGAGTCTCTCAGTTGAGACCAAAA 1137  
Db |||||  
QY 1141 CAATGTGTCTCCAGCAAGTTACTTAAAAAATACCCGAGGTCTCTCAGTTGAGACCAAG 1200  
QY 1138 ACTGGAGTCAAGGATTTGATAGTCACTCACTGATGTGGCTCTGGAACACACGAGGAA 1197  
Db |||||  
QY 1201 ACCGGTGTGAGGGATTTGACAAATCACTACCGAGGTGGCCCTGGAGCACTGAGGAG 1260  
QY 1198 TGTGACTGTGTGTAGAGAAACGAGGAGGTAACTGCGAGCTTGTAGCAGCAC 1254  
Db |||||  
QY 1261 TGTGACTGTGTGTGAGAGGAGCAGAGGAGTAGCGGCATCACCAACGAGCAGCTC 1317

RESULT 12

ID ABS57294  
XX ABS57294 standard; DNA; 2825 BP.

AC ABS57294;

DT 31-JAN-2003 (first entry)

XX DNA encoding human vascular endothelial cell growth factor-E (VEGF-E).

DE Human; vascular endothelial cell growth factor-E; VEGF-E; PRO:200;  
XX VEGF; bone morphogenetic protein 1; wound repair; tissue regeneration;  
KW cardiovascular disorder; endothelial disorder; angiogenic disorder;  
KW cancer; diabetes mellitus; cardiac hypertrophy; atherosclerosis;  
KW cardiast; cytostatic; antidiabetic; antiarteriosclerotic;  
KW gene therapy; gene; ds.

XX Homo sapiens.

XX Key Location/Qualifiers  
FH 259..1296  
FT CDS /\*tag= a  
FT /\*product= "VEGF-E"

XX US6455283-B1.

XX 24-SEP-2002.

XX 10-MAR-1999; 99US-0265686.

XX 17-MAR-1998; 98US-0040220.

XX 02-NOV-1998; 98US-0184216.

XX (GETH ) GENENTECH INC.

XX Ferrara N, Kuo SS;

XX WPI; 2003-086231/06.

XX P-PSDB; ABG72132.

XX New nucleic acid encoding endothelial cell growth factor-E polypeptide,  
PT useful for diagnosing or treating a cardiovascular, endothelial or  
PT angiogenic disorder such as cancer, diabetes mellitus or  
PT atherosclerosis

XX Claim 2; Fig 1; 46pp; English.

XX The present invention relates to the isolation of human vascular

XX endothelial cell growth factor-E (VEGF-E, also referred to as

XX PRO:200), and the polynucleotide sequence encoding it. VEGF-E is

XX related to VEGF and bone morphogenetic protein 1. VEGF-E is useful

CC in wound repair, as well as in the generation and regeneration of  
CC tissue. The sequences of the invention are useful for diagnosing or  
CC treating cardiovascular, endothelial or angiogenic disorders such as  
CC cancer, diabetes mellitus, cardiac hypertrophy and atherosclerosis.  
CC The polynucleotide encoding VEGF-E is useful in the gene therapy of  
CC such disorders. The present sequence encodes human VEGF-E.

XX Sequence 2825 BP; 849 A; 522 C; 605 G; 848 T; 1 other;

Query Match 62.0%; Score 914.2; DB 25; Length 2825;  
Best Local Similarity 83.5%; Pred. No. 1.7e-267;  
Matches 1050; Conservative 0; Mismatches 203; Indels 4; Gaps 1;

QY 2 ACCTGAGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTATGTGAAACTA 61

Db 61 AACTGAGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTATGTGAAACTA 120

QY 62 CCTCGGATTTCTGCTGCCAGAGCGCGCCAGCGCTTCCACCGCAGCGAGCTTTCCC 121

Db 121 CCTCGGATTTCTGCTGCCAGAGCGCGCTTCCACCGCAGCGAGCTTTCCC 180

QY 122 CGG---GCTGGGCTGAGCCTTCGAGTCTGCTCTCCCGAGTCCCGCCGAGTGAGCC 177

Db 181 TGGCGGTGTGAAAGAGACTCGGAGTCTGCTGTTTCAAAGTCCCGCCGCTGAGTGAGCT 240

QY 178 CTCGCCCCAGTCTAGCCAAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCCCTGGCC 237

Db 241 CTCACCCCGAGTCTAGCCAAATGAGCTCTCTCGGCTCTCTCTGCTGACATCTGCCCTGGCC 300

QY 238 GGCCTAAGAACGGGAGTCTGGGCTGAGTCCAACTGAGCAGCAAGTTGCACTCTCCAGC 297

Db 301 GGCCTAAGAACGGGAGTCTGAGGGGAAATCCAACTGAGTAAATTTCCAGTTTTCAGC 360

QY 298 GACAGGAACAGAACGGAGTGCAGATCCCGGCTGAGAGAGTTGTCACTATCTCGT 357

Db 361 AACAAGAACAGAACGGAGTGCAGATCCCGGCTGAGAGAGTTGTCACTATCTCGT 420

QY 358 AATGGGAGCATCCACAGCCGAAAGTTTCTCATACGCTACCCAGAAATATGGTCTGGTG 417

Db 421 AATGGAAATATCCACAGCCCAAGTTTCTCTCATACTTATCCAGAAATACGGTCTTGTA 480

QY 418 TGGAGATTAGTTCAGTAGATGAAATGTGGGATCCAGCTGACATTTGATGAGAGATT 477

Db 481 TGGAGATTAGTTCAGTAGAGGAAATATGATGATACCACTTACCTTTGATGAAAGATT 540

QY 478 GGCCTGAAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAGTTGAGCAGCC 537

Db 541 GGCCTTGAAGACCCAGAAATGACATATGCAAGTATGATTTTGTAGAGTTGAGGACCC 600

QY 538 AGTGATGGAAGTGTTTTAGGACGCTGCTGTTCTGGGACTGTGCCAGGAAAGCAGACT 597

Db 601 AGTGATGGAATATATTAGGCGCTGCTGTTCTGGTACTGTACACAGGAAACAGATT 660

QY 598 TCTAAGGAAATCATATCAGGATAAGATTGTGATCTGATGAGTATTTTCCATCTGAACCC 657

Db 661 TCTAAGGAAATCAAATTAGGATAAGATTGTGATCTGATGAATATTTTCTCTTGAACCA 720

QY 658 GGATTCGCAATCCACTACAGTATTATCATGCCAAGTCCACAGAAACACAGGCTCTTCG 717

Db 721 GGGTTCTGCATTCCTACAAATTTGTATGCCAATTTCAAGAGCTGTGAGTCTTCA 780

QY 718 GTGTGCCCCCTTCATCTTTGTATGAGCCTGTCTCAACATGCTGTGACTGCTTCACT 777

Db 781 GTGTACCCCTTCAGCTTTGCCACTGACCTGCTTAATAATGCTATAAATGCTTAACT 840

QY 778 ACCTTGAAGAGCTGATTCGGTACCTAGAGCAGATCGATGGCAGGTGGACTTGGACAGC 837

Db 841 ACCTTGAAGAGCTTATTCGATATCTTGAACACAGAGATGGCAGTTGGAGTTGAAAGAT 900

QY 838 CTCTACAGCCCAATGCGAGCTTTTGGCAAGCTTTTCTGTATGGGAAAAAGCAAA 897

Db 901 CTATATAGGCCCACTTGGCAACTTCTTGGCAAGCTTTTGTGTTTGAAGAAAAATCCAGA 960

QY 898 GTGGTGAATCTGAATCTCTCAAGGAAGAGGTAAACTCTACAGCTGCACACCCCGGAAC 957  
 Db 961 GTGGTGAATCTGAATCTCTCAAGGAAGAGGTAAAGATTATACAGCTGCACACCTCGTAAC 1020  
 QY 958 TTCTCAGTGTCCATACCGGAAGAGCTAAAGAGGACAGATACCATATTCTGGCCAGGTTGT 1017  
 Db 1021 TTCTCAGTGTCCATACCGGAAGAGCTAAAGAGGACAGATACCATATTCTGGCCAGGTTGT 1080  
 QY 1018 CTCTGCTCAAGCGCTGTGGAGGAATTTGCTCTGTTGCTCTCCATAATTGCAATGAATGT 1077  
 Db 1081 CTCTGCTGTTAAACGCTGTGGGGAAGCTGTGCTGTTGCTCTCCATAATTGCAATGAATGT 1140  
 QY 1078 CAGTGTGTCCACAGTAAGTTTACAAAAGATACCATAGGAGTCTCTCAGTTGAGACCAAAA 1137  
 Db 1141 CAATGTGTCCACAGTAAGTTTACTAAAAGATACCATAGGAGTCTCTCAGTTGAGACCAAAA 1200  
 QY 1138 ACTGGAGTCAAGGATTCATTAAGTCACTCACTGATGTGGCTCTGGACACACGAGGAA 1197  
 Db 1201 ACCGTTGTCAAGGATTCATTAAGTCACTCACTGATGTGGCTCTGGACACACGAGGAG 1260  
 QY 1198 TGTGACTGTGTGTAGAGGAAACGACAGAGGATTAACCTGACAGCTTCTGTAGCAGCAC 1254  
 Db 1261 TGTGACTGTGTGTAGAGGAAACGACAGAGGATTAACCTGACAGCTTCTGTAGCAGCAC 1317

## RESULT 13

AAD06812  
 ID AAD06812 standard; DNA; 2827 BP.

XX AC AAD06812;

XX DT 10-AUG-2001 (first entry)

XX DE Human LP8, a PDGF-related protein encoding DNA.

XX KW Human; LP8; platelet-derived growth factor-related protein; PGDF  
 cytosolic; vulnary; bone growth; therapy; bone fracture;  
 KW prophylaxis; osteoblast proliferation; osteoporosis; muscle loss;  
 KW bone loss; endocrine disorder; arthritis; sarcopenia;  
 KW periodontal disease; cartilage differentiation; wound healing; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 276..1313

XX FT FT /\*tag= a

XX FT FT /product= "Human LP8, a PDGF-related protein"

XX PN WO200132197-A2.

XX PD 10-MAY-2001.

XX PF 24-OCT-2000; 2000WO-US26272.

XX PR 02-NOV-1999; 99US-0163056.

XX PR 02-NOV-1999; 99US-0163203.

XX PR 02-NOV-1999; 99US-0163204.

XX PA (ELIL ) LILLY & CO ELI.

XX PI Hock JM, Na S, Hammond LJ, Kharitonov A, Krishnan V, Becker GW;

XX DR WPI; 2001-316384/33.

XX DR P-PSDB; AAE02649.

XX PT New LP8 protein or its fragment for promoting bone growth, treating  
 bone fractures, increasing or maintaining bone density, and treating  
 osteoporosis, arthritis, sarcopenia and periodontal disease -

XX PS Example 1; Page 57-59; 61pp; English.

XX CC The present sequence is a DNA encoding human LP8, platelet-derived

XX CC growth factor (PDGF)-related protein or its fragment. LP8 or its

CC fragment is useful for promoting bone growth, treating bone fractures,  
 CC prophylactically increasing or maintaining bone density in a subject  
 CC having a substantially normal bone density, so as to stimulate  
 CC osteoblast proliferation, treating osteoporosis, muscle or bone loss  
 CC due to malignancy, endocrine disorder, arthritis, sarcopenia and  
 CC periodontal disease, preventing cartilage differentiation, and  
 CC wound healing.

XX SQ Sequence 2827 BP; 864 A; 522 C; 589 G; 852 T; 0 other;

Query Match 62.0%; Score 914.2; DB 22; Length 2827;

Best Local Similarity 83.5%; Pred. No. 1.7e-267;

Matches 1050; Conservative 0; Mismatches 203; Indels 4; Gaps 1;

QY 2 ACCTGGAGACACAGAGGGCTCTAGGAAAAATTTTGGATGGGATATATGGAAACTA 61

Db 78 AACTGGATACACAGAGGGCTCTAGGAAAAATTTTGGATGGGATATATGGAAACTA 137

QY 62 CCCTCGGATTTCTGCTGCCAGAGCCGCGGCTTCCACCGCAGCGAGCTTTCC 121

Db 138 CCCTCGGATTTCTGCTGCCAGAGCGCTCGGGCTTCCACCGCAGCGAGCTTTCC 197

QY 122 CGG---GCTGGGCTGAGCTTGGAGTCTGCTTCCCGAGTCCCGCGGAGTGAGCC 177

Db 198 TGGCGGTGTAAGAGACTCGGGAGTCTGCTTCCAAAGTCCCGCGGAGTGAGCT 257

QY 178 CTCGCCCCAGTCAGCCAAATGCTCCTCTCGGCTCTCTCTGCTGACATCTGCCCTGGCC 237

Db 258 CTCACCCAGTCAGCCAAATGAGCTCTTTCGGGCTCTCTCTGCTGACATCTGCCCTGGCC 317

QY 238 GGCCTGAGGAGTCCAGGAGTCCAGGCTGAGTCCACCTGAGCAGCAGTTCGAGCTCCACG 297

Db 318 GGCCTGAGGAGTCCAGGAGTCCAGGCTGAGTCCACCTGAGTGAATTCAGTTTCCAGC 377

QY 298 GACAGGAACACAGACGAGTGCAGATCCCGGCAATGAGAGAGTTGTCTATATCTGT 357

Db 378 AACAGGAACACAGACGAGTGCAGATCCCGGCAATGAGAGAGTTGTCTATATCTGT 437

QY 358 AATGGAGATCCACAGCCCGAGTTCTCTATAGTACCCAGAAATATGCTGCTGGTG 417

Db 438 AATGGAATTTTCAAGCCCAAGTTTCTCTATATCTTATCCAAAGAAATACGGTCTTGGTA 497

QY 418 TGGAGATTAGTTCAGTAGATGAAAATGTGGGATCCAGCTGACATTTGATCAGAGATT 477

Db 498 TGGAGATTAGTTCAGTAGATGAAAATGTGGGATCCAGCTGACATTTGATCAGAGATT 557

QY 478 GGGCTGGAAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAGTTGAGGAGCC 537

Db 558 GGGCTGGAAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAGTTGAGGAGCC 617

QY 538 AGTGTGGAAGTGTGTTTAGGACGCTGTTGGGCTGTTGGGCTGTTGGGAGAGCAGACT 597

Db 618 AGTGTGGAAGTGTGTTTAGGACGCTGTTGGGCTGTTGGGCTGTTGGGAGAGCAGACT 677

QY 598 TCTAAGGAATCATATATCAGGATAGATTTGATCTGATGATGATTTTCCATCTGAACCC 657

Db 678 TCTAAGGAATCATATATCAGGATAGATTTGATCTGATGATGATTTTCCATCTGAACCC 737

QY 658 GGATTTCTGATCCACTACAGTATTATCATGCCCAAGTCCACAGAAACACGAGTCTCTCG 717

Db 738 GGATTTCTGATCCACTACAGTATTATCATGCCCAAGTCCACAGAAACACGAGTCTCTCG 797

QY 718 GTGTTGCCCTTCTATCTTTTGTGCTTGGACCTGCTCAACATGCTGTGATGCTTCACT 777

Db 798 GTGTTGCCCTTCTATCTTTTGTGCTTGGACCTGCTCAACATGCTGTGATGCTTCACT 857

QY 778 ACCTTGGAGAGTGTATTCGGTACCTAGAGCAGATTCGATGGCAGTGGAGCTTGGACAGC 837

Db 858 ACCTTGGAGAGTGTATTCGGTACCTAGAGCAGATTCGATGGCAGTGGAGCTTGGAGAT 917

QY 838 CTCCTCAAGCCCAACATGCGAGCTTTTGGGCAAGGCTTTCTGTATGGGAAAAAAGCAAA 897

Db 918 CTCCTCAAGCCCAACATGCGAGCTTTTGGGCAAGGCTTTCTGTATGGGAAAAAAGCAAA 977

QY 898 GTGGTGAATCTGATCTCTCAAGGAGGCTAAACCTCTACAGTGCACACCCCGGAAC 957

Db 978 GTGGTGAATCTGAAACCTCTCAAGAGGAGTAAGATTATACAGCTGCACACCTCGTAAC 1037

QY 958 TTCTCAGTGTCCATACCGGAAAGAGCTAAAGAGGACAGATACCATATTTCTGGCCAGTTGT 1017

Db 1038 TTCTCAGTGTCCATACCGGAAAGAGCTAAAGAGGAAACCGATACCATATTTCTGGCCAGTTGT 1097

QY 1018 CTCCTGTGTCAGCGTGTGGAGGAATTTGTCCTGTGTCTCCATTAATGCAATGAATGT 1077

Db 1098 CTCCTGTGTCAGCGTGTGGAGAACTGTGCGCTGTGTCTCCATTAATGCAATGAATGT 1157

QY 1078 CAGTGTGTCCAGCTTAAAGTTTACAAAAGAGTACCATGAGTCCCTTCACTTGAGACCAAAA 1137

Db 1158 CAATGTGTCCAGTAAAGTTTACTTAAATAATCCACAGAGTCCCTTCACTTGAGACCAAAA 1217

QY 1138 ACTGAGTCAAGGGATTGCATTAAGTCACTCACTGATGTGGTCTTGGAAACACACAGAGAA 1197

Db 1218 ACCGTGTGAGGGATTGCACAAATCACTACCGAGCTGGGCTTGGAGCACCATGAGGAG 1277

QY 1198 TGTGACTGTGTGTAGAGGAACCGAGAGGTAACCTGACGCTTCTGTAGCAGCAC 1254

Db 1278 TGTGACTGTGTGTGAGAGGGAGCACAGAGGATAGCCGCATCACACAGCAGCTC 1334

RESULT 14

AAAA47452

ID AAA47452 standard; cDNA; 2839 BP.

XX AC AAA47452;

XX DT 20-OCT-2000 (first entry)

XX DE Human TANGO 128 coding sequence.

XX KW TANGO; 128; 140; 197; 212; 213; 224; 239; modulating agent; asthma;

XX KW graft versus-host diseases; rheumatoid arthritis; psoriasis;

XX KW inflammatory bowel disease; septic shock; ulcerative colitis;

XX KW Crohn's disease; chronic myelogenous leukemia; cancer; liver

XX KW disease; Hodgkin's disease; osteoarthritis; Lyme's disease;

XX KW cachexia; autoimmune disease; myasthenia gravis; autoimmune diabetes;

XX KW systemic lupus erythematosus; transgenic animal; diagnosis;

XX KW prognosis; prophylactic; therapeutic; human; ds.

XX OS Homo sapiens.

XX FH Key

XX CDS Location/Qualifiers

FT 288..1325

FT /\*tag= a

FT /product= TANGO 128

XX WO200039284-A1.

XX PN 06-JUL-2000.

XX PD 23-DEC-1999; 99WO-US31025.

XX PF 30-DEC-1998; 98US-0223546.

XX PR (MILL-) MILLENNIUM PHARM INC.

XX PA Holtzman DA;

XX PI WPI; 2000-465743/40.

XX DR P-PSDB; AAB01419.

XX DR Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213,

XX PT 224 and 239 polypeptides useful for the treatment of asthma, rheumatoid

XX PT arthritis, psoriasis and autoimmune diseases

XX PS Claim 1; Fig 1; 209pp; English.

XX XX

CC Nucleic acids encoding TANGO polypeptides are useful as modulating

CC agents for regulating cellular processes like asthma, graft

CC versus-host diseases, rheumatoid arthritis, psoriasis, inflammatory

CC bowel disease, septic shock, ulcerative colitis, Crohn's disease,

CC chronic myelogenous leukemia, cancer, liver disease, Hodgkin's

CC disease, osteoarthritis, Lyme's disease, cachexia and autoimmune

CC diseases e.g. myasthenia gravis, autoimmune diabetes and systemic

CC lupus erythematosus. The nucleic acids are also useful for producing

CC transgenic animals and the TANGO polypeptides themselves. Partial

CC TANGO-128, 140, 197, 212, 213, 224, 239 sequences are useful in

CC forensic biology, for diagnostic assays, prognostic assays,

CC pharmacogenomics and for monitoring clinical trials. TANGO

CC polypeptides are suitable for both prophylactic and therapeutic

CC methods for treating a subject at risk of a disorder or having a

CC disorder associated with aberrant TANGO expression. A wide range

CC of cellular disorders can be treated.

XX

SQ Sequence 2839 BP; 858 A; 532 C; 600 G; 849 T; 0 other;

Query Match 62.0%; Score 914.2; DB 21; Length 2839;

Best Local Similarity 83.5%; Pred. No. 1.7e-267;

Matches 1050; Conservative 0; Mismatches 203; Indels 4; Gaps 1;

QY 2 ACCTGACACACAGAGAGGCTCTAGGAAATTTTGGATGGGATATATGGAACATA 61

Db 90 AACTGGACACACAGAGAGGCTCTAGGAAATTTTGGATGGGATATATGGAACATA 149

QY 62 CCTCTCGATTTCTCTGCTCCAGAGCCGCGCTTCCACCGCAGCCAGCTTTTCCC 121

Db 150 CCTCTCGATTTCTCTGCTCCAGAGCAGCTCGGCTTCCACCGCAGCTTTTCCC 209

QY 122 CGG----GCTGGGCTGAGCTTTGGAGTGTCTGCTTCCCGAGTCCCGCGGAGTGAGCC 177

Db 210 TGGCGGTGTGAAAGAGACTCGGGAGTGTCTGCTTCCAAAGTGCCTGAGTGAGCT 269

QY 178 CTCGCCCGCAGTCAGCCAAATGCTCTCTCGCGCTCTCTCTGTCACATCTGCTGGCC 237

Db 270 CTCACCCCGAGTCAGCCAAATGAGCTCTTTCGGGCTTCTCTCTGTCACATCTGCTGGCC 329

QY 238 GGCCTAAAGAAACGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGTCAGCTCTCCAGC 237

Db 330 GGCCTAAGACAGGAGACTCAGCGGATCCACCTGAGTAGTAATTCAGTTTCCAGC 389

QY 298 GACAAGGAACAGAACGGAGTCAAGATCCCGCATGAGAGAGTTCTACTATATCTGCT 357

Db 390 AACCAAGGAACAGAACGGAGTCAAGATCCCTGAGCATGAGAGATATATTACTGTCTACT 449

QY 358 AATGGGAGCATCCACAGCCCGAAGTTTCTCTATACGTACCCAGAAATATGGTCTGGTG 417

Db 450 AATGGAAGTATTCACAGCCCAAGTTTCTCTATATCTATCTTCCAGAAATACGGTCTGGTA 509

QY 418 TGGAGATTAGTTGTCAGTAGATAAATGTCCGATCCAGCTGACATTTGATGAGAGATT 477

Db 510 TGGAGATTAGTAGCAGTAGAGGAAATGTATGGATACAACTTACGTTTGTATGAAGATT 569

QY 478 GGGCTGGAAGATCCAGAACGATATATGCAAGTATGATTTTGTAGAGTTGAGGACCC 537

Db 570 GGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTTGTAGAGTTGAGGACCC 629

QY 538 AGTGATGGAAGTGTTTTGGAGCGCTGGTGGTTCTGGGACTGTCAGGAGAAAGACACT 597

Db 630 AGTGATGGAAGTGTATTTAGGCGCTGGTGGTTCTGGTACTGTACCGAGAAACAGATT 689

QY 598 TCTAAAGGAAATCATATCAGGATAAGATTGTATCTGATGAGTATTTTTCATCTGAACCC 657

Db 690 TCTAAAGGAAATCAAAATTAGGATAAGATTGTATCTGATGAATATTTTCTTCTGAACCA 749

QY 658 GGAATCTGATTCACATACAGTATATATGAGCCCAAGATCAGAGAACCAAGTCTCTCG 717

Db 750 GGGTTCTGATCCACTACAAATGTGATGCCCAATTCATGAGAGCTGTGAGTCTCTCA 809

QY 718 GTGTGCCCCCTTCATCTTTGTTCATTTGACCTCTCAACATCTGTGATGCTCTCAGT 777

```
Db      810 GTGCTACCCCTTCAGCTTTGCCACTGACCTGCTTAATAATGCTATTAAGTCCCTTTAGT 869
QY      778 ACCTTGGAGAGCTGATTGCGTACCTAGACGACAGATCGATGCGAGTGCAGTTCGACAGC 837
Db      870 ACCTTGGAGAGCTTATTTCGATATCTTGAACGAGAGATGGCAGTTGGACTTGAAGAT 929
QY      838 CTCTACAAGCCCAACATGGCAGCTTTTGGGCAAGGCTTTCCCTGTATGGGAAAAAAGCAAA 897
Db      930 CTATATAGCCCACTTGGCACTTCTTGGCAAGGCTTTTGTGTTTGAAGAAAAATCCAGA 989
QY      898 GTGGTGAATCTGAATCTCCTCAAGGAAGAGGTAAATCTTACAGTGCACACCCCGGAC 957
Db      990 GTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAAC 1049
QY      958 TTCTCAGTGTCCATACGGGAAGAGCTTAAAGAGGACAGATACCATATCTCGGCCAGGTTGT 1017
Db      1050 TTCTCAGTGTCCATTAAGGAAGAACTTAAGAGAACCGATACCATTTTCTGGCCAGGTTGT 1109
QY      1018 CTCCTGGTCAAGCGCTGTGGAGGAAATTGTGCTGTGTCTCCATTAATTCGAATGAATGT 1077
Db      1110 CTCCTGGTTAAACGCTGTGGTGGAACTGTGCTGTGTCTCCATTAATTCGAATGAATGT 1169
QY      1078 CAGTGTGTCACGTAAGTTACAAAAGTACCATGAGTCTTCCAGTTGAGACCAAAA 1137
Db      1170 CAATGTGTCACCAAGCAAGTTACTAAATAATACCAGAGGTCTTCCAGTTGAGACCAAG 1229
QY      1138 ACTGGAGTCAAGGGATTGCATAAGTCACCTCACTGATGTGGCTCTGGAAACACCAAGAGAA 1197
Db      1230 ACCGTGTTCAGGGGATTGCACAAATCACTACCGAGCTGGCCCTGGAGACCATGAGGAG 1289
QY      1198 TGTGACTGTGTGTAGAGAAACGAGAGGGTAACTGCGACCTTTCGTAGCAGCAC 1254
Db      1290 TGTGACTGTGTGTGACAGGGAGCACAGAGGATAGCCGCATCACACCAGCAGCTC 1346

RESULT 15
AAZ34296
ID      AAZ34296 standard; cdNA; 2849 BP.
XX
AC      AAZ34296;
XX
DT      07-DEC-1999 (first entry)
XX
DE      Human PRO200 nucleotide sequence.
XX
KW      Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW      probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW      secreted protein; transmembrane protein; ss.
XX
OS      Homo sapiens.
XX
PN      WO9946281-A2.
XX
PD      16-SEP-1999.
XX
PF      08-MAR-1999; 99WO-U050528.
XX
PR      10-MAR-1998; 98US-0077450.
PR      11-MAR-1998; 98US-0077632.
PR      11-MAR-1998; 98US-0077641.
PR      11-MAR-1998; 98US-0077649.
PR      12-MAR-1998; 98US-0077791.
PR      13-MAR-1998; 98US-0078004.
PR      17-MAR-1998; 98US-0040220.
PR      20-MAR-1998; 98US-0078886.
PR      20-MAR-1998; 98US-0078910.
PR      20-MAR-1998; 98US-0078936.
PR      20-MAR-1998; 98US-0078939.
PR      25-MAR-1998; 98US-0079294.
PR      26-MAR-1998; 98US-0079656.
PR      27-MAR-1998; 98US-0079663.
PR      27-MAR-1998; 98US-0079664.
PR      27-MAR-1998; 98US-0079689.
XX
```

```
PR      27-MAR-1998; 98US-0079728.
PR      27-MAR-1998; 98US-0079786.
PR      30-MAR-1998; 98US-0079920.
PR      30-MAR-1998; 98US-0079923.
PR      31-MAR-1998; 98US-0080105.
PR      31-MAR-1998; 98US-0080107.
PR      31-MAR-1998; 98US-0080165.
PR      31-MAR-1998; 98US-0080194.
PR      01-APR-1998; 98US-0080327.
PR      01-APR-1998; 98US-0080328.
PR      01-APR-1998; 98US-0080333.
PR      01-APR-1998; 98US-0080334.
PR      08-APR-1998; 98US-0081049.
PR      08-APR-1998; 98US-0081070.
PR      08-APR-1998; 98US-0081071.
PR      09-APR-1998; 98US-0081195.
PR      09-APR-1998; 98US-0081203.
PR      09-APR-1998; 98US-0081229.
PR      15-APR-1998; 98US-0081817.
PR      15-APR-1998; 98US-0081838.
PR      15-APR-1998; 98US-0081952.
PR      15-APR-1998; 98US-0081955.
PR      21-APR-1998; 98US-0082568.
PR      21-APR-1998; 98US-0082569.
PR      22-APR-1998; 98US-0082700.
PR      22-APR-1998; 98US-0082704.
PR      22-APR-1998; 98US-0082804.
PR      23-APR-1998; 98US-0082767.
PR      23-APR-1998; 98US-0082796.
PR      27-APR-1998; 98US-0083336.
PR      28-APR-1998; 98US-0083322.
PR      29-APR-1998; 98US-0083392.
PR      29-APR-1998; 98US-0083495.
PR      29-APR-1998; 98US-0083496.
PR      29-APR-1998; 98US-0083499.
PR      29-APR-1998; 98US-0083500.
PR      29-APR-1998; 98US-0083545.
PR      29-APR-1998; 98US-0083554.
PR      29-APR-1998; 98US-0083558.
PR      30-APR-1998; 98US-0083559.
PR      30-APR-1998; 98US-0083742.
PR      05-MAY-1998; 98US-0084366.
PR      06-MAY-1998; 98US-0084414.
PR      06-MAY-1998; 98US-0084441.
PR      07-MAY-1998; 98US-0084598.
PR      07-MAY-1998; 98US-0084600.
PR      07-MAY-1998; 98US-0084627.
PR      07-MAY-1998; 98US-0084637.
PR      07-MAY-1998; 98US-0084639.
PR      07-MAY-1998; 98US-0084640.
PR      13-MAY-1998; 98US-0084643.
PR      13-MAY-1998; 98US-0085323.
PR      13-MAY-1998; 98US-0085338.
PR      13-MAY-1998; 98US-0085339.
PR      15-MAY-1998; 98US-0085573.
PR      15-MAY-1998; 98US-0085579.
PR      15-MAY-1998; 98US-0085580.
PR      15-MAY-1998; 98US-0085582.
PR      15-MAY-1998; 98US-0085689.
PR      15-MAY-1998; 98US-0085697.
PR      15-MAY-1998; 98US-0085700.
PR      15-MAY-1998; 98US-0085704.
PR      18-MAY-1998; 98US-0086023.
PR      22-MAY-1998; 98US-0086392.
PR      22-MAY-1998; 98US-0086414.
PR      22-MAY-1998; 98US-0086430.
PR      22-MAY-1998; 98US-0086486.
PR      28-MAY-1998; 98US-0087098.
PR      28-MAY-1998; 98US-0087106.
PR      28-MAY-1998; 98US-0087208.
PR      30-JUL-1998; 98US-0094651.
PR      11-SEP-1998; 98US-0100038.
XX
```

PA	(GETH ) GENENTECH INC.	Db	687	TCCTAAGGAAATCAAAATTAGGATAAGATTGTATCTGATGAATATTTTCTCTTCTGAACCA	746
XX		QY	658	GGATTCTGCATCCACTACAGTATTTATCATGCCCAAGTACAGAAACACAGAGTCCTTCG	717
XX	Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;	Db	747	GGGTTCTGCATCCACTACAACTTGTCTGTCACCAATTCACAGAGCTGTGAGTCTTCA	806
DR	WPI; 1999-551358/46.	QY	718	GTGTTGCCCTTTCATCTTTTGTTCATTTGGACCTGCTCTCAAACTGCTGTGATGCTTTCAGT	777
XX	P-PSDB; AAY41766.	Db	807	GTGCTACCCCTTTCAGCTTTTGCCTGAGCTTCTTAATAATGCTATACTGCTTTCAGT	866
PT	New secreted and transmembrane polypeptides and their polynucleotides,	QY	778	ACCTTGGAGAGCTGATTTCGGTACCTAGAGCCAGATCGATGGCAGGTGGACTTTGGACAGC	837
PT	adhesion disorders -	Db	867	ACCTTGGAGAGCTTATTCGATATCTTGAACAGAGATGGCAGTTGGACTTAGAGAT	926
XX	Claim 2; Fig 206; 530pp; English.	QY	838	CTCTCAAGCCCAACATGGCAGCTTTTGGCAAGCTTTCTCTGATGGGAAAAAAGCAAA	897
XX	The present invention describes secreted and transmembrane polypeptides	Db	927	CTATATAGCCCAACTTGGCAACTTCTTGGCAAGCTTTTGTGGAAGAAAAATCCAGA	986
CC	and their polynucleotides. The nucleotide sequences are useful as	QY	898	GTGCTGAATCTGAATCTCTCTCAAGGAGAGGTAAACTCTACAGCTGCACACCCCGAAC	957
CC	sources of probes, primers, for chromosome mapping, and for generation	Db	987	GTGCTGATCTGAACCTTCTTAACAGAGGAGGTAAAGATTATACAGCTGCACACCTCGTAAC	1046
CC	of antisense sequences. They can also be used to treat a variety of diseases and	QY	958	TTCTCAGTGTCCATACGGAAGAGCTAAAGAGGACAGATACCATATTTCTGCCCAGGTGT	1017
CC	animals. The proteins can be used to treat a variety of diseases and	Db	1047	TTCTCAGTGTCCATAGGAGGAGAACTTAAGAGAACCGATACCAATTTCTGCCCAGGTGT	1106
CC	disorders, depending on their function. Diseases that may be treated	QY	1018	CTCTCTGCTCAAGCGCTGTGGAGGAAATTTGTCCTGTTGTCTCCATATTTGCAATGAATGT	1077
CC	include blood coagulation disorders, cancers and cellular adhesion	Db	1107	CTCTCTGTTAAACGCTGTGGTGGAACTGTGCTGTTGTCTCCCAATTTGCAATGAATGT	1166
CC	disorders. They may also be used to raise antibodies. AAZ33891 to	QY	1078	CAGTGTGTCCTCCAGTAAAGTTACAAAAAGTACATGAGGTCTCTCAGTTGAGACCAAAA	1137
CC	AAZ34338, and AAY41685 to AAY41774 represent polynucleotide and	Db	1167	CAATGTGTCCCAAGCAAAAGTTACTAAAAAATACCAAGGTCTCTCAGTTGAGACCAAAAG	1226
CC	polypeptide sequence given in the exemplification of the present	QY	1138	ACTGAGTCAAGGGATTGCAATAGTCACTCACTGATGTGGCTCTGGAACACCAACGAGAA	1197
CC	invention.	Db	1227	ACCGTGTGAGGGGANTTGAACAATCACTACCGAGTGGCCCTTGGAGCACTGAGGAG	1286
XX	Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;	QY	1198	TGTGACTGTGTGTAGAGGAAACGACAGGAGGTAACTGACAGCTTCTGATAGCAGCAC	1254
SQ	Query Match 62.0%; Score 914.2; DB 20; Length 2849;	Db	1287	TGTGACTGTGTGTGACAGGGAGCACAGGAGGATAGCCGATCACCACCGACGCTC	1343

Search completed: November 26, 2003, 00:11:33  
Job time : 276.163 secs

QY	2	ACCTGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTATGTGAAACTA	61
Db	87	AACCTGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTATGTGAAACTA	146
QY	62	CCCTGAGATCTCTGCTGCAGAGCGGCGAGCGCTTCCACCGCAGCGAGCTTTCCTC	121
Db	147	CCCTGAGATCTCTGCTGCAGAGCGGCTCGGCGCTTCCACCGCAGCTTTCCTCCTC	206
QY	122	CGG---GCTGGGCTGAGCCTTGGAGTGTGCTGCTTCCCAAGTCCCGCCGAGTGAGCC	177
Db	207	TGGCGGTGTGAAGAGACTCGGGAGTGTGCTGCTTCCAAAGTGCCTGAGTGAGCT	266
QY	178	CTCGCCCGAGTCAGCCAAATGCTCTCTCGGCTCTCTGCTGACATTCGCTGCTG	237
Db	267	CTCACCCAGTCAGCCAAATGAGCTTCTCGGCTTCTCTGCTGACATTCGCTGCTG	326
QY	238	GGCCAAAGACGGGCTCGGCTGAGTCCCACTGAGCAGCAAGTTGCACTCTCAGC	297
Db	327	GGCCAGAGACAGGGACTCAGGCGGAATCCAACTGAGTAGTAATTTCCAGTTTTCAGC	386
QY	298	GACAAAGAACAGAGTGCAGATCCCGGCTGAGAGATTGTCACTATATCTGCT	357
Db	387	AACAAGAACAGAGTGCAGATCCCTGAGTGCAGATGAGAGATTATTAATCTGCTACT	446
QY	358	AATGGAGCATTCACAGCCGAGTTTCTCTATACGTACCCAGAAATATGCTGCTG	417
Db	447	AATGGAAGTATTCACAGCCCAAGTTTCTCTATATTCAGAAATATACGCTTCTG	506
QY	418	TGAGATAGTTCAGTGTAGATGAATGTGCGATCCAGCTGACATTTGATGAGAGTTT	477
Db	507	TGAGATAGTGTAGAGGAGAAATGTATGGATACAACTTACGTTTGTATGAAGATT	566
QY	478	GGGCTGAAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAGTTTGGAGCCC	537
Db	567	GGGCTTGAAGACCCAGAGATGATATGCAAGTATGATTTTGTAGAGTTGAGAACCC	626
QY	538	AGTGATGAAGTGTGTTTGAAGCGCTGTGTTCTCGGACTGTGCGAGAAACAGACT	597
Db	627	AGTGATGAAGTATTTAGGCGCTGTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTG	686
QY	598	TCCTAAGGAATCATATCAGATGAAGATTGTATCTGATGATTTTCTCATCTGACCC	657

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 25, 2003, 23:46:56 ; Search time 72.0008 Seconds  
(without alignments)  
9035.995 Million cell updates/sec

Title: US-09-852-209A-6  
Perfect score: 1474  
Sequence: 1 cacttgagacacagaag.....aatcacaaagcactgcacgc 1474

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA.\*  
1: /cgm2\_6/ptodata/2/ina/5A.COMB.seq:\*  
2: /cgm2\_6/ptodata/2/ina/5B.COMB.seq:\*  
3: /cgm2\_6/ptodata/2/ina/6A.COMB.seq:\*  
4: /cgm2\_6/ptodata/2/ina/6B.COMB.seq:\*  
5: /cgm2\_6/ptodata/2/ina/PCTUS.COMB.seq:\*  
6: /cgm2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1444.8	98.0	3571	4	US-09-564-595D-34
2	1444.8	98.0	3571	4	US-09-706-968-42
3	1432.8	97.2	3573	4	US-09-457-066-42
4	914.2	62.0	2825	4	US-09-040-220D-1
5	914.2	62.0	2825	4	US-09-255-686-1
6	878.8	59.6	1760	4	US-09-564-595D-32
7	878.8	59.6	1760	4	US-09-706-968-1
8	878.8	59.6	1764	4	US-09-457-066-1
9	745.8	50.6	1095	4	US-09-457-066-50
10	745.8	50.6	1095	4	US-09-706-968-50
11	650.8	44.8	1035	4	US-09-457-066-6
12	650.8	44.8	1035	4	US-09-706-968-6
13	175	11.9	1110	4	US-09-564-595D-6
14	137.2	9.3	1472	4	US-09-540-224-3
15	137.2	9.3	1472	4	US-09-564-595D-52
16	125.6	8.5	1910	4	US-09-457-066-36
17	123.2	8.4	1882	4	US-09-540-224-1
18	123.2	8.4	1882	4	US-09-564-595D-1
19	123.2	8.4	1882	4	US-09-706-968-36
20	45	3.1	7218	1	US-08-232-463-14
21	38.4	2.6	1836	4	US-09-328-352-1536
22	36.2	2.5	900	4	US-09-370-976-1
23	36.2	2.5	1806	4	US-09-351-229-3
24	35.6	2.4	2828	4	US-09-016-434-1458
25	35.6	2.4	2980	4	US-09-266-225D-11
26	35.4	2.4	1428	4	US-09-252-991A-9266
27	35.4	2.4	1545	4	US-09-252-991A-9274

c 28	35.4	2.4	1977	4	US-09-252-991A-9290	Sequence 9290, Ap
c 29	35.4	2.4	2539	4	US-09-620-312D-454	Sequence 454, App
c 30	34.4	2.3	828	4	US-09-252-991A-181	Sequence 181, App
c 31	34.4	2.3	1560	4	US-09-252-991A-166	Sequence 166, App
c 32	34.4	2.3	1686	4	US-09-252-991A-155	Sequence 155, App
c 33	34.4	2.3	1803	4	US-09-252-991A-170	Sequence 170, App
c 34	34.4	2.3	2610	4	US-09-252-991A-175	Sequence 175, App
c 35	34.2	2.3	77536	4	US-09-410-551B-1	Sequence 1, Appli
c 36	34	2.3	501	4	US-09-252-991A-1347	Sequence 1347, Ap
c 37	34	2.3	582	4	US-09-252-991A-1257	Sequence 1257, Ap
c 38	34	2.3	1370	3	US-09-111-470-9	Sequence 9, Appli
c 39	34	2.3	1458	3	US-09-111-470-3	Sequence 3, Appli
c 40	33.6	2.3	40	4	US-09-040-220D-4	Sequence 4, Appli
c 41	33.6	2.3	40	4	US-09-265-686-4	Sequence 4, Appli
c 42	33.6	2.3	531	4	US-09-704-139-3	Sequence 3, Appli
c 43	33.6	2.3	1390	4	US-09-704-139-1	Sequence 1, Appli
c 44	33.6	2.3	1424	1	US-08-403-634-3	Sequence 3, Appli
c 45	33.6	2.3	1424	3	US-08-913-441B-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1  
US-09-564-595D-34  
; Sequence 34, Application US/09564595D  
; Patent No. 6495668  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4  
; FILE REFERENCE: 99-19  
; CURRENT APPLICATION NUMBER: US/09/564,595D  
; PRIOR FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: US 09/304,216  
; PRIOR FILING DATE: 1999-05-03  
; PRIOR APPLICATION NUMBER: US 60/164,463  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: US 60/180,169  
; PRIOR FILING DATE: 2000-02-04  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 34  
; LENGTH: 3571  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1049)...(2086)  
US-09-564-595D-34

Query Match	98.0%;	Score 1444.8;	DB 4;	Length 3571;
Best Local Similarity	99.4%;	Pred. No. 0;		
Matches 1460;	Conservative	0;	Mismatches	8;
			Indels	1;
			Gaps	1;
Qy	2	ACCTGGAGACACAGAGAGGCTCTAGGAAAATTTTGGATGGGATTTATGGAACTA	61	
Db	856	AACCTGGAGACACAGAGAGGCTCTAGGAAAATTTTGGATGGGATTTATGGAACTA	915	
Qy	62	CCCTGCGATTCTTGTGTCGACAGCCGGCCAGGCGCTTCCACCGCAGCGACCTTTCCC	121	
Db	916	CCCTGCGATTCTTGTGTCGACAGCCGGCCAGGCGCTTCCACCGCAGCGACCTTTCCC	975	
Qy	122	CGGGCTGGGCTGAGCCTTGGAGTGTGCTTCCCGAGTCCCGCGGAGTGAGCCCTCG	181	
Db	976	C-GGCTGGGCTGAGCCTTGGAGTGTGCTTCCCGAGTCCCGCGGAGTGAGCCCTCG	1034	
Qy	182	CCCAGTTCAGCAAAATGCTCTCTCGGCTCTCTCTGTCGATCTGACATCTGCGCCGCCGCC	241	
Db	1035	CCCAGTTCAGCAAAATGCTCTCTCGGCTCTCTCTGTCGATCTGACATCTGCGCCGCCGCC	1094	
Qy	242	AAAGACGGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTCAGCTCTCCAGCGACA	301	

Db 1095 AAAGACGGGACTCGGGCTAGTCCAACTGAGCAGCAAGTTGCAGCTCTCCAGCGACA 1154  
Qy 302 AGGAACAGAACGGAGTCAAGATCCCGGATGAGAGAGTTGTCACTATATCTCTGTAATG 361  
Db 1155 AGGAACAGAACGGAGTCAAGATCCCGGATGAGAGAGTTGTCACTATATCTCTGTAATG 1214  
Qy 362 GGAGCATCCACAGCCGAAAGTTCTCATACGTACCCAAAGAAATATGGTGTGGTGA 421  
Db 1215 GGAGCATCCACAGCCGAAAGTTCTCATACGTACCCAAAGAAATATGGTGTGGTGA 1274  
Qy 422 GATTAGTTCAGTAGATGAATAATGTGGGATCCAGCTGACATTTGATGAGAGATTGGGC 481  
Db 1275 GATTAGTTCAGTAGATGAATAATGTGGGATCCAGCTGACATTTGATGAGAGATTGGGC 1334  
Qy 482 TGGAGATCCAGAAAGACATATATGCAAGTAGTATTTTGTAGAAGTTGAGGAGCCAGTG 541  
Db 1335 TGGAGATCCAGAAAGACATATATGCAAGTAGTATTTTGTAGAAGTTGAGGAGCCAGTG 1394  
Qy 542 ATGAAAGTGTTTTAGGACGCTGGTGTGGTCTGGGACTGTGCCAGGAAAGCAGACTTCTA 601  
Db 1395 ATGAAAGTGTTTTAGGACGCTGGTGTGGTCTGGGACTGTGCCAGGAAAGCAGACTTCTA 1454  
Qy 602 AAGGAATCATATCAGATAGATTGTATCTGATGAGTATTTTCCATCTGAACCCGGAT 661  
Db 1455 AAGGAATCATATCAGATAGATTGTATCTGATGAGTATTTTCCATCTGAACCCGGAT 1514  
Qy 662 TCTGCATCCACTACAGTATTATATGCAAGTACAGAAACACAGAGTCTCTCGGTGT 721  
Db 1515 TCTGCATCCACTACAGTATTATATGCAAGTACAGAAACACAGAGTCTCTCGGTGT 1574  
Qy 722 TGCCCCCTTCATCTTGTGATGACCTGCTCAACATGCTGTGACTGCTTCAGTACCT 781  
Db 1575 TGCCCCCTTCATCTTGTGATGACCTGCTCAACATGCTGTGACTGCTTCAGTACCT 1634  
Qy 782 TGGAGAGCTGATTCGGTACCTAGAGCAGATCGATGGCAGTGGACTTGGACAGCTCT 841  
Db 1635 TGGAGAGCTGATTCGGTACCTAGAGCAGATCGATGGCAGTGGACTTGGACAGCTCT 1694  
Qy 842 ACAAGCCAACTGACGCTTTTGGGCAAGGCTTCTGTATGGGAAAAAGCAAGTGG 901  
Db 1695 ACAAGCCAACTGACGCTTTTGGGCAAGGCTTCTGTATGGGAAAAAGCAAGTGG 1754  
Qy 902 TGATCTGAATCTCTCAAGAAAGGTAAACTCTACAGCTGCACACCCCGGAACTTCT 961  
Db 1755 TGAATCTGAATCTCTCAAGAAAGGTAAACTCTACAGCTGCACACCCCGGAACTTCT 1814  
Qy 962 CAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACCATATCTGGCCAGTTGTCTCC 1021  
Db 1815 CAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACCATATCTGGCCAGTTGTCTCC 1874  
Qy 1022 TGGTCAAGCGCTGGAGGAAATTTGCTGCTTGTCTCCATAATGCAATGAATGTCAGT 1081  
Db 1875 TGGTCAAGCGCTGGAGGAAATTTGCTGCTTGTCTCCATAATGCAATGAATGTCAGT 1934  
Qy 1082 GTGTCCACGTAAGTTACAAAAGTACCAATGAGTCCCTCAGTTCAGACCAAAACTG 1141  
Db 1935 GTGTCCACGTAAGTTACAAAAGTACCAATGAGTCCCTCAGTTCAGACCAAAACTG 1994  
Qy 1142 GAGTCAAGGATTCATAGTCACTCACTGATGTGGCTCTGGAAACACACGAGGAATGTG 1201  
Db 1995 GAGTCAAGGATTCATAGTCACTCACTGATGTGGCTCTGGAAACACACGAGGAATGTG 2054  
Qy 1202 ACTGTGTGTAGAGGAAACGACAGAGGTAATCTGACGCTTCGTAGCAGCACAGTGAG 1261  
Db 2055 ACTGTGTGTAGAGGAAACGACAGAGGTAATCTGACGCTTCGTAGCAGCACAGTGAG 2114  
Qy 1262 CACTGGCATTTCTGTATCCCCCAACAGCACTTCATCCCCACAGGTTGGCCGAGGG 1321  
Db 2115 CACTGGCATTTCTGTATCCCCCAACAGCACTTCATCCCCACAGGTTGGCCGAGGG 2174  
Qy 1322 CTCTCAGCTGTGATGCTGGCTATGGTAAAGATCTTACTGTCTCCAAACCAAAATTTCTCAG 1381

Db 2175 CTCTCAGCTGTGATGCTGGCTATGGTAAAGATCTTACTCTCTCCAAACCAAAATTTCTCAG 2234  
Qy 1382 TTGTTTGTCTTCAATAGCTTCCCTCTCAGGACTTCAAGTGTCTTCTTAAAGACCCAGAGGC 1441  
Db 2235 TTGTTTGTCTTCAATAGCTTCCCTCTCAGGACTTCAAGTGTCTTCTTAAAGACCCAGAGGC 2294  
Qy 1442 ACCAANAGGAGTCAATCACAAGCACTGC 1470  
Db 2295 ACCAAGAGGAGTCAATCACAAGCACTGC 2323  
RESULT 2  
US-09-706-968-42  
; Sequence 42, Application US/09706968  
; Patent No. 6528050  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60C1  
; CURRENT APPLICATION NUMBER: US/09/706,968  
; CURRENT FILING DATE: 2000-11-06  
; PRIOR APPLICATION NUMBER: US/09/541,752  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 42  
; LENGTH: 3571  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1049) ... (2086)  
US-09-706-968-42  
Query Match 98.0%; Score 1444.8; DB 4; Length 3571;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 1460; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  
Qy 2 ACCTGGAGACACAGAGAGGCTCTAGGAAAAATTTTGGATGGGATATATGTGAAACTA 61  
Db 856 AACTGGAGACACAGAGAGGCTCTAGGAAAAATTTTGGATGGGATATATGTGAAACTA 915  
Qy 62 CCCTGCCATTCTCTGCTGCCAGAGCCGGCCAGGGCTTCCACCGCAGCGAGCCTTTCCC 121  
Db 916 CCCTGCCATTCTCTGCTGCCAGAGCCGGCCAGGGCTTCCACCGCAGCGAGCCTTTCCC 975  
Qy 122 CGGGCTGGGCTGAGCCTTGGAGTGGTGGTCTTCCAGTGGCCGCGGAGTGAGCCCTCG 181  
Db 976 C-GGCTGGGCTGAGCCTTGGAGTGGTGGTCTTCCAGTGGCCGCGGAGTGAGCCCTCG 1034  
Qy 182 CCCAGTCAAGCAAAATGCTCCTCTCGGCTCTCTCTGCTGACATCTGCTCCCTGGCCGCC 241  
Db 1035 CCCAGTCAAGCAAAATGCTCCTCTCGGCTCTCTCTGCTGACATCTGCTCCCTGGCCGCC 1094  
Qy 242 AAGAACCGGAGCTCGGGCTGAGTCCAACTGAGCAGCAAGTTGACGCTCTCCAGCGACA 301  
Db 1095 AAGAACCGGAGCTCGGGCTGAGTCCAACTGAGCAGCAAGTTGACGCTCTCCAGCGACA 1154  
Qy 302 AGGAACAGAACGGAGTCAAGATCCCGGATGAGAGAGTTGTCACTATATCTCTGTAATG 361  
Db 1155 AGGAACAGAACGGAGTCAAGATCCCGGATGAGAGAGTTGTCACTATATCTCTGTAATG 1214  
Qy 362 GGAGCATCCACAGCCGAAAGTTCTCATACGTACCCAAAGAAATATGGTGTGGTGA 421  
Db 1215 GGAGCATCCACAGCCGAAAGTTCTCATACGTACCCAAAGAAATATGGTGTGGTGA 1274  
Qy 422 GATTAGTTCAGTAGATGAATAATGTGGGATCCAGCTGACATTTGATGAGAGATTGGGC 481



1275 GATTAGTTCAGTAGTGAATGTGGGATCCAGTGCATTTGATGAGATTTGGC 1334  
482 TGAAGATCCAGAGCAGATATATGCAAGTATGTTGTAGAGTTGAGAGCCAGTG 541  
1335 TGAAGATCCAGAGCAGATATATGCAAGTATGTTGTAGAGTTGAGAGCCAGTG 1394  
542 ATGGAAGTGTGTTTGAAGCCTGGTGGTCTCGGAGCTGTCAGGAAAGCAGACTTCTA 601  
1395 ATGGAAGTGTGTTTGAAGCCTGGTGGTCTCGGAGCTGTCAGGAAAGCAGACTTCTA 1454  
602 AAGGAATCATATCAGGATPAAGATTGTATCTGATGAGTATTTTCATCTGAACCCGAT 661  
1455 AAGGAATCATATCAGGATPAAGATTGTATCTGATGAGTATTTTCATCTGAACCCGAT 1514  
662 TGTGATCAGTACAGTATATCAGGATGATGATGATGATGATGATGATGATGATGATGAT 721  
1515 TGTGATCAGTACAGTATATCAGGATGATGATGATGATGATGATGATGATGATGATGAT 1574  
722 TGTGATCAGTACAGTATATCAGGATGATGATGATGATGATGATGATGATGATGATGAT 781  
1575 TGTGATCAGTACAGTATATCAGGATGATGATGATGATGATGATGATGATGATGATGAT 1634  
782 TGAAGAGCTGATTCGGTACCTAGAGCCAGATGATGATGATGATGATGATGATGATGATGAT 841  
1635 TGAAGAGCTGATTCGGTACCTAGAGCCAGATGATGATGATGATGATGATGATGATGATGAT 1694  
842 ACAGGCAACATGCGAGCTTTTGGGCAAGCTTCTGATGATGATGATGATGATGATGATGATGAT 901  
1695 ACAAGCAACATGCGAGCTTTTGGGCAAGCTTCTGATGATGATGATGATGATGATGATGATGAT 1754  
902 TGAATCTGAATCTCTCAAGGAAGAGGTAAATCTACAGCTGCACACCCCGAATCTCT 961  
1755 TGAATCTGAATCTCTCAAGGAAGAGGTAAATCTACAGCTGCACACCCCGAATCTCT 1814  
962 CAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACCATATTTCTGGCCAGGTTGCTCC 1021  
1815 CAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACCATATTTCTGGCCAGGTTGCTCC 1874  
1022 TGTCAAGCGCTGTGGAGGAAATTTGTGCTGTTGTCTCCATAATTTGCAATGATGTCAGT 1081  
1875 TGTCAAGCGCTGTGGAGGAAATTTGTGCTGTTGTCTCCATAATTTGCAATGATGTCAGT 1934  
1082 GTGTCCACAGTAAAGTTACAAAAGAGTACCAGTACAGTCTTTCAGTTGAGACCAAAACTG 1141  
1935 GTGTCCACAGTAAAGTTACAAAAGAGTACCAGTACAGTCTTTCAGTTGAGACCAAAACTG 1994  
1142 GAGTCAAGGATTTGATTAAGTCACTGATGATGATGATGATGATGATGATGATGATGATGAT 1201  
1995 GAGTCAAGGATTTGATTAAGTCACTGATGATGATGATGATGATGATGATGATGATGATGAT 2054  
1202 ACTGTGTGTAGAGGAAACGAGAGGTAATCTGACGCTTCTGATGATGATGATGATGATGATGAT 1261  
2055 ACTGTGTGTAGAGGAAACGAGAGGTAATCTGACGCTTCTGATGATGATGATGATGATGATGAT 2114  
1262 CACTGGCAATCTGTGTACCCCAACAGCAACTTTCATCCCAACAGCGTGGCCGAGG 1321  
2115 CACTGGCAATCTGTGTACCCCAACAGCAACTTTCATCCCAACAGCGTGGCCGAGG 2174  
1322 CTCTCAGTGTGATGCTGGTATGTTAAAGATCTTACTGCTCTCCAAACCAAAATCTCAG 1381  
2175 CTCTCAGTGTGATGCTGGTATGTTAAAGATCTTACTGCTCTCCAAACCAAAATCTCAG 2234  
1382 TTGTTTCTTCAATAGCCTTCCCTGCGAGGACTTCAAGTGTCTTCTAAAGACCAAGGC 1441  
2235 TTGTTTCTTCAATAGCCTTCCCTGCGAGGACTTCAAGTGTCTTCTAAAGACCAAGGC 2294  
1442 ACCAANAGGAGTCAATCAAAAGCACTGC 1470  
2295 ACCAANAGGAGTCAATCAAAAGCACTGC 2323

US-09-457-066-42  
; Sequence 42, Application US/09457066  
; Patent No. 6432673  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60  
; CURRENT APPLICATION NUMBER: US/09/457,066  
; CURRENT FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 42  
; LENGTH: 3571  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1049)...(2086)  
US-09-457-066-42  
Query Match 97.2%; Score 1432.8; DB 4; Length 3573;  
Best Local Similarity 99.3%; Pred. No. 0;  
Matches 1460; Conservative 0; Mismatches 8; Indels 3; Gaps 2;  
QY 2 ACTGAGACACAGAGAGGGCTCTAGGAAATTTTGGATGGGATATGTGAAACTA 61  
DB 856 AACTGAGACACAGAGAGGGCTCTAGGAAATTTTGGATGGGATATGTGAAACTA 915  
QY 62 CCCTGCGATTCTCTGTCGACAGCGGCCGAGCGCTTCCACCGCAGCGAGCCTTTCCC 121  
DB 916 CCCTGCGATTCTCTGTCGACAGCGGCCGAGCGCTTCCACCGCAGCGAGCCTTTCCC 975  
QY 122 CGGCTGGGCTGAGCCTTGAGTGTGCTTCCCACTGCGCCGCGGAGTGAGCCCTCG 181  
DB 976 C-GCTGGGCTGAGCCTTGAGTGTGCTTCCCACTGCGCCGCGGAGTGAGCCCTCG 1034  
QY 182 CCCAGTCAGCCAAAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCTGCGCCGCC 241  
DB 1035 CCCAGTCAGCCAAAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCTGCGCCGCC 1094  
QY 242 AAAGAACGGGAGCTCGGGCTGAGTCCAACTGACAGCAAGTTCAGCTCTCCAGCGACA 301  
DB 1095 AAAGAACGGGAGCTCGGGCTGAGTCCAACTGACAGCAAGTTCAGCTCTCCAGCGACA 1154  
QY 302 AGGAACAGAGCGGAGTCCAAAGATCCCGGCATGAGAGTGTGCTATATCTGTTATG 361  
DB 1155 AGGAACAGAGCGGAGTCCAAAGATCCCGGCATGAGAGTGTGCTATATCTGTTATG 1214  
QY 362 GGAGCATCCAGCGCCGAGTTCCTCATAGTACCCAGAAATATGCTGCTGTTGCGA 421  
DB 1215 GGAGCATCCAGCGCCGAGTTCCTCATAGTACCCAGAAATATGCTGCTGTTGCGA 1274  
QY 422 GATTAGTTGAGTATGATAATGTCGGATCCAGCTGACATTTTCATGAGAGATTTGGGC 481  
DB 1275 GATTAGTTGAGTATGATAATGTCGGATCCAGCTGACATTTTCATGAGAGATTTGGGC 1334  
QY 482 TGAAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAGTGTGAGAGCCAGTG 541  
DB 1335 TGAAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAGTGTGAGAGCCAGTG 1394  
QY 542 ATGGAAGTGTGTTTGAAGAGCTGTTGCTGGAGTGTGCTGGAGGAAAGCAGACTTCTA 601  
DB 1395 ATGGAAGTGTGTTTGAAGAGCTGTTGCTGGAGTGTGCTGGAGGAAAGCAGACTTCTA 1454  
QY 602 AAGGAATCATATCAGGATPAAGATTGTATCTGATGAGTATTTTCCATCTCAACCCGAT 661  
DB 1455 AAGGAATCATATCAGGATPAAGATTGTATCTGATGAGTATTTTCCATCTCAACCCGAT 1514



662 TCTGATCCACTACAGTATTATCATGCCACAAGTCACAGAACACAGAGTCCTTCGGTGT 721  
1515 TCTGATCCACTACAGTATTATCATGCCACAAGTCACAGAACACAGAGTCCTTCGGTGT 1574  
722 TGCCCCCTTCATCTTTGTTCATTTGGACCTGCTCAACAAATGCTGTGACTGCTTCAGTACCT 781  
1575 TGCCCCCTTCATCTTTGTTCATTTGGACCTGCTCAACAAATGCTGTGACTGCTTCAGTACCT 1634  
782 TGAAGAGAGTATTCCGGTACCTAGAGCCAGATTCGATGGCAGGTGGACTTGGACGCTCT 841  
1635 TGAAGAGAGTATTCCGGTACCTAGAGCCAGATTCGATGGCAGGTGGACTTGGACGCTCT 1694  
842 ACAAGCCAACTAGGAGCTTTTGGCAAGCTTTTGGCAAGCTTTTGGCAAGCTTTTGGCAAGCTTT 901  
1695 ACAAGCCAACTAGGAGCTTTTGGCAAGCTTTTGGCAAGCTTTTGGCAAGCTTTTGGCAAGCTTT 1754  
902 TGAATCTGAATCTCTCAAGGAAGAGTAAACTCTACAGCTGCACACCCCGAACTCT 961  
1755 TGAATCTGAATCTCTCAAGGAAGAGTAAACTCTACAGCTGCACACCCCGAACTCT 1814  
962 CAGTGTCCATACGGGAAGAGCTAAAGAGACAGATACATATTTCTGGCCAGGTTGTCTCC 1021  
1815 CAGTGTCCATACGGGAAGAGCTAAAGAGACAGATACATATTTCTGGCCAGGTTGTCTCC 1874  
1022 TGGTCAAGCGCTGTGGAGGAATTTGTCCTGTTGCTCCATAATTTGCAATGAATGTCACT 1081  
1875 TGGTCAAGCGCTGTGGAGGAATTTGTCCTGTTGCTCCATAATTTGCAATGAATGTCACT 1934  
1082 GTGTCCACGCTAAAGTTACAAAAGTACCATGAGTCTCTTCAAGTTGAGACCAAAAAGT 1141  
1935 GTGTCCACGCTAAAGTTACAAAAGTACCATGAGTCTCTTCAAGTTGAGACCAAAAAGT 1994  
1142 GAGTCAAGGATTCATAGTACTCACTGATGTGCTCTGAGAGCTCTTCAAGTTGAGACCAAAAAGT 1201  
1995 GAGTCAAGGATTCATAGTACTCACTGATGTGCTCTGAGAGCTCTTCAAGTTGAGACCAAAAAGT 2054  
1202 ACTGTGTGTAGAGGAAGAGGAGGTTAACTGAGAGCTCTTCAAGTTGAGACCAAAAAGT 1261  
2055 ACTGTGTGTAGAGGAAGAGGAGGTTAACTGAGAGCTCTTCAAGTTGAGACCAAAAAGT 2114  
1262 CACTGCAATCTGTGTACCCCC--ACAAGCAACCTTCATCCCCACAGCGTTGGCCGAG 1319  
2115 CACTGCAATCTGTGTACCCCC--ACAAGCAACCTTCATCCCCACAGCGTTGGCCGAG 2174  
1320 GGCCTCAGCTGTGATGTGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1379  
2175 GGCCTCAGCTGTGATGTGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2234  
1380 AGTTGTTTGTCTCAATAGCTTCTCCCTGCAGGACTTCAAGTGTCTTCTTAAAGACCAAG 1439  
2235 AGTTGTTTGTCTCAATAGCTTCTCCCTGCAGGACTTCAAGTGTCTTCTTAAAGACCAAG 2294  
1440 GCACCAAGGAGTCAATCAAGCACTGC 1470  
2295 GCACCAAGGAGTCAATCAAGCACTGC 2325

## RESULT 4

US-09-040-220D-1  
; Sequence 1, Application US/09040220D  
; Patent No. 6391311  
; GENERAL INFORMATION:  
; APPLICANT: Kuo, Sophia S.  
; TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR  
; TITLE OF INVENTION: ENDOTHELIAL CELL GROWTH FACTOR AND BONE MORPHOGENETIC  
; TITLE OF INVENTION: PROTEIN 1 AND NUCLEIC ACIDS ENCODING SAME, THEIR USES,  
; TITLE OF INVENTION: AND PROCESSES FOR THEIR PRODUCTION  
; FILE REFERENCE: P1122  
; CURRENT APPLICATION NUMBER: US/09/040,220D  
; CURRENT FILING DATE: 1998-03-17  
; NUMBER OF SEQ ID NOS: 8

; SEQ ID NO 1  
; LENGTH: 2825  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: Human  
; LOCATION: 2689  
; OTHER INFORMATION: N is A, T, C or G  
US-09-040-220D-1

Query Match 62.0%; Score 914.2; DB 4; Length 2825;  
Best Local Similarity 83.5%; Pred. No. 1.2e-270;  
Matches 1050; Conservative 0; Mismatches 203; Indels 4; Gaps 1;  
QY 2 ACCTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATCGGGATTATGTGGAACTA 61  
DB 61 AACTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTATGTGGAACTA 120  
QY 62 CCCTCGATTCTCTGCTGCCAGAGCGCGCCAGCGCTTCCACCGCAGCGCAGCTTTTCCC 121  
DB 121 CCCTCGATTCTCTGCTGCCAGAGCGCGCTCGCGCTTCCACCGCAGCTTCCGCC 180  
QY 122 CGG---GCTGGGCTGAGCCTTGGAGTGTCTGCTTCCCGAGTCCCGCGCGAGTGAGCC 177  
DB 181 TGGCGGTGGTGAAGAGACTCGGGAGTGTCTGCTTCCAAAGTCCCGCGCTGAGTGAGCT 240  
QY 178 CTGCCCCAGTCAGCCAAATGCTCTCTCGGCCCTCTCTGCTGACATCTGCCCCCTGGCC 237  
DB 241 CTCACCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCTGCTGACATCTGCCCCCTGGCC 300  
QY 238 GGCCAAAGAAACGGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGAGCTCTCCAGC 297  
DB 301 GGCCAGAGACAGGGGACTCAGCGGAATCCAACTGAGTAGTAAATTCAGATTTTCCAGC 360  
QY 298 GACAGAAACAGAACGAGTGCAGATCCCGGCATGAGAGATTGCTACTATATCTGGT 357  
DB 361 AAACAGGAAACAGAACGAGTGCAGATCCCGGCATGAGAGATTATTAATCTGTGTCTACT 420  
QY 358 AATGGAGCATCCACAGCCGGAAGTTTCTCTACGTACCTACCCAGAAATATGGTGGTG 417  
DB 421 AATGGAAGTATTCACAGCCCAAGTTTCTCTATCTATNTTCAAGAAATACGGTCTGGTA 480  
QY 418 TGAGATTATGTGCTAGTGAATAATGTCGGATCCAGCTGACATTTGATGAGAGATT 477  
DB 481 TGGAGATTATGAGCTAGAGGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 540  
QY 478 GGGCTGGAAGATCCAGAGACGATATATGCAAGTATGATTTGTAGAGTTGAGAGCCC 537  
DB 541 GGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTGTAGAGTTGAGAGACC 600  
QY 538 AGTGTAGGAAGTGTTTTAGACGCTGTGTGGTCTCTGGGACTGTGCCAGGAAAGCAGACT 597  
DB 601 AGTGTAGGAATATATATAGGGCTGTGTGGTCTCTGGTACTGTATCCAGGAAACAGATT 660  
QY 598 TCTAAAGGAAATCATATCAGGATTAAGATTGTATCTGATGAGTATTTTCCATCTGAACCC 657  
DB 661 TCTAAAGGAAATCAAATTTAGGATTAAGATTGTATCTGATGATTTTCTTCTGAACCA 720  
QY 658 GGATTTCTGATCCACTACAGTATTATATGCCCAAGTACAGAAACCAAGCTCTCTCG 717  
DB 721 GGGTCTGATCCACTACCAATTTGTATGCCCAATTTCAAGAGCTGTGTGCTCTCA 780  
QY 718 GTGTGCCCTCTCACTTTTGTCTATTTGGACCTGCTCAACAACTGCTGTGACTGCTTCAGT 777  
DB 781 GTGCTACCCCTTCAGCTTTGCACTGGACCTGCTTAAATGCTATATACTGCTTTAGT 840  
QY 778 ACCTTGAAGAGCTGATTCGGTACCTAGAGCCAGATTCGATGGCAGGTGGAGCTTGAAGC 837  
DB 841 ACCTTGAAGAGCTTATTCGATATCTTGAACACAGAGATGGCAGTTGGAGCTTAGAGAT 900  
QY 838 CTCTACAGCCAACTGGAGCTTTTGGGCAAGGCTTCTCTGTATGGGAAAGAAAGCAAA 897  
DB 901 CTATATAGGCCAACTTGGCAAGCTTCTTGGCAAGGCTTTTGTGTTTGGAGAAATCCAGA 960

QY 898 GTGGTGAATCTGAATCTCTCAAGAGAGAGGTAAACTCTACAGCTGCACACCCCGGAAC 957  
Db |||||  
QY 961 GTGGTGAATCTGAACCTTCTAAACAGAGAGGTAGATATACAGCTGCACACCTCGTAAC 1020  
Db |||||  
QY 958 TTCTCAGTGTCCATACCGGAGAGCTAAAGAGGACAGATACCATATCTTGGCCAGGTTGT 1017  
Db |||||  
QY 1021 TTCTCAGTGTCCATACCGGAGAGCTAAAGAGAGACCGATACCATATCTTGGCCAGGTTGT 1080  
Db |||||  
QY 1018 CTCCTGTCTCAAGCCCTGTGGAGGAATGTGCGCTGTGTCTCTCCATATTTGCAATGAATGT 1077  
Db |||||  
QY 1081 CTCCTGTCTCAAGCCCTGTGGAGGAATGTGCGCTGTGTCTCTCCATATTTGCAATGAATGT 1140  
Db |||||  
QY 1078 CAGTGTGTCCACAGCTAAAGTTTACAAAAGATACCATGAGGTCTTCAAGTTCAGAGCCAAA 1137  
Db |||||  
QY 1141 CAATGTGTCCACAGCTAAAGTTTACAAAAGATACCATGAGGTCTTCAAGTTCAGAGCCAAA 1200  
Db |||||  
QY 1138 ACTGGAGTCAAGGATTCATTAAGTCACTCACTGATGAGGTCTTGGAAACACACAGAGAA 1197  
Db |||||  
QY 1201 ACCGGTGTGAGGGATTCACAAATCACTCACCGAGTGGCCCTGGAGCACCATGAGGAG 1260  
Db |||||  
QY 1198 TGTGACTGTGTGTGAGAGGAACGACGAGGAGTAACTGACGAGCTTCTGTAGCAGCAC 1254  
Db |||||  
QY 1261 TGTGACTGTGTGTGAGAGGAGGACACAGAGGATAGCCGCATCACCAACGAGGCTC 1317  
Db |||||

## RESULT 5

US-09-265-686-1  
; Sequence 1, Application US/09265686  
; Patent No. 6455283  
; GENERAL INFORMATION:  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Kuo, Sophia S.  
; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1  
; FILE REFERENCE: P1122P2  
; CURRENT APPLICATION NUMBER: US/09/265,686  
; CURRENT FILING DATE: 1999-03-10  
; PRIOR APPLICATION NUMBER: US 09/040,220  
; PRIOR FILING DATE: 1998-03-17  
; PRIOR APPLICATION NUMBER: US 09/184,216  
; PRIOR FILING DATE: 1998-11-02  
; NUMBER OF SEQ ID NOS: 8  
; SEQ ID NO 1  
; LENGTH: 2825  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: Unknown  
; LOCATION: 2689  
; OTHER INFORMATION: Any nucleotide  
US-09-265-686-1

Query Match 62.0%; Score 914.2; DB 4; Length 2825;  
Best Local Similarity 83.5%; Pred. No. 1.2e-270;  
Matches 1050; Conservative 0; Mismatches 203; Indels 4; Gaps 1;  
QY 2 ACCTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATATGTGGAAACTA 61  
Db |||||  
QY 61 AACTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATATGTGGAAACTA 120  
Db |||||  
QY 62 CCCTCGATTTCTCTGTGTCAGAGCGGCGCACGCGCTTCCACGACGAGCGCTTTTCCC 121  
Db |||||  
QY 121 CCCTCGATTTCTCTGTGTCAGAGCGGCTCGCGCTTCCACGAGTGCAGCTTTCCC 180  
Db |||||  
QY 122 CGG----GCTGGGCTGAGCTTGGAGTGTCTGCTTCCCGAGTGGCGCGCGAGTGAGCC 177  
Db |||||  
QY 181 TGGCGGTGGTGAAGAGACTCGGGAGTCTGCTTCCAAAAGTGCCCGCGTGAAGTGA 240  
Db |||||  
QY 178 CTCGCGCCAGTCAGCCAAATGTCTCTCGGCTCTCTGCTGACATCTGCTCTGGCC 237  
Db |||||  
QY 241 CTCACCCAGTCAGCCAAATGAGCCCTCTTGGGCTCTCTGCTGACATCTGCTCTGGCC 300  
Db |||||  
QY 238 GGCCAAAGAACGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGAGCTCTCCAGC 297  
Db |||||

## RESULT 6

US-09-564-595D-32  
; Sequence 32, Application US/09564595D  
; Patent No. 6495668  
; GENERAL INFORMATION:

Db |||||  
QY 301 GGCCAGAGACAGGGGACTCAGGCGGAATCCAACCTAGTAGTAATTCAGTTTCCAGC 360  
QY 298 GACAAGGAACAGAACGGAGTCCAAGATCCCCCGCATGAGAGAGTTGTCACTATATCTGT 357  
Db |||||  
QY 361 AACAGGAACAGAACGGAGTCCAAGATCCCCCGCATGAGAGAGTTATTTACTGTGTCTACT 420  
Db |||||  
QY 358 AATGGGAGCATCCAAGCGGAGTTTCTCATAGTACCAAGAAATATGGTGTCTGGTG 417  
Db |||||  
QY 421 AATGGAGTATTTCAAGCGGAGTTTCTCATATCTTATCCAAGAAATACGGTCTTGSTA 480  
QY 418 TGGAGATTAGTTGCAATAGATGAAGATGCGGATCCAGCTGACATTTGATGAGAGATTT 477  
Db |||||  
QY 481 TGGAGATTAGTAGCAGTAGAGGAAATGTATGGATACAACTTACGTTTGTATGAAGATTT 540  
Db |||||  
QY 478 GGGCTTGGAGATCCAGAGAGCATATATGCAAGTATGATTTTGTAGAAAGTTGAGGAGCC 537  
Db |||||  
QY 541 GGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTTGTAGAGTTGAGGAGCC 600  
QY 538 AGTGAATGAAGTGTATTTAGGACGCTGTGGTCTCTGGAGCTGTGCCAGGAAAGAGACT 597  
Db |||||  
QY 601 AGTGAATGAAGTATATATTAGGCGCTGTGGTCTCTGGTACTGTACCAAGAAACAGATT 660  
QY 598 TCTAAAGAAATCATATCAGGATAGATTTGTATCTGATGAGTATTTTCCATCTGAACCC 657  
Db |||||  
QY 661 TCTAAAGAAATCAAAATTAGGATAGATTTGTATCTGATGAATATTTTCTTCTGAACCA 720  
QY 658 GGATTTCTGCATCCACTCAGATATTTATCATGCCCACAAAGTCAAGAAACACGAGTCTCTCG 717  
Db |||||  
QY 721 GGGTCTGCTCATCCACTCAACATTTGTCATGCCAATTTCAAGAGCTGTGAGTCTCTTCA 780  
QY 718 GTGTTGCCCTTCACTTTTGTGATGACCTGTCTCAACATGCTGTGATGCTGCTTCACT 777  
Db |||||  
QY 781 GTGCTACCCCTTCACTTTTGTGCTGACCTGTCTTAAATGCTATTAATGCTTCTTCTT 840  
QY 778 ACCTTGGAGAGCTGATTTGGTACTTAGAGCCAGATCGATGCGAGTGTGACTTGGACAGC 837  
Db |||||  
QY 841 ACCTTGGAGAGCTTATTTGATATCTTGAACAGAGAGATGCGAGTGTGACTTGAAGAT 900  
QY 838 CTCTCAAGCCCAACATGCGAGCTTTTGGCAAGGCTTCTCTGTATGGGAAAAAAGCAAA 897  
Db |||||  
QY 901 CTATATAGCCCAACTTGGCACTTCTTGGCAAGGCTTTTGTGTTTGGAGAAATCCAGA 960  
QY 898 GTGTTGAATCTGAATCTCTCTCAAGGAAGAGTAAACTCTACAGCTGCAACCCCGGAC 957  
Db |||||  
QY 961 GTGGTGGATCTGAACCTTCTAAGAGAGGAGTAAAGTATATACAGCTGCAACCTCTGTAAC 1020  
QY 958 TTCTCAGTGTCCATACGGGAGAGCTTAAGAGGACAGATACCATATTTCTGGCCAGGTTGT 1017  
Db |||||  
QY 1021 TTCTCAGTGTCCATTAAGGAGAGAACTTAAGAGAACCGATACCATTTTCTGGCCAGGTTGT 1080  
QY 1018 CTCCTGGTCAAGCGCTGTGGAGGAAATGTGCTGTGTCTCCATAATTTGCAATGAATGT 1077  
Db |||||  
QY 1081 CTCCTGGTAAACGCTGTGGTGGAACTGTGCTGTGTCTCCCAATTTGCAATGAATGT 1140  
QY 1078 CAGTGTGTCCCAGTAAAGTTTACAAAAGTACCAGTGTGCTTCAAGTGTGAGACCAAA 1137  
Db |||||  
QY 1141 CAATGTGTCCCAGCAAGTTACTTAAATAATACCAGAGGTCTTCAAGTGTGAGACCAAG 1200  
QY 1138 ACTGAGTCAAGGATTCATAGTCACTCACTGATGCTGTGCTGTGAGAACACCAAGGAA 1197  
Db |||||  
QY 1201 ACCGGTGTGAGGGATTCACAAATCACTCACCGAGTGGCCCTGGAGCACCATGAGGAG 1260  
QY 1198 TGTGACTGTGTGTGAGAGGAAACGAGGAGGTAACTGACGCTTCTGTAGCAGCAC 1254  
Db |||||  
QY 1261 TGTGACTGTGTGTGAGAGGAGGACAGAGGATAGCCGCATCACCAACGAGGCTC 1317  
Db |||||

```
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 1760
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (154)...(1191)
US-09-564-595D-32

Query Match      59.6%; Score 878.8; DB 4; Length 1760;
Best Local Similarity 83.4%; Pred. No. 6.9e-260;
Matches 1011; Conservative 0; Mismatches 197; Indels 4; Gaps 1;

QY 47 ATTATGTGGAACTACCTCGGATCTCTGCTGCGGAGTCTGGAGTCTGCTTCCCGAGTCCC 106
Db 1 ATTATGTGGAACTACCTCGGATCTCTGCTGCGGAGTCTGGAGTCTGCTTCCCGAGTCCC 60
QY 107 AGCGCAGCCTTTCCTCCGG---GCTGGGCTGAGCCTTGGAGTCTGCTTCCCGAGTCCC 162
Db 61 AGTGACGCTTCCCTCGGGTGGTGAAGAGACTCGGGAGTCTGCTTCCCGAGTCCC 120
QY 163 CGCGCGAGTGAAGCCTCGCCCGAGTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 222
Db 121 CGCGCGAGTGAAGCCTCGCCCGAGTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 223 ACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 282
Db 181 ACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 283 TTGCACTCTTCAGCGGCAAGGAAACAGACGAGTCAAGATCCCGCGGATCAGAGAGT 342
Db 241 TTCCAGTCTTCAGCAACAGGAAACAGACGAGTCAAGATCCCGCGGATCAGAGAGT 300
QY 343 GTCATATATCTGTTAATGGAGATCCACGCCGAGTTCCTCATAGTACCGCAAGA 402
Db 301 ATTACTGTCTCTACTAATGGAAGTATTCACGCCCAAGGTTTCTCATATCTATCAAGA 360
QY 403 AATATGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 462
Db 361 AATAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 463 TTTGATGAGATTTGGCTGGAAGATCCAGAGACGATATATGCAAGTATGATTTGTA 522
Db 421 TTTGATGAAAGATTTGGGCTTCAAGACCCAGAGATGACATATGCAAGTATGATTTGTA 480
QY 523 GAAGTTGAGGACCCAGTGAAGTATTTAGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 582
Db 481 GAAGTTGAGGACCCAGTGAAGTATTTAGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 583 CCAGGAAGACGACTTCTAAGGAATCATATCAGATGAAGATTTGATCTCATGATAT 642
Db 541 CCAGGAAGACGACTTCTAAGGAATCATATCAGATGAAGATTTGATCTCATGATAT 600
QY 643 TTTCCATCTGAACCCGAGTTTGCATCCACTACAGTATTTATCATGCCCAAGTACAGAA 702
Db 601 TTTCCATCTGAACCCGAGTTTGCATCCACTACAGTATTTATCATGCCCAAGTACAGAA 660
QY 703 ACCAGAGTCTTCGGTGTGCCCCCTTCATCTTTGTCATTTGGACCTGCTCAACATGCT 762
```

## RESULT 7

US-09-706-968-1

; Sequence 1, Application US/09706968

; Patent No. 6528050

; GENERAL INFORMATION:

; APPLICANT: Gao, Zeren

; APPLICANT: Hart, Charles E.

; APPLICANT: Sheppard, Paul O.

; APPLICANT: Shoemaker, Kimberly E.

; APPLICANT: Gilbertson, Debra G.

; APPLICANT: West, James W.

; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3

; FILE REFERENCE: 98-60CI

; CURRENT APPLICATION NUMBER: US/09/706,968

; CURRENT FILING DATE: 2000-11-06

; PRIOR APPLICATION NUMBER: US/09/541,752

; PRIOR FILING DATE: 2000-03-31

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 1760

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (154)...(1191)

US-09-706-968-1

Query Match

Best Local Similarity 59.6%; Score 878.8; DB 4; Length 1760;

Matches 1011; Conservative 0; Mismatches 197; Indels 4; Gaps 1;

```
QY 47 ATTATGTGAAACTACCTCGCATCTCTGTGCGAGAGCCGGCAGGCGCTTCCACCGC 106
Db 1 ATTATGTGAAACTACCTCGCATCTCTGTGCGAGAGCCGGCAGGCGCTTCCACCGC 60
QY 107 AGCGCAGCCTTCCCGG----GCTGGGCTGAGCCTTGAGTCGTCGCTTCCCGAGTGC 162
Db 61 AGTGCAGCCTTCCCGTGGCGTGGTAAAGAGACTCGGGAGTCGCTGCTTCCAAAGTGC 120
QY 163 CGCCGAGTGAAGCCTCGCCCGAGTCAGCCAAATGCTCCTCCTCGGCTCCTCTGCTG 222
Db 121 CGCGGTGAGTGAAGCTCACCCCGAGTCAGCCAAATGAGCCTTCTCGGCTTCTCCTGCTG 180
QY 223 ACATCTGCCCTGGCGGCCAAAGACGGGACTCGGCTGAGTCGAACTGAGCAGCAG 282
Db 181 ACATCTGCCCTGGCGGCCAGAGACGGGACTCGAGCGGAATCCAACTGAGTAGTAA 240
QY 283 TTGCAGCTCTCAGCGCAAGAAACAGAACGAGTGAAGATCCCGGCTCAGAGAGTT 342
Db 241 TTCCAGTTTTCAGCAACAGAGAACAGAACGAGTGAAGATCCAGATGAGAGATT 300
QY 343 GTCACTATATCTGTAATGGGAGCATCCACGCCGGAAGTTTCTCATACGTACCCAGA 402
Db 301 ATTACTGTGCTACTTAATGGAGTATTCACGCCCAAGTTTCTCATACTTATCCAGA 360
QY 403 AATATGGTCTGGTGGAGATTAGTTGAGTAGATAAAATGTGCGGATCCAGCTGACA 462
Db 361 AATACGGTCTTGGTATGAGATTAGTAGCAGTAGAGGAAATGTATGGATCAACTTAC 420
QY 463 TTTGATGAGAGATTGGGCTGGAAGATCCAGAACGATATATGCAAGTATGATTTGTA 522
Db 421 TTTGATGAAAGATTGGGCTTGAAGCCAGAGATGACATATGCAAGTATGATTTGTA 480
QY 523 GAAGTTGAGGACCCAGTGAAGTGTATTAGGACGCTGTGTGGTCTCGGACTGTG 582
Db 481 GAAAGTTGAGAACCCAGTGAAGTATATATTAGGCGCTGTGTGGTCTCGTACTGTA 540
QY 583 CCAGAAAGCAGACTTCTAAAGGAATCATATCAGATGAAGTTTGTATCTGATGATAT 642
Db 541 CCAGAAACAGATTCTTAAGGAATCAATATGAGTAAAGTTTGTATCTGATGAATAT 600
QY 643 TTTTCATCTGAACCCGAGTTCTGTCACTACAGTATTATATGCAAGTATCAAGAA 702
Db 601 TTTCTCTGACACAGGTTCTGTCACTACAGTATTATGCAAGTATCAAGAA 660
QY 703 ACCAGAGTCTTCCGCTGTGCCCCCTTCATCTTTGTCAATGGAAGTCTCAACAATGT 762
Db 661 GCTGTGAGTCTTCAAGTGTACCCCTTCAAGTGTGCAAGTCTGCAAGTCTGATTAATGT 720
QY 763 GTGACTGCTTCAAGTGTGCAAGTGTATTCGTAAGTGTGCAAGTGTGCAAGTGTG 822
Db 721 ATAACTGCTTGTAGTGTGCAAGTGTATTCGTAAGTGTGCAAGTGTGCAAGTGTG 780
QY 823 GTGACTGCTTCAAGTGTGCAAGTGTATTCGTAAGTGTGCAAGTGTGCAAGTGTG 882
Db 781 TTGGACTTGAAGTGTATATAGGCAACTTGTGCAAGTGTGCAAGTGTGCAAGTGTG 840
QY 883 GGGAAAAAGCAAGTGTGATCTGAATCTCTCAAGGAAAGAGTAAATCTTACAGC 942
Db 841 GGAAGAAAAATCAGAGTGTGATCTGAACCTTCTAAAGAGAGTGAAGTAAATATACAG 900
QY 943 TGCAACCCCGGAACTTCTCAGTGTCCATACGGAAGAGCTTAAAGAGGACAGATACCATA 1002
Db 901 TGCAACCTCTGTAATCTTCTCAGTGTCCATACGGAAGAGCTTAAAGAGGACAGATACCATA 960
QY 1003 TTTGCGCCAGGTTGTCTCTGCTCAAGCCTGTGGAGGAAATTTGTGCTGTTGTCTCCAT 1062
Db 961 TTTGCGCCAGGTTGTCTCTGCTTAAACGCTGTGTGGGAACTGTGCTGTTGTCTCCAC 1020
QY 1063 AATTGCAATGAATGTGCTGTCCCAAGTAAAGTTAAGTTAAGTTAAGTTAAGTTAAGTT 1122
Db 1021 AATTGCAATGAATGTGCTGTCCCAAGTAAAGTTAAGTTAAGTTAAGTTAAGTTAAGTT 1080
QY 1123 CAGTTGAGACCAAAACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1182
```

```
Db 1081 CAGTTGAGACCAAAAGACCGGTGTGAGGGGATTGCAAAATCACTCACCGAGTGGCCCTG 1140
QY 1183 GAACACCAAGAGAAATGTGCTGTGTAGAGGAAACGAGAGGGGTAACTGAGCCT 1242
Db 1141 GAGCACCATGAGAGTGTGCTGTGTGTCAGAGGGAGCACAGGAGATAGCCGCATCAC 1200
QY 1243 TCGTAGCAGCAC 1254
Db 1201 CACCAGCAGCTC 1212

RESULT 8
US-09-457-066-1
; Sequence 1, Application US/09457066
; Patent No. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1760
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (154)...(1191)
US-09-457-066-1

Query Match 59.6%; Score 878.8; DB 4; Length 1764;
Best Local Similarity 83.4%; Pred. No. 6.9e-260;
Matches 1011; Conservative 0; Mismatches 197; Indels 4; Gaps 1;

QY 47 ATTATGTGAAACTACCTCGCATCTCTGTGCGAGAGCCGGCAGGCGCTTCCACCGC 106
Db 1 ATTATGTGAAACTACCTCGCATCTCTGTGCGAGAGCCGGCAGGCGCTTCCACCGC 60
QY 107 AGCGCAGCCTTCCCGG----GCTGGGCTGAGCCTTGAGTCGTCGCTTCCCGAGTGC 162
Db 61 AGTGCAGCCTTCCCGTGGCGTGGTAAAGAGACTCGGGAGTGCCTTCCAAAGTGC 120
QY 163 CGCCGAGTGAAGCCTCGCCCGAGTCAGCCAAATGCTCCTCCTCGGCTCCTCTGCTG 222
Db 121 CGCGGTGAGTGAAGCTCACCCCGAGTCAGCCAAATGAGCCTTCTCGGCTTCTCCTGCTG 180
QY 223 ACATCTGCCCTGGCGGCCAAAGACGGGACTCGGCTGAGTGAAGTGAAGTGAAGTGAAG 282
Db 181 ACATCTGCCCTGGCGGCCAGAGACGGGACTCGAGCGGAATCCAACTGAGTAGTAA 240
QY 283 TTGCAGCTCTCAGCGCAAGAAACAGAACGAGTGAAGATCCCGGCTCAGAGAGTT 342
Db 241 TTCCAGTTTTCAGCAACAGAGAACAGAACGAGTGAAGATCCAGATGAGAGATT 300
QY 343 GTCACTATATCTGTAATGGGAGCATCCACGCCGGAAGTTTCTCATACGTACCCAGA 402
Db 301 ATTACTGTGCTACTTAATGGAGTATTCACGCCCAAGTTTCTCATACTTATCCAGA 360
QY 403 AATATGGTCTGGTGGAGATTAGTTGAGTAGATAAAATGTGCGGATCCAGCTGACA 462
Db 361 AATACGGTCTTGGTATGAGATTAGTAGCAGTAGAGGAAATGTATGGATCAACTTAC 420
QY 463 TTTGATGAGAGATTGGGCTGGAAGATCCAGAACGATATATGCAAGTATGATTTGTA 522
```













```

; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1472
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (93)...(1205)
; US-09-540-224-3

Query Match          9.3%; Score 137.2; DB 4; Length 1472;
Best Local Similarity 52.5%; Pred. No. 6.7e-32;
Matches 496; Conservative 0; Mismatches 373; Indels 75; Gaps 6;

QY 356 GTAATGGGAGATCCACAGCCCGAAGTTTCTCATAGTACCCAGAAATATGGTCTGG 415
Db 271 GCAATGGCCATGTGCAGATCTCTCCGAAACAGCTACCCAGGAACCTCTCTGA 330
QY 416 TGTGGAGATTAGTTCAGTAGATGAAATGTGCGGATCCAGCTGACATTTGATGAGAT 475
Db 331 CATGTGGCTCGTTC---CCAGGAGAAAACACGGATACAACTGTCTTGGACATCAAT 387
QY 476 TTGGCTGGAGATCCAGAGACGATATATGCAAGTATGATTTGTAGAGTTGAGGAGC 535
Db 388 TCGGACTAGAGAGACGAGAAATGACATTTGTAGTATGACTTTGTGGAAGTTGAAGA 447
QY 536 CCAGTGTAGTGAAG-----TGTTTATGAGACGCTGTGTGGTTCTGGGACTGTGCCAG 589
Db 448 TCTCAGAGAGCAGACTGTGTGCAGAGGAGATGTGTGGCCACAGGAGATCCCTCCAA 507
QY 590 AGCAGACTCTTAAAGGAAATCATATCAGGATAAGATTTGTATCTGATGAGTATTTCCAT 649
Db 508 GGATAACGTCAAGAACAAACAGATTAATAATCAATTTAAGTCTGATGACTACTTTGTGG 567
QY 650 CTGACCCCGGATTCGCTATCCACTACATATAT-----CATGCCACAGTCA 697
Db 568 CAAACCTCGGATTAAGATTTATTATTCATTTGTGGAAAGATTTCCAAACCGAAGCAGCT 627
QY 698 CAGAACCCAGCAGTCTTCGGTGTGGCCCTTTCATCTTTGTTCATTTGTTCATTTGACCTG 750
Db 628 CAGAGACCACTGGGAATCAGTCAAGACTCTTTCTCTGGGTGTCTTATCCTCTCCAT 687
QY 751 -----CTCAACAAATGCTGTGACTGCGCTTCAGTA 778
Db 688 CAATAACGGACCCCACTCTCACTGCTGATGCCCTGGACAAAACCTGTGCAGAAATTCGATA 747
QY 779 CCTTGGAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGGATTCGACAGCC 838
Db 748 CCGTGGAGATCTACTTAAGCACTTCAATCAGTGTCTTGGCAGATGATCTGGAAT 807
QY 839 TCTCAAGCCCAACATGCGAGCTTTTGGGAGGCTTTCCCTGTATGGGAAAAAAGCAAAG 898
Db 808 TGTATCTGGACACCCCTCATTTATAGAGCGAGGTATACCATGATCGGAAGTCCA----- 861
QY 899 TGGTGAATCTGAATCTCTCAAGGAGAGGTAAACTCTACAGTGCACACCCCGAAT 958
Db 862 AAGTGGACCTTGGACAGGCTCAATGATGATCAAGCGTTTACAGTTGCACCTCCAGGAATC 921
QY 959 TCTCAGTGTCCATACGGGAAGAGCTTAAAGAGGACAGATACATATTTCTGGCCAGGTGTGC 1018
Db 922 ACTCTGTGAACCTCAGGGAGAGCTGAAGCTGACCAATGACATCTTCTCCAGATGCC 981
QY 1019 TCCTGGTCAAGCGCTGTGGAGAAATTTGTGCTGTTCTTCCATATTAATGCAATGAATGC 1078
Db 982 TCCTCGTGCAGCGTGTGGTGGCAACTGTGTTGGGAACTGTCAACTGGAAGTCTCTGCA 1041

; US-09-564-595D-52
; Sequence 52, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 1472
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (93)...(1205)
; US-09-564-595D-52

Query Match          9.3%; Score 137.2; DB 4; Length 1472;
Best Local Similarity 52.5%; Pred. No. 6.7e-32;
Matches 496; Conservative 0; Mismatches 373; Indels 75; Gaps 6;

QY 356 GTAATGGGAGATCCACAGCCCGAAGTTTCTCATAGTACCCAGAAATATGGTCTGG 415
Db 271 GCAATGGCCATGTGCAGAGTCTCTCCGAAACAGCTACCCAGGAACCTCTCTGA 330
QY 416 TGTGGAGATTAGTTCAGTAGATGAAATGTGCGGATCCAGCTGACATTTGATGAGAT 475
Db 331 CATGTGGCTCGTTC---CCAGGAGAAAACACGGATACAACTGTCTTGGACATCAAT 387
QY 476 TTGGCTGGAGATCCAGAGACGATATATGCAAGTATGATTTGTAGAGTTGAGGAGC 535
Db 388 TCGGACTAGAGAGACGAGAAATGACATTTGTAGTATGACTTTGTGGAAGTTGAAGA 447
QY 536 CCAGTGTAGTGAAG-----TGTTTATGAGACGCTGTGTGGTTCTGGGACTGTGCCAG 589
Db 448 TCTCAGAGAGCAGACTGTGTGCAGAGGAGATGTGTGGCCACAGGAGATCCCTCCAA 507
QY 590 AGCAGACTCTTAAAGGAAATCATATCAGGATAAGATTTGTATCTGATGAGTATTTCCAT 649
Db 508 GGATAACGTCAAGAACAAACAGATTAATAATCAATTTAAGTCTGATGACTACTTTGTGG 567
QY 650 CTGACCCCGGATTCGCTATCCACTACATATAT-----CATGCCACAGTCA 697
Db 568 CAAACCTCGGATTAAGATTTATTATTCATTTGTGGAAAGATTTCCAAACCGAAGCAGCT 627
QY 698 CAGAACCCAGCAGTCTTCGGTGTGGCCCTTTCATCTTTGTTCATTTGTTCATTTGACCTG 750
Db 628 CAGAGACCACTGGGAATCAGTCAAGACTCTTTCTCTGGGTGTCTTATCCTCTCCAT 687
QY 751 -----CTCAACAAATGCTGTGACTGCGCTTCAGTA 778
Db 688 CAATAACGGACCCCACTCTCACTGCTGATGCCCTGGACAAAACCTGTGCAGAAATTCGATA 747
QY 779 CCTTGGAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGGATTCGACAGCC 838
Db 748 CCGTGGAGATCTACTTAAGCACTTCAATCAGTGTCTTGGCAGATGATCTGGAAT 807
QY 839 TCTCAAGCCCAACATGCGAGCTTTTGGGAGGCTTTCCCTGTATGGGAAAAAAGCAAAG 898
Db 808 TGTATCTGGACACCCCTCATTTATAGAGCGAGGTATACCATGATCGGAAGTCCA----- 861
QY 899 TGGTGAATCTGAATCTCTCAAGGAGAGGTAAACTCTACAGTGCACACCCCGAAT 958
Db 862 AAGTGGACCTTGGACAGGCTCAATGATGATCAAGCGTTTACAGTTGCACCTCCAGGAATC 921
QY 959 TCTCAGTGTCCATACGGGAAGAGCTTAAAGAGGACAGATACATATTTCTGGCCAGGTGTGC 1018
Db 922 ACTCTGTGAACCTCAGGGAGAGCTGAAGCTGACCAATGACATCTTCTCCAGATGCC 981
QY 1019 TCCTGGTCAAGCGCTGTGGAGAAATTTGTGCTGTTCTTCCATATTAATGCAATGAATGC 1078
Db 982 TCCTCGTGCAGCGTGTGGTGGCAACTGTGTTGGGAACTGTCAACTGGAAGTCTCTGCA 1041
```

QY 751 -----CTCAACAATGCTGTGACTGCCTTCAGTA 778  
Db CAATAACGGACCCCACTCTACTGCTGATGCCCTGGACAAACTGTGCGAATTCGATA 747  
QY 779 CCTTGGAAAGAGCTGATTCCGTACCTTAGAGCCAGATCGATGGCAGGTGGACTTGGACAGCC 838  
Db CCGTGGAAAGATCTACTTAAGCACCTTCAATCCAGTGTCTTGGCAAGATGATCTGGAGAATT 807  
QY 839 TCTACAAGCCCAACATGGCAGCTTTTGGGCAAGGCTTCTGTATGGGAAAAAAGCAAG 898  
Db TGTATCTGGACACCCCTCATTTATAGAGCGAGGTCAACCATGATCGGAAGTCCA----- 861  
QY 899 TGGTGAATCTGNAATCTCTCAAGGAAGAGGTAATAACTCTACAGCTGCACACCCCGAACT 958  
Db AAGTGGACCTGGACAGGCTCAATGATGATGTCAAGCGTTACAGTTGCACTCCAGGAATC 921  
QY 959 TCTCAGTGTCCATACGGGAAGAGCTTAAAGAGGACAGATACCATATTTCTGGCCAGGTTGTC 1018  
Db ACTCTGTGAACCTCAGGGAGGAGCTGAAGCTGACCAATGCAGTCTTCTTCCCAOGATGCC 981  
QY 1019 TCCTGGTCAAGCGCTGTGGAGGAAATTTGGCCTGTGTCTCCATTAATTGCAATGAATGTC 1078  
Db TCCTCGTGCAGCGCTGTGGTGGCAACTGTGTGTGGCAACTGTCAACTGGAAGTCTCTGCA 1041  
QY 1079 AGTGTGTCCCAAGTAAAGTTACAAAAAGTACCATGAGGTCTTTCAGTTTGAGACC----- 1133  
Db CATGCAGCTCAGGGAAGACAGTGAAGAGTATCATGAGGATTTGAAGTTGAGCCTGGAC 1101  
QY 1134 -----AAAAACTGGAGTCAAGGATTGCATAAGTCACTCACTGATGTGGCTCTGGAAACCC 1189  
Db ATTTCAAGAGAAGGGGCAAGCTAAGAAATATGGCTCTTGTGTATATCCAGCTGGATCATC 1161  
QY 1190 ACGAGGAATGTGACTGTGTGTGTAGAGGAAACGCAGGAGGGTAA 1233  
Db ATGAGCGATGTGACTGTATCTCAGCTCAAGACCACCTCGATAA 1205

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 26, 2003, 03:42:52 ; Search time 362.884 Seconds  
(without alignments)  
13382.717 Million cell updates/sec

Title: US-09-852-209A-6

Perfect score: 1474

Sequence: 1 cacttgagacagaagag.....aatcacaagcactgcaccg 1474

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2190069 seqs, 1647345023 residues

Total number of hits satisfying chosen parameters: 4380138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.\*

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/FCR\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*  
13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*  
14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*  
15: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*  
16: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
17: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1473	99.9	1474	10	US-09-852-209A-6
2	1473	99.9	1474	14	US-10-131-600-6
3	1444.8	98.0	3571	9	US-09-823-033-3
4	1444.8	98.0	3571	13	US-10-139-583-42
5	1444.8	98.0	3571	14	US-10-264-361-3
6	914.2	62.0	2825	14	US-10-178-442-1
7	914.2	62.0	2839	11	US-09-796-753-5
8	914.2	62.0	2849	10	US-09-978-295A-487
9	914.2	62.0	2849	10	US-09-978-697-487
10	914.2	62.0	2849	10	US-09-978-132A-487
11	914.2	62.0	2849	10	US-09-999-832A-487
12	914.2	62.0	2849	11	US-09-978-189-487
13	914.2	62.0	2849	11	US-09-978-608A-487
14	914.2	62.0	2849	11	US-09-978-585A-487
15	914.2	62.0	2849	11	US-09-978-191A-487
16	914.2	62.0	2849	11	US-09-978-403A-487

17 914.2 62.0 2849 11 US-09-978-564A-487 Sequence 487, App  
18 914.2 62.0 2849 11 US-09-999-833A-487 Sequence 487, App  
19 914.2 62.0 2849 11 US-09-981-915A-487 Sequence 487, App  
20 914.2 62.0 2849 11 US-09-978-824-487 Sequence 487, App  
21 914.2 62.0 2849 11 US-09-918-585A-487 Sequence 487, App  
22 914.2 62.0 2849 11 US-09-978-423A-487 Sequence 487, App  
23 914.2 62.0 2849 11 US-09-978-193A-487 Sequence 487, App  
24 914.2 62.0 2849 11 US-09-999-830A-487 Sequence 487, App  
25 914.2 62.0 2849 11 US-09-978-757B-487 Sequence 487, App  
26 914.2 62.0 2849 11 US-09-978-187B-487 Sequence 487, App  
27 914.2 62.0 2849 11 US-09-978-643A-487 Sequence 487, App  
28 914.2 62.0 2849 12 US-09-978-375A-487 Sequence 487, App  
29 914.2 62.0 2849 12 US-09-978-188A-487 Sequence 487, App  
30 914.2 62.0 2849 12 US-09-978-298A-487 Sequence 285, App  
31 914.2 62.0 2849 12 US-10-137-870-285 Sequence 285, App  
32 914.2 62.0 2849 12 US-10-140-018-285 Sequence 285, App  
33 914.2 62.0 2849 12 US-10-140-021-285 Sequence 285, App  
34 914.2 62.0 2849 12 US-10-140-274-285 Sequence 285, App  
35 914.2 62.0 2849 12 US-10-140-471-285 Sequence 285, App  
36 914.2 62.0 2849 12 US-10-140-807-285 Sequence 285, App  
37 914.2 62.0 2849 12 US-10-140-922-285 Sequence 285, App  
38 914.2 62.0 2849 12 US-10-140-924-285 Sequence 285, App  
39 914.2 62.0 2849 12 US-10-140-926-285 Sequence 285, App  
40 914.2 62.0 2849 12 US-10-141-702-285 Sequence 285, App  
41 914.2 62.0 2849 12 US-10-141-704-285 Sequence 285, App  
42 914.2 62.0 2849 12 US-10-142-421-285 Sequence 285, App  
43 914.2 62.0 2849 12 US-10-142-432-285 Sequence 285, App  
44 914.2 62.0 2849 12 US-10-142-432-285 Sequence 285, App  
45 914.2 62.0 2849 12 US-10-142-767-285 Sequence 285, App

#### ALIGNMENTS

#### RESULT 1

US-09-852-209A-6  
; Sequence 6, Application US/09852209A  
; Patent No. US20020164687A1  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: RASE, Karin  
; APPLICANT: LEE, Xuri  
; APPLICANT: PONTEN, Annica  
; APPLICANT: UUTELA, Marko  
; APPLICANT: ALITALO, Kari  
; APPLICANT: OESTMAN, Arne  
; APPLICANT: HELDIN, Carl-Henrik  
; APPLICANT: BETHSOLTZ, Christer  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C,  
; FILE REFERENCE: THEREFOR, AND USES THEREOF  
; CURRENT APPLICATION NUMBER: US/09/852,209A  
; CURRENT FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: 09/410,349  
; PRIOR FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: 60/110,749  
; PRIOR FILING DATE: 1998-12-03  
; PRIOR APPLICATION NUMBER: 60/113,002  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 60/135,426  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: 60/144,022  
; PRIOR FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 1474  
; TYPE: DNA  
; ORGANISM: Murinae gen. sp.  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1447)  
; OTHER INFORMATION: can be a, c, g or t

DNA CODING

US-09-852-209A-6

Query Match 99.9%; Score 1473; DB 10; Length 1474; Best Local Similarity 100.0%; Pred. No. 0; Matches 1474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	CACCTGGAGACACAGAGAGGCTCTAGGAAAAATTTTGGATGGGATATGTGAAACT	60						
Db	1	CACCTGGAGACACAGAGAGGCTCTAGGAAAAATTTTGGATGGGATATGTGAAACT	60						
Qy	61	ACCTTGGATTCCTGCTGCAGAGCCGCCAGGCGCTTCCACCGCAGCGAGCTTTCC	120						
Db	61	ACCTTGGATTCCTGCTGTCAGAGCCGCCAGGCGCTTCCACCGCAGCGAGCTTTCC	120						
Qy	121	CGGGCTGGGCTGAGCCCTTGGAGTCGTCTGCTTCCCCAGTCCCGCGCGAGTGAGCCCTC	180						
Db	121	CGGGCTGGGCTGAGCCCTTGGAGTCGTCTGCTTCCCCAGTCCCGCGCGAGTGAGCCCTC	180						
Qy	181	GCCCGAGTCAGCCAAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCCCTGGCGGC	240						
Db	181	GCCCGAGTCAGCCAAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCCCTGGCGGC	240						
Qy	241	CAAGAACGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCGAGCTCTCCAGCGAC	300						
Db	241	CAAGAACGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCGAGCTCTCCAGCGAC	300						
Qy	301	AAGGAACAGAACGGAGTGCAGATCCCGGCATGAGAGAGTTGTCACTATCTGTAAT	360						
Db	301	AAGGAACAGAACGGAGTGCAGATCCCGGCATGAGAGAGTTGTCACTATCTGTAAT	360						
Qy	361	GGGAGCATCCAGCGCCGAGTTTCTCATAGTACCCAGAAATATGCTGTGTGG	420						
Db	361	GGGAGCATCCAGCGCCGAGTTTCTCATAGTACCCAGAAATATGCTGTGTGG	420						
Qy	421	AGATTAGTTGCAGTAGATGAAATGTGCGGATCCAGCTGACATTTGATGAGAGTTTGGG	480						
Db	421	AGATTAGTTGCAGTAGATGAAATGTGCGGATCCAGCTGACATTTGATGAGAGTTTGGG	480						
Qy	481	CTGGAAGATCCAGAAACGATATATGCAAGTATGATTTTGTAGAGTTGAGAGCCCACT	540						
Db	481	CTGGAAGATCCAGAAACGATATATGCAAGTATGATTTTGTAGAGTTGAGAGCCCACT	540						
Qy	541	GATGGAAGTGTTTTGGACGCTGGTGTCTGGGACTGTGCCAGGAAGCAGACTTCT	600						
Db	541	GATGGAAGTGTTTTGGACGCTGGTGTCTGGGACTGTGCCAGGAAGCAGACTTCT	600						
Qy	601	AAAGGAATCATATCAGGATAAGATTTGTATCTGATGAGTATTTTCCATCTGAACCCGGA	660						
Db	601	AAAGGAATCATATCAGGATAAGATTTGTATCTGATGAGTATTTTCCATCTGAACCCGGA	660						
Qy	661	TTCTGCATCCACTACAGTATATCATGCCACAGTCAAGAAACCAAGAGTCTTGGTG	720						
Db	661	TTCTGCATCCACTACAGTATATCATGCCACAGTCAAGAAACCAAGAGTCTTGGTG	720						
Qy	721	TTGCCCTTCTATCTTGTGATGGACCTGTCTCAACAAATGCTGTGACTGCCCTCAGTACC	780						
Db	721	TTGCCCTTCTATCTTGTGATGGACCTGTCTCAACAAATGCTGTGACTGCCCTCAGTACC	780						
Qy	781	TTGGAAGAGCTGATTCGGTACTAGAGCAGATCGATGGCAGGTGGACTTGGAAGCCTC	840						
Db	781	TTGGAAGAGCTGATTCGGTACTAGAGCAGATCGATGGCAGGTGGACTTGGAAGCCTC	840						
Qy	841	TACAAGCCAACTGCGAGCTTTTGGCAAGGCTTTCTGTATGGAAAAAAGCAAGTG	900						
Db	841	TACAAGCCAACTGCGAGCTTTTGGCAAGGCTTTCTGTATGGAAAAAAGCAAGTG	900						
Qy	901	GTGAATCTGAATCTCTCAAGGAAGAGGTAAAACTTACAGCTGCACACCCCGGAACTTC	960						
Db	901	GTGAATCTGAATCTCTCAAGGAAGAGGTAAAACTTCTACAGCTGCACACCCCGGAACTTC	960						
Qy	961	TCAGTGTCCATACGGGAAGAGCTTAAAGAGGACAGATACCATATTTCTGGCCAGGTTGTCTC	1020						
Db	961	TCAGTGTCCATACGGGAAGAGCTTAAAGAGGACAGATACCATATTTCTGGCCAGGTTGTCTC	1020						

RESULT 2

US-10-131-600-6  
; Sequence 6, Application US/10131600  
; Publication No. US20030082670A1  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: AASE, Karin  
; APPLICANT: LEE, Xuri  
; APPLICANT: PONTEN, Amica  
; APPLICANT: UTELA, Marko  
; APPLICANT: ALITALO, Kari  
; APPLICANT: OESTMAN, Arne  
; APPLICANT: HELDIN, Carl-Henrik  
; APPLICANT: BETHOLITZ, Christer  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING  
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740  
; CURRENT APPLICATION NUMBER: US/10131,600  
; CURRENT FILING DATE: 2002-04-25  
; PRIOR APPLICATION NUMBER: US/09/410,349  
; PRIOR FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: 60/108,109  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: 60/110,749  
; PRIOR FILING DATE: 1998-12-03  
; PRIOR APPLICATION NUMBER: 60/113,002  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 60/135,426  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: 60/144,022  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 1474  
; TYPE: DNA  
; ORGANISM: Murinae gen. sp.  
; FEATURE:  
; NAME/KEY: unsure

```
; LOCATION: (1447)
; OTHER INFORMATION: can be a, c, g or t
US-10-131-600-6

Query Match          99.9%; Score 1473; DB 14; Length 1474;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACCTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGAAACT 60
Db 1 CACCTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGAAACT 60

QY 61 ACCCTGCGATCTCTGCTGTCAGAGCCGCGCAGCGCTTCCACCGCAGCGAGCCTTTC 120
Db 61 ACCCTGCGATCTCTGCTGTCAGAGCCGCGCAGCGCTTCCACCGCAGCGAGCCTTTC 120

QY 121 CCGGGCTGGGCTGAGCCTTGGAGTCTGCTTCCCGAGTGCCTTCCCGAGTGCAGCCCTC 180
Db 121 CCGGGCTGGGCTGAGCCTTGGAGTCTGCTTCCCGAGTGCCTTCCCGAGTGCAGCCCTC 180

QY 181 GCGCCAGTACGCAAAATGCTCTCTCGGCTCTCTCTGCTGCAATCTGCCCTGGCCGGC 240
Db 181 GCGCCAGTACGCAAAATGCTCTCTCGGCTCTCTCTGCTGCAATCTGCCCTGGCCGGC 240

QY 241 CAAAGAACGGGACTCGGGCTGAGTCCCACTGAGCAGCAAGTTCAGCTATCTGGTAAT 300
Db 241 CAAAGAACGGGACTCGGGCTGAGTCCCACTGAGCAGCAAGTTCAGCTATCTGGTAAT 300

QY 301 AAGGAAACAGAACGGAGTGCAGATCCCGGATGAGAGAGTTCATCTATCTGGTAAT 360
Db 301 AAGGAAACAGAACGGAGTGCAGATCCCGGATGAGAGAGTTCATCTATCTGGTAAT 360

QY 361 GGGAGCATCCACAGCCCGAATTTCTCTACGTAACGTAACCAAGAAATATGGTGGTGG 420
Db 361 GGGAGCATCCACAGCCCGAATTTCTCTACGTAACGTAACCAAGAAATATGGTGGTGG 420

QY 421 AGATTAGTTCAGTAGATGAATATGCGGATCCAGTCCAGTCCAGTTCAGTATGAGAGTTGG 480
Db 421 AGATTAGTTCAGTAGATGAATATGCGGATCCAGTCCAGTTCAGTATGAGAGTTGG 480

QY 481 CTGGAAGATCCAGAACGATATATGCAAGTATGATTTCTGAGAGTTGAGGAGCCAGT 540
Db 481 CTGGAAGATCCAGAACGATATATGCAAGTATGATTTCTGAGAGTTGAGGAGCCAGT 540

QY 541 GATGGAAGTCTTTAGAACGCTGGTGGTCTGCGGACTGTCGAGAAAGCAGACTTCT 600
Db 541 GATGGAAGTCTTTAGAACGCTGGTGGTCTGCGGACTGTCGAGAAAGCAGACTTCT 600

QY 601 AAAGGAAATCATATCAGATAAGATTTGTATCTGATGAGTATTTTCCATCTGACCCGGA 660
Db 601 AAAGGAAATCATATCAGATAAGATTTGTATCTGATGAGTATTTTCCATCTGACCCGGA 660

QY 661 TTCTGATCCTACATAGTATTTATCATGCCCAAGTCAAGAACCCAGAGTCTCTTCGGTG 720
Db 661 TTCTGATCCTACATAGTATTTATCATGCCCAAGTCAAGAACCCAGAGTCTCTTCGGTG 720

QY 721 TTGCGCCCTTCATCTTTGCTATGGAAGTCTGCTCAAGTCTGATGAGTCTTCAAGTACC 780
Db 721 TTGCGCCCTTCATCTTTGCTATGGAAGTCTGCTCAAGTCTGATGAGTCTTCAAGTACC 780

QY 781 TTGGAAGAGCTGATTCGGTACCTAGAGCCAGATGCGAGTGGAGTGGACAGCCTC 840
Db 781 TTGGAAGAGCTGATTCGGTACCTAGAGCCAGATGCGAGTGGAGTGGACAGCCTC 840

QY 841 TACAAGCAACATGGCAGCTTTTGGCAAGCTTTTCTGTATGGAAAAAAGCAAGTG 900
Db 841 TACAAGCAACATGGCAGCTTTTGGCAAGCTTTTCTGTATGGAAAAAAGCAAGTG 900

QY 901 GTGAATCTGAATCTCTCAAGGAGAGGTAAACTCTACAGCTGCAACCCCGAACTTC 960
Db 901 GTGAATCTGAATCTCTCAAGGAGAGGTAAACTCTACAGCTGCAACCCCGAACTTC 960

QY 961 TCAGTGTCCATACGGGAAGAGCTAAAGAGACAGATACCATATTTCTGGCCAGGTTGCTC 1020
Db 961 TCAGTGTCCATACGGGAAGAGCTAAAGAGACAGATACCATATTTCTGGCCAGGTTGCTC 1020

QY 1021 CTGCTCAAGCGCTGCTGGAGAAATTTGCTGTTGCTTCCATAATTTGCAATGTAATGTCAG 1080
Db 1021 CTGCTCAAGCGCTGCTGGAGAAATTTGCTGTTGCTTCCATAATTTGCAATGTAATGTCAG 1080

QY 1081 TGTGTCCCAAGTAAAGTTTACAAAAAGTACCATGAGTCTTCAAGTTGAGACCAAAACT 1140
Db 1081 TGTGTCCCAAGTAAAGTTTACAAAAAGTACCATGAGTCTTCAAGTTGAGACCAAAACT 1140

QY 1141 GGAGTCAAGGATTCATTAAGTCACTCACTGATGCTCTGGAACACCCAGAGGAATGT 1200
Db 1141 GGAGTCAAGGATTCATTAAGTCACTCACTGATGCTCTGGAACACCCAGAGGAATGT 1200

QY 1201 GACTGTGTGTAGAGAAACGAGGAGGTAACCTGAGCTTCTGAGCAGCACACGCTGA 1260
Db 1201 GACTGTGTGTAGAGAAACGAGGAGGTAACCTGAGCTTCTGAGCAGCACACGCTGA 1260

QY 1261 GCACTGCAATTCCTGATGCTGCTATGTAAGATCTTACTCTCCAAACCAAAATTTCTCA 1380
Db 1261 GCACTGCAATTCCTGATGCTGCTATGTAAGATCTTACTCTCCAAACCAAAATTTCTCA 1380

QY 1381 GTTGTGTTCTCAATAGCTTCCCTCGAGGACTTCAAGTGTCTTCTAAAGACACAGAGG 1440
Db 1381 GTTGTGTTCTCAATAGCTTCCCTCGAGGACTTCAAGTGTCTTCTAAAGACACAGAGG 1440

QY 1441 CACCAANAGAGTCAATCAAAAGCACTGCACCG 1474
Db 1441 CACCAANAGAGTCAATCAAAAGCACTGCACCG 1474

RESULT 3
US-09-823-033-3
; Sequence 3, Application US/09823033
; Patent No. US20020004225A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE
; FILE REFERENCE: 00-12
; CURRENT APPLICATION NUMBER: US/09/823,033
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 3571
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1049)... (2086)
US-09-823-033-3

Query Match          98.0%; Score 1444.8; DB 9; Length 3571;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1460; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 2 ACCTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGAAACTA 61
Db 856 AACTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGAAACTA 915

QY 62 CCTGCGAATTTCTGCTGCGCAGAGCCGCGCAGGCTTCCACCGCAGCGAGCCTTTCCC 121
Db 916 CCCTGCGAATTTCTGCTGCGCAGAGCCGCGCAGGCTTCCACCGCAGCGAGCCTTTCCC 975

QY 122 CGGGCTGGGCTGAGCCTTGGAGTCTGCTTCCCGAGTGCCTGCGCGCGAGTGAGCCCTCG 181
Db 122 CGGGCTGGGCTGAGCCTTGGAGTCTGCTTCCCGAGTGCCTGCGCGCGAGTGAGCCCTCG 181
```

976 C-GGCTGGGCTGAGCCTTGGAGTCGTGCTCTCCCGAGTGCCTGAGCCCTCG 1034  
182 CCCAGTCAGCAAAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCTGCGCGCC 241  
1035 CCCAGTCAGCAAAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCTGCGCGCC 1094  
242 AAAGAACGGGACTCGGCTGAGTCCAACTTGAGCAGCAAGTTCGAGCTCTCCAGCGACA 301  
1095 AAAGAACGGGACTCGGCTGAGTCCAACTTGAGCAGCAAGTTCGAGCTCTCCAGCGACA 1154  
302 AGGACAGAACGGAGTCAAGATCCCGGCTGAGAGAGTGTCTCATATATCTGGTAATG 361  
1155 AGGACAGAACGGAGTCAAGATCCCGGCTGAGAGAGTGTCTCATATATCTGGTAATG 1214  
362 GGAGCATCCACAGCCGAGTTTCTCTATAGTACCCCAAGAAATATGCTGCTGGTGGGA 421  
1215 GGAGCATCCACAGCCGAGTTTCTCTATATATATATATATATATATATATATATAT 1274  
422 GATTAGTTGAGTATGAAATATGTCGAGTCCAGTGCATATTTGATGAGAGATTGGGC 481  
1275 GATTAGTTGAGTATGAAATATGTCGAGTCCAGTGCATATTTGATGAGAGATTGGGC 1334  
482 TGGAGATCCAGAGACATATATGCAAGTATGATTTGTAGAGTTGAGGAGCCAGTG 541  
1335 TGGAGATCCAGAGACATATATGCAAGTATGATTTGTAGAGTTGAGGAGCCAGTG 1394  
542 ATGGAAGTGTGTTAGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601  
1395 ATGGAAGTGTGTTAGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1454  
602 AAGGAATCATATCAGGATAGATTGTTATCTGATGAGTATTTTCCATCTGAACCCGAT 661  
1455 AAGGAATCATATCAGGATAGATTGTTATCTGATGAGTATTTTCCATCTGAACCCGAT 1514  
662 TCTGATCCATACAGTATATATGTCACCAAGTCCAGAGAACCAAGTCTCTGCGGT 721  
1515 TCTGATCCATACAGTATATATGTCACCAAGTCCAGAGAACCAAGTCTCTGCGGT 1574  
722 TGCCCCCTTCACTTTGCTATGGAACCTGCTCAACAATGCTGTGATGCTGCTGCTGCT 781  
1575 TGCCCCCTTCACTTTGCTATGGAACCTGCTCAACAATGCTGTGATGCTGCTGCTGCT 1634  
782 TGGAGAGCTGATTCGCTACCTAGGACCATGATGCTGCTGCTGCTGCTGCTGCTGCT 841  
1635 TGGAGAGCTGATTCGCTACCTAGGACCATGATGCTGCTGCTGCTGCTGCTGCTGCT 1694  
842 ACAAGCCAACTGCGAGCTTTGGCAAGGCTTCTCTATGGAAGAAAGCAAGTGG 901  
1695 ACAAGCCAACTGCGAGCTTTGGCAAGGCTTCTCTATGGAAGAAAGCAAGTGG 1754  
902 TGAATCTGAATCTCTCAAGGAAGGTAAACTCTACAGTGCACACCCCGGAACCTTCT 961  
1755 TGAATCTGAATCTCTCAAGGAAGGTAAACTCTACAGTGCACACCCCGGAACCTTCT 1814  
962 CAGTGTCCATACGGGAGAGCTAAAGAGGACAGATACCATATTTCTGGCAGGTTGCTCC 1021  
1815 CAGTGTCCATACGGGAGAGCTAAAGAGGACAGATACCATATTTCTGGCAGGTTGCTCC 1874  
1022 TGGTCAAGCGCTGTGGAGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1081  
1875 TGGTCAAGCGCTGTGGAGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1934  
1082 GTGTCCACGTAAGTTTCAAAAAGTACCATGAGTCTCTTCAAGTGAAGCAAAAATG 1141  
1935 GTGTCCACGTAAGTTTCAAAAAGTACCATGAGTCTCTTCAAGTGAAGCAAAAATG 1994  
1142 GAGTCAAGGGATTCATAGTCACTCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1201  
1995 GAGTCAAGGGATTCATAGTCACTCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2054  
1202 ACTGTGTGTAGAGGAACGAGAGGTTAACTGACGCTTCTGATGAGCAGCAGTGTGAG 1261  
2055 ACTGTGTGTAGAGGAACGAGAGGTTAACTGACGCTTCTGATGAGCAGCAGTGTGAG 2114

1362 CACTGGCATTCTGTGTACCCCAAGCAACTTTCATCCCAAGCAGTGTGGCCGCGAGG 1321  
2115 CACTGGCATTCTGTGTACCCCAAGCAACTTTCATCCCAAGCAGTGTGGCCGCGAGG 2174  
1322 CTCTCAGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1381  
2175 CTCTCAGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2234  
1382 TTGTTTGGTTCATAGAGTCTTCCCTGCGAGTCTCAAGTGTCTTCTTAAAGACGAGG 1441  
2235 TTGTTTGGTTCATAGAGTCTTCCCTGCGAGTCTTCAAGTGTCTTCTTAAAGACGAGG 2294  
1442 ACCAAGAGGAGTCAATCAAAAGCACTGC 1470  
2295 ACCAAGAGGAGTCAATCAAAAGCACTGC 2323

RESULT 4  
US-10-139-583-42  
; Sequence 42, Application US/10139583  
; Publication No. US2002017193A1  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVGF3  
; FILE REFERENCE: 98-60  
; CURRENT APPLICATION NUMBER: US/10139,583  
; CURRENT FILING DATE: 2002-05-02  
; PRIOR APPLICATION NUMBER: 09/457,066  
; PRIOR FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 42  
; LENGTH: 3571  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1049)...(2086)  
US-10-139-583-42

Query Match 98.0%; Score 1444.8; DB 13; Length 3571;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 1460; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 2 ACCTGGAGACACAGAGAGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGGAACCTA 61  
DB 856 AACTGGAGACACAGAGAGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGGAACCTA 915  
QY 62 CCCTGCGATTCTCTGCTGCCAGAGCGCGCCAGGCGCTTCCACCGCAGCGAGCCTTTCC 121  
DB 916 CCCTGCGATTCTCTGCTGCCAGAGCGCGCCAGGCGCTTCCACCGCAGCGAGCCTTTCC 975  
QY 122 CGGCTGGGCTGAGCCTTGGAGTGTGCTTCCAGTGTGCTGCTGCTGCTGCTGCTGCTG 181  
DB 976 C-GGCTGGGCTGAGCCTTGGAGTGTGCTTCCAGTGTGCTGCTGCTGCTGCTGCTGCTG 1034  
QY 182 CCCAGTCAAGCAATGCTCTCTGCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 241  
DB 1035 CCCAGTCAAGCAATGCTCTCTGCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1094  
QY 242 AAAGAACGGGACTCGGCTGAGTCCAACTTGAGCAGCAAGTTCGAGCTCTCCAGCGACA 301  
DB 1095 AAAGAACGGGACTCGGCTGAGTCCAACTTGAGCAGCAAGTTCGAGCTCTCCAGCGACA 1154  
QY 302 AGGAACAGAGCGAGTGCAGAGATCCCGGAGATGAGAGTGTGCTATATATCTGGTAATG 361

Db 1155 AGGAACGACGAGTGCAGATCCCGCATGAGAGAGTTGTCACATATATCTGTTAATG 1214  
QY 362 GGAGCATCCACAGCCGGAAGTTTCTCATACGTAACCAAGAAATATGGTGTGGTGA 421  
Db 1215 GGAGCATCCACAGCCGGAAGTTTCTCATACGTAACCAAGAAATATGGTGTGGTGA 1274  
QY 422 GATTAGTTGACATAGATGAAATGTGCGATCCAGTGCATTTGATGAGATTTGGC 481  
Db 1275 GATTAGTTGACATAGATGAAATGTGCGATCCAGTGCATTTGATGAGATTTGGC 1334  
QY 482 TGAAGATCCAGACGATATATGCAAGTATGATTTGTAGAAATTTGAGGAGCCAGTG 541  
Db 1335 TGAAGATCCAGACGATATATGCAAGTATGATTTGTAGAAATTTGAGGAGCCAGTG 1394  
QY 542 ATGGAAGTGTGTTAGAACGCTGGTGTGTTCTGGACTGTGCAGGAAAGCAGACTTCTA 601  
Db 1395 ATGGAAGTGTGTTAGAACGCTGGTGTGTTCTGGACTGTGCAGGAAAGCAGACTTCTA 1454  
QY 602 AAGGAAATCATATCAGGATTAAGTATGATCTGATGAGTATTTCCATCTGAACCGGAT 661  
Db 1455 AAGGAAATCATATCAGGATTAAGTATGATCTGATGAGTATTTCCATCTGAACCGGAT 1514  
QY 662 TCTGCATCCACTACAGTATTTATCATGCCACAAGTACAGAAACCCAGTCTCTCGGTG 721  
Db 1515 TCTGCATCCACTACAGTATTTATCATGCCACAAGTACAGAAACCCAGTCTCTCGGTG 1574  
QY 722 TGCCCCCTTCATCTTGTGATTTGAGACCTGCTCAAAATGCTGTGACTGCTTCAGTACT 781  
Db 1575 TGCCCCCTTCATCTTGTGATTTGAGACCTGCTCAAAATGCTGTGACTGCTTCAGTACT 1634  
QY 782 TGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGCGAGTGCAGTTCGACGCTTCT 841  
Db 1635 TGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGCGAGTGCAGTTCGACGCTTCT 1694  
QY 842 ACAAGCCAACTGCGAGCTTTTGGCAAGGCTTCTGTATGGGAAAAAAGCAAGTGG 901  
Db 1695 ACAAGCCAACTGCGAGCTTTTGGCAAGGCTTCTGTATGGGAAAAAAGCAAGTGG 1754  
QY 902 TGAATCTGAATCTCTCAAGNAGAGGTAAACTCTACAGTGCACACCCCGGAATCTTCT 961  
Db 1755 TGAATCTGAATCTCTCAAGNAGAGGTAAACTCTACAGTGCACACCCCGGAATCTTCT 1814  
QY 962 CAGTGTCCATACGGAAGAGCTAAAGAGACAGATACCATATTTCTGGCCAGGTTCTTCC 1021  
Db 1815 CAGTGTCCATACGGAAGAGCTAAAGAGACAGATACCATATTTCTGGCCAGGTTCTTCC 1074  
QY 1022 TGGTCAAGCGCTGTGGAGGAAATTTGCTGTGTTCTCCATAATTTGCAATGCTCAGT 1081  
Db 1875 TGGTCAAGCGCTGTGGAGGAAATTTGCTGTGTTCTCCATAATTTGCAATGCTCAGT 1934  
QY 1082 GTGTCCCAAGTAAAGTTACAAAAGTACCATGAGTCTTTCAGTTGAGACCAAAAATG 1141  
Db 1935 GTGTCCCAAGTAAAGTTACAAAAGTACCATGAGTCTTTCAGTTGAGACCAAAAATG 1994  
QY 1142 GAGTCAAGGGATTCATTAAGTCACTCACTGATGTGGCTCTGGAAACCCAGCAGGAATGTG 1201  
Db 1995 GAGTCAAGGGATTCATTAAGTCACTCACTGATGTGGCTCTGGAAACCCAGCAGGAATGTG 2054  
QY 1202 ACTGTGTGTAGAGGAAACCCAGAGGTAACCTGCAGCCTTCGTAGCAGCAGCAGTG 1261  
Db 2055 ACTGTGTGTAGAGGAAACCCAGAGGTAACCTGCAGCCTTCGTAGCAGCAGCAGTG 2114  
QY 1262 CACTGGCAATCTGTGTACCCCAAGCAACCTTCATCCCAAGCAGGTTGGCCGAGGG 1321  
Db 2115 CACTGGCAATCTGTGTACCCCAAGCAACCTTCATCCCAAGCAGGTTGGCCGAGGG 2174  
QY 1322 CTCTCAGTGTGTGTGCTGTGCTATGTTAAAGATCTTACTGTCTCCCAACCAAAATCTCAG 1381  
Db 2175 CTCTCAGTGTGTGTGCTGTGCTATGTTAAAGATCTTACTGTCTCCCAACCAAAATCTCAG 2234  
QY 1382 TTGTTTGTTCATATAGCCTTCCCTGAGGACTTCAAGTGTCTTCTAAAGACAGAGGC 1441  
Db 2235 TTGTTTGTTCATATAGCCTTCCCTGAGGACTTCAAGTGTCTTCTAAAGACAGAGGC 2294

QY 1442 ACCAANAGGAGTCAATCACAAGCACTGC 1470  
Db 2295 ACCAAGAGGAGTCAATCACAAGCACTGC 2333

## RESULT 5

US-10-264-361-3  
; Sequence 3, Application US/10264361  
; Publication No. US20030087870A1  
; GENERAL INFORMATION:  
; APPLICANT: Gilbertson, Debra G.  
; TITLE OF INVENTION: METHOD OF TREATING FIBROSIS  
; FILE REFERENCE: 00-53  
; CURRENT APPLICATION NUMBER: US/10/264,361  
; PRIOR FILING DATE: 2002-10-03  
; PRIOR APPLICATION NUMBER: US/09/695,121  
; PRIOR FILING DATE: 2000-10-23  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 3571  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1049)...(2086)  
US-10-264-361-3

Query Match 98.0%; Score 1444.8; DB 14; Length 3571;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 1460; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 2 ACCTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGGAACCTA 61  
Db 856 AACTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGGAACCTA 915  
QY 62 CCTCGGATTTCTGCTGTCAGAGCGGCGCCAGGCGCTTCCACCGAGCGCAGCCTTTTCC 121  
Db 916 CCTCGGATTTCTGCTGTCAGAGCGGCGGCGGCGCTTCCACCGAGCGCAGCCTTTTCC 975  
QY 122 CGGCTGGGCTGAGCCTTGGAGTCTGCTTCCCGAGTCCCGCGCGAGTGAAGCCTCG 181  
Db 976 C-GGCTGGGCTGAGCCTTGGAGTCTGCTTCCCGAGTCCCGCGCGAGTGAAGCCTCG 1034  
QY 182 CCCAGTCAGCAAAATGCTCTCTCGGCTCTCTCTGATGATCTGCTGCGGCGC 241  
Db 1035 CCCAGTCAGCAAAATGCTCTCTCGGCTCTCTCTGATGATCTGCTGCGGCGC 1094  
QY 242 AAAGAACCGGAGCTGGGCTGAGTCCAACTGAGCAGCAAGTTGCAAGTCTCTCAGCGACA 301  
Db 1095 AAAGAACCGGAGCTGGGCTGAGTCCAACTGAGCAGCAAGTTGCAAGTCTCTCAGCGACA 1154  
QY 302 AGGACAGAAACGAGTCAAGATCCCGGATGAGAGGTTGTCTATATCTGTTAATG 361  
Db 1155 AGGACAGAAACGAGTCAAGATCCCGGATGAGAGGTTGTCTATATCTGTTAATG 1214  
QY 362 GGAGCATCCACAGCCGGAAGTTTCTCATAGTACCAAGAAATATGCTGCTGTTGGA 421  
Db 1215 GGAGCATCCACAGCCGGAAGTTTCTCATAGTACCAAGAAATATGCTGCTGTTGGA 1274  
QY 422 GATTAGTTGCAAGTGAATAATGCGGATCCAGCTGACATTTGATGAGAGATTTGGC 481  
Db 1275 GATTAGTTGCAAGTGAATAATGCGGATCCAGCTGACATTTGATGAGAGATTTGGC 1334  
QY 482 TGAAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAGTTGAGAGCCAGTG 541  
Db 1335 TGAAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAGTTGAGAGCCAGTG 1394  
QY 542 ATGGAAGTGTGTTTAGGACGCTGTTGTTCTGGAGTGTGCTGAGGAAAGCAGACTTCTA 601  
Db 1395 ATGGAAGTGTGTTTAGGACGCTGTTGTTCTGGAGTGTGCTGAGGAAAGCAGACTTCTA 1454

```
QY 602 AAGGAAATCATATCAGGATAAGATTGTATCTGATGAGTATTTTCATCTGAACCCGGAT 661
    |||||
Db 1455 AAGGAAATCATATCAGGATAAGATTGTATCTGATGAGTATTTTCATCTGAACCCGGAT 1514
    |||||
QY 662 TCTGATCCACTACAGTATATCATGCCACAAGTCCAGAGAACCCAGAGTCTTCCGGTGT 721
    |||||
Db 1515 TCTGATCCACTACAGTATATCATGCCACAAGTCCAGAGAACCCAGAGTCTTCCGGTGT 1574
    |||||
QY 722 TCGCCCTTCATCTTGTTCATTTGGACCTCTCAACAAATCTGTGATGCTGCTTCAGTACCT 781
    |||||
Db 1575 TCGCCCTTCATCTTGTTCATTTGGACCTCTCAACAAATCTGTGATGCTGCTTCAGTACCT 1634
    |||||
QY 782 TGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGCGAGGTGGACTTTGGACAGCCTCT 841
    |||||
Db 1635 TGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGCGAGGTGGACTTTGGACAGCCTCT 1694
    |||||
QY 842 ACAAGCCACATGGCGAGCTTTTGGGCAAGGCTTCTGTATGGGAAAAAAGCAAGTGG 901
    |||||
Db 1695 ACAAGCCACATGGCGAGCTTTTGGGCAAGGCTTCTGTATGGGAAAAAAGCAAGTGG 1754
    |||||
QY 902 TGAATCTGAATCTCTCAAGGAAGAGGTAAACTCTACAGCTGCACACCCCGGAACCTCT 961
    |||||
Db 1755 TGAATCTGAATCTCTCAAGGAAGAGGTAAACTCTACAGCTGCACACCCCGGAACCTCT 1814
    |||||
QY 962 CAGTGTCCATACGGAAGAGCTAAAGAGGACAGATACCATATTTCTGGCCAGGTTGTCTCC 1021
    |||||
Db 1815 CAGTGTCCATACGGAAGAGCTAAAGAGGACAGATACCATATTTCTGGCCAGGTTGTCTCC 1874
    |||||
QY 1022 TGGTCAAGGCTGTGGAGAAATGTGCTGTGCTCTCCATTAATTCATGATGAATGTCTCAGT 1081
    |||||
Db 1875 TGGTCAAGGCTGTGGAGAAATGTGCTGTGCTCTCCATTAATTCATGATGAATGTCTCAGT 1934
    |||||
QY 1082 GTGTCCCAAGTAAAGTTACAAAAAGTACCATGAGGTCTCTCAGTTGAGACCAAAAACTG 1141
    |||||
Db 1935 GTGTCCCAAGTAAAGTTACAAAAAGTACCATGAGGTCTCTCAGTTGAGACCAAAAACTG 1994
    |||||
QY 1142 GAGTCAAGGATGTCATTAAGTCACTACATGATGTGGCTCTGAAACACCAAGGAAATGTG 1201
    |||||
Db 1995 GAGTCAAGGATGTCATTAAGTCACTACATGATGTGGCTCTGAAACACCAAGGAAATGTG 2054
    |||||
QY 1202 ACTGTGTGTAGAGGAACGAGGAGGTAACTGCGAGCTTCGTAGCAGCACAGTGGAG 1261
    |||||
Db 2055 ACTGTGTGTAGAGGAACGAGGAGGTAACTGCGAGCTTCGTAGCAGCACAGTGGAG 2114
    |||||
QY 1262 CACTGGCATTCCTGTGTACCCCAAGCAACCTTCATCCCAAGCAAGCTGTGGCCGAGGG 1321
    |||||
Db 2115 CACTGGCATTCCTGTGTACCCCAAGCAACCTTCATCCCAAGCAAGCTGTGGCCGAGGG 2174
    |||||
QY 1322 CTCTCAGCTGCTGATGCTGGCTATGTTAAAGATCTTACTCGTCTCCAAACAAATTCCTCAG 1381
    |||||
Db 2175 CTCTCAGCTGCTGATGCTGGCTATGTTAAAGATCTTACTCGTCTCCAAACAAATTCCTCAG 2234
    |||||
QY 1382 TTGTTTGTCTCAATAGCTTCCCTGCGAGGACTTCAAGTGTCTCTTAAAGACCAAGAGGC 1441
    |||||
Db 2235 TTGTTTGTCTCAATAGCTTCCCTGCGAGGACTTCAAGTGTCTCTTAAAGACCAAGAGGC 2294
    |||||
QY 1442 ACCAAGAGGATCAATCAAAAGCACTGC 1470
    |||||
Db 2295 ACCAAGAGGATCAATCAAAAGCACTGC 2323
    |||||
```

## RESULT 6

```
US-10-178-442-1
; Sequence 1, Application US/10178442
; Publication No. US20030113870A1
; GENERAL INFORMATION:
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Kuo, Sophia S.
; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1
; FILE REFERENCE: 11669.112USD2
; CURRENT APPLICATION NUMBER: US/10178,442
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US 09/265,686
```

```
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: US 09/184,216
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: US 09/040,220
; PRIOR FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2825
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2689)..(2689)
; OTHER INFORMATION: Any nucleotide
US-10-178-442-1
```

Query Match 62.0%; Score 914.2; DB 14; Length 2825;

Best Local Similarity 83.5%; Pred. No. 4.6e-296;

Matches 1050; Conservative 0; Mismatches 203; Indels 4; Gaps 1;

```
QY 2 ACCTGGAGACACAGAGAGGCTCTAGGAAAAATTTTGGATGGGATATATGTGAAACTA 61
    |||||
Db 61 AACTGGAGACACAGAGAGGCTCTAGGAAAAATTTTGGATGGGATATATGTGAAACTA 120
    |||||
QY 62 CACTCGATTTCTGTGCGAGAGCGGCGAGGCTTCCACCGCAGCGCAGCCTTTTCCC 121
    |||||
Db 121 CACTCGATTTCTGTGCGAGAGCAGGCTCGGCGCTTCCACCCAGTCGACGCTTCCC 180
    |||||
QY 122 CGG----GCTGGGCTGAGCCTTTGGAGTGTGCTTCCCGAGTCCCGCGCAGTAGGCC 177
    |||||
Db 181 TGGCGGTGTGAAAGAGACTCGGGAGTGTGCTTCCAAAGTGCCGCGTGTGAGTGT 240
    |||||
QY 178 CTCGCCCCAGTCAGCCAAATGCTCTCTCGGCTCTCTCTGATGATCTGCTGCTGCTG 237
    |||||
Db 241 CTCACCCAGTCAGCCAAATGAGCCTCTTTCGGGCTTCTCTCTGATGATCTGCTGCTG 300
    |||||
QY 238 GGCCAAAGAACCGGAGCTCGGGCTGAGTCCAACTTGAGCAGCAAGTTGCGAGCTCTCCAGC 297
    |||||
Db 301 GGCCAGAGACAGGAGACTCAGCGGAAATCCAACTGAGTAGTAAATTCAGATTTCCAGC 360
    |||||
QY 298 GACAAAGGAACAGAACGGAGTGCAGATCCCGGCATGAGAGAGTTGTCTACTATATCTGGT 357
    |||||
Db 361 AACAAAGGAACAGAACGGAGTGCAGATCCCGGCATGAGAGAGTTGTCTACTGTCTACT 420
    |||||
QY 358 AATGGAGCATCCACAGCCCGAGTTTCTCTATAGTACCCAGAAATATGTGCTGGTG 417
    |||||
Db 421 AATGGAAGTATTCACAGCCCAAGGTTTCTCTATATTCCTCAAGAAATACGGTCTTGGTA 480
    |||||
QY 418 TGGAGATTAGTTGCGAGTAGATGAAAAATGTCCGGATCCAGCTGACATTTTGTATGAGAGATT 477
    |||||
Db 481 TGGAGATTAGTTGCGAGTAGAGGAAATGTATGATACAACTTACGTTTGTATGAAAGATT 540
    |||||
QY 478 GGGCTGGAAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAAATGAGGAGGCC 537
    |||||
Db 541 GGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTTGTAGAAATGAGGAGGCC 600
    |||||
QY 538 AGTGATGGAAGTGTATTAGGACGCTGTGGTCTGGGACTGTGCCAGGAAAGCAGACT 597
    |||||
Db 601 AGTGATGGAACATATATTAGGCGCTGGTGTGTTCTGTACTGTATCCAGGAAACAGATT 660
    |||||
QY 598 TCTAAAGGAATCATATCAGGATAAGATTGTATCTGATGAGTATTTTCCATCTGAACCC 657
    |||||
Db 661 TCTAAAGGAATCAATATTAGGATAGATTGTATCTGATGATATTTTCTTCTGAACCA 720
    |||||
QY 658 GGATTTCTGCATCCACTACAGTATTAATGACCAAGTCAAGAAACCAAGAGTCTTCTCG 717
    |||||
Db 721 GGGTTCTGCATCCACTACAAATTTGTCTATGTCACAAATTCACAGAAAGCTGTGAGTCTTCA 780
    |||||
QY 718 GTGTTGCCCTTCTCATCTTTGTGATGAGCTGCTCAACAATGCTGTGATGCTGCTCAGT 777
    |||||
Db 781 GTGCTACCCCTTCTGCTTTGCCACTGCGCTTAAATATGCTATATACTGCTCTTGTAGT 840
    |||||
```



QY 778 ACCTTGGAAAGCTGATTCGGTACTAGAGCCAGATCGATGCGAGGTGACTTGGACAGC 837  
Db |  
QY 841 ACCTTGGAAAGCTTATTCGATATCTTGAACAGAGAGATGCGACTTGAAGAT 900  
Db |  
QY 838 CTCTACAAAGCAACATGCGAGCTTTTGGCAAGGCTTCTCTATGGGAAAAAGCAAA 897  
Db |  
QY 901 CTATATAGGCCAACCTTGGCAACTTCTTGGCAAGGCTTTGTTTTGGAGAAAAATCCAGA 960  
Db |  
QY 898 GTGGTGAATCTGAATCTCTCAAGGAAGAGGTAAATCTCTACAGTGCACACCCCGGAAC 957  
Db |  
QY 961 GTGGTGAATCTGAATCTCTCAAGGAAGAGGTAAATCTCTACAGTGCACACCCCGGAAC 1020  
QY 958 TTCTCAGTGTCCATACGGAAGAGCTTAAAGGACAGATACCATATCTTGGCCAGGTGT 1017  
Db |  
QY 1021 TTCTCAGTGTCCATACGGAAGAGCTTAAAGGACAGATACCATATCTTGGCCAGGTGT 1080  
QY 1018 CTCTCTGGTCAAGCGCTGTGGAGGAATGTGCTGTCTCTCAATTTGCAATCAATGT 1077  
Db |  
QY 1081 CTCTCTGGTAAACGCTGTGGGAACTGTGCTGTCTCTCAATTTGCAATCAATGT 1140  
QY 1078 CAGTGTGTCCACGCTAAAGTTTACAAAAAAGTACCATGAGTCTCTTCACTTGAAGCAAAA 1137  
Db |  
QY 1141 CAATGTGTCCCAAGCAAGTTTACTAAAAAATACCAAGGCTCTTCACTTGAAGCAAAA 1200  
QY 1138 ACTGAGTCAAGGATTCGATAGTCACTCACTGATGTGGCTCTGGAACACACAGGAA 1197  
Db |  
QY 1201 ACCGCTGTCAAGGATTCGATAGTCACTCACTGATGTGGCTCTGGAACACACAGGAA 1260  
QY 1198 TGTGACTGTGTGTAGAGGAAACCGAGGAGGTAACTGCGAGCTTCTGAGCAGCAC 1254  
Db |  
QY 1261 TGTGACTGTGTGTAGAGGAGGACACAGAGGATAGCGCATCCACCAGCAGCTC 1317

## RESULT 7

US-09-796-753-5  
; Sequence 5, Application US/09796753  
; Publication No. US20030027998A1  
; GENERAL INFORMATION:  
; APPLICANT: McCarthy, Sean A.  
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF  
; FILE REFERENCE: 7853-227-999  
; CURRENT APPLICATION NUMBER: US/09/796,753  
; CURRENT FILING DATE: 2001-03-01  
; PRIOR APPLICATION NUMBER: 09/183,175  
; PRIOR FILING DATE: 1998-10-30  
; PRIOR APPLICATION NUMBER: 09/223,094  
; PRIOR FILING DATE: 1998-12-30  
; PRIOR APPLICATION NUMBER: 09/223,546  
; PRIOR FILING DATE: 1998-12-30  
; PRIOR APPLICATION NUMBER: 09/224,246  
; PRIOR FILING DATE: 1998-12-30  
; PRIOR APPLICATION NUMBER: 09/259,388  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/122,458  
; PRIOR FILING DATE: 1999-03-01  
; PRIOR APPLICATION NUMBER: 09/312,359  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: 09/336,536  
; PRIOR FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: 09/342,687  
; PRIOR FILING DATE: 1999-06-29  
; PRIOR APPLICATION NUMBER: 09/345,464  
; PRIOR FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: 09/365,164  
; PRIOR FILING DATE: 1999-07-30  
; PRIOR APPLICATION NUMBER: 09/399,723  
; PRIOR FILING DATE: 1999-09-20  
; PRIOR APPLICATION NUMBER: 09/409,634  
; PRIOR FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: 09/471,179  
; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 09/474,071  
; PRIOR FILING DATE: 1999-12-29

Query Match  
Best Local Similarity 62.0%; Score 914.2; DB 11; Length 2839;  
Matches 1050; Conservative 0; Mismatches 203; Indels 4; Gaps 1;  
US-09-796-753-5

QY 2 ACCTGGAGACACAGAGAGGCTCTAGGAAAAATTTGGATGGGGATTATGTGGAACATA 61  
Db |  
QY 90 AACTGGAGACACAGAGAGGCTCTAGGAAAAATTTGGATGGGGATTATGTGGAACATA 149  
Db |  
QY 62 CCCTGGGATTTCTGCTGCGAGAGCGGCGAGGCGCTTCCACCGAGCGAGCCTTTCC 121  
Db |  
QY 150 CCCTGGGATTTCTGCTGCGAGAGCGGCTGCGGCGCTTCCACCGAGCGAGCCTTTCC 209  
QY 122 CGG----GCTGGGCTGAGCTTGGAGTCTGCTTCCCGAGTCCCGCGCGAGTGAGCC 177  
Db |  
QY 210 TGGCGGTGGTGAAGAGACTCGGAGTCTGCTTCCAAAGTCCCGCGCGAGTGAGT 269  
QY 178 CTGCGCCCGAGTCAGCCAAATGCTCTCTCGGCGCTTCTCTGCTGACATCTGCGCTGGCC 237  
Db |  
QY 270 CTCACCCCGAGTCAGCCAAATGAGCCTCTTGGGCTTCTCTGCTGACATCTGCGCTGGCC 329  
QY 238 GGCCAAAGAACGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGAGCTCTCCAGC 297  
Db |  
QY 330 GGCCAGAGACAGGGGACTCAGGCGGAATCCAACTGAGTAGTAATTCAGTTTCCAGC 389  
QY 298 GACAAGGAACAGAACCGAGTCCAAGATCCCGGCGATGAGAGTGTCTCACTATATCTGCT 357  
Db |  
QY 390 AACAGGAACAGAACCGAGTCCAAGATCCCGGCGATGAGAGTGTCTCACTATATCTGCT 449  
QY 358 AATGGAGATTCACAGCCCAAGGTTTCTCATAGTACCAAGAAATATGCTGCTGGTG 417  
Db |  
QY 418 TGGAGATTAGTTCAGTAGATGAAAAATGTGGGATTCGCGTGAATTTGATGAGAGATT 477  
Db |  
QY 510 TGGAGATTAGTTCAGTAGATGAAAAATGTGGGATTCGCGTGAATTTGATGAGAGATT 569  
QY 478 GGGCTGGAAGATCCAGAGAGATATATGCAAGTATGATTTTGTAGAGTTGAGAGCCC 537  
Db |  
QY 570 GGGCTGGAAGATCCAGAGAGATATATGCAAGTATGATTTTGTAGAGTTGAGAGCCC 629  
QY 538 AGTGATGGAAGTGTTTTAGGACGCTGTGTGTTTCTGGGACTGTGCGGAAAGCAGACT 597

Db 630 AGTGATGGAATATATTAGGCGCTGTGTGTTCTGCTACTGACAGGAAAAACAGATT 689  
Qy 598 TCTAAAGGAATCATATCAGATTAAGATTGTGTATCTGATGATATTTTCCATCTGAACCC 657  
Db 690 TCTAAAGGAATCAAAATAGGATAAGATTGTGTATCTGATGATATTTTCTCTGAACCA 749  
Qy 658 GGATTCTCATCCACTCAGATTATATCATGCAAGTCAAGAACACAGAGTCCTTCG 717  
Db 750 GGGTTCTGATCCACTACAAATGTGTATGCAACAAATTCAGAAAGCTGTGAGTCTTCA 809  
Qy 718 GTGTGCCCCCTTCATCTTTGTCTATGCACTGTCTCAACAAATGTGTGACCTTCAGT 777  
Db 810 GTGCTACCCCTTCAGCTTTGCACTGTGCACTGTCTTAATAATGCTATTAAGTCCCTTAGT 869  
Qy 778 ACCTTGAAGAGCTGATTTCGGTCACTAGACGACAGATCGATGCGAGGTGAGCTTGACAGC 837  
Db 870 ACCTTGAAGACCTTATTCGATATCTTGAACAGAGAGATGCGAGTTCGATTTAGAAGT 929  
Qy 838 CTCTACAGCCAAATGCGAGCTTTTGGCAAGGCTTTCTGTATGGAAAAAAGCAAA 897  
Db 930 CTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTGGAAGAAATCCAGA 989  
Qy 898 GTGTGGAATCTGAATCTCTCAAGGAAGAGGTAAATCTCTACAGCTGCACACCCCGGAAC 957  
Db 990 GTGTGGAATCTGAATCTCTCAAGGAAGAGGTAAATCTCTACAGCTGCACACCCCGTAAC 1049  
Qy 958 TTCTCAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACCATATTTCTGCGCCAGGTGT 1017  
Db 1050 TTCTCAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACCATATTTCTGCGCCAGGTGT 1109  
Qy 1018 CTCCTGTGCAAGCGCTGTGAGGAAATGTGCTGTCTTCTCCATATTTGCAATGCAATGT 1077  
Db 1110 CTCCTGTGTAACGCTGTGTGGGAACCTGTGCTGTCTTCTCCCAATTTGCAATGCAATGT 1169  
Qy 1078 CAGTGTGTCACAGCTTAAGTTTACAAAAGTACCATGAGTCTTCTGAGTTCAGACCAAAA 1137  
Db 1170 CAATGTGTGTCACAGCAAAAGTTACTAAAAAATACCAAGAGGTCTTCTGAGTTCAGACCAAG 1229  
Qy 1138 ACTGAGTCAAGGATTCATTAAGTCACTCACTGATGCTGTGGAACACACAGAGAA 1197  
Db 1230 ACCGGTGTGAGGATTCACAAATCACTACCGAGTGGCCCTTGAGACCATGAGAG 1289  
Qy 1198 TGTGACTGTGTGTAGAGGAAACCGAGAGGTAAGTTCAGTTCAGTTCAGTTCAGTTCAGT 1254  
Db 1290 TGTGACTGTGTGTGAGAGGAGGACAGAGGATAGCGCATCACCACAGCAGCTC 1346

RESULT 8

US-09-978-295A-487  
; Sequence 487, Application US/09978295A  
; Patent No. US20020156006A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas P.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630FIC11  
; CURRENT APPLICATION NUMBER: US/09/978,295A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/077450  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 60/077632  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077641  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077649  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077791  
; PRIOR FILING DATE: 1998-03-12  
; PRIOR APPLICATION NUMBER: 60/078004  
; PRIOR FILING DATE: 1998-03-13  
; PRIOR APPLICATION NUMBER: 60/078886  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078936  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078939  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079664  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079663  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079786  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079920  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 60/079923  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 60/080105  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080107  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080165  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080194  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080327  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080328  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080333





1 PRIOR FILING DATE: 1998-04-01  
2 PRIOR APPLICATION NUMBER: 60/080334  
3 PRIOR FILING DATE: 1998-04-01  
4 PRIOR APPLICATION NUMBER: 60/081070  
5 PRIOR FILING DATE: 1998-04-08  
6 PRIOR APPLICATION NUMBER: 60/081049  
7 PRIOR FILING DATE: 1998-04-08  
8 PRIOR APPLICATION NUMBER: 60/081071  
9 PRIOR FILING DATE: 1998-04-08  
10 PRIOR APPLICATION NUMBER: 60/081195  
11 PRIOR FILING DATE: 1998-04-08  
12 PRIOR APPLICATION NUMBER: 60/081203  
13 PRIOR FILING DATE: 1998-04-09  
14 PRIOR APPLICATION NUMBER: 60/081229  
15 PRIOR FILING DATE: 1998-04-09  
16 PRIOR APPLICATION NUMBER: 60/081955  
17 PRIOR FILING DATE: 1998-04-15  
18 PRIOR APPLICATION NUMBER: 60/081817  
19 PRIOR FILING DATE: 1998-04-15  
20 PRIOR APPLICATION NUMBER: 60/081819  
21 PRIOR FILING DATE: 1998-04-15  
22 PRIOR APPLICATION NUMBER: 60/081952  
23 PRIOR FILING DATE: 1998-04-15  
24 PRIOR APPLICATION NUMBER: 60/081838  
25 PRIOR FILING DATE: 1998-04-15  
26 PRIOR APPLICATION NUMBER: 60/082568  
27 PRIOR FILING DATE: 1998-04-21  
28 PRIOR APPLICATION NUMBER: 60/082569  
29 PRIOR FILING DATE: 1998-04-21  
30 PRIOR APPLICATION NUMBER: 60/082704  
31 PRIOR FILING DATE: 1998-04-22  
32 PRIOR APPLICATION NUMBER: 60/082804  
33 PRIOR FILING DATE: 1998-04-22  
34 PRIOR APPLICATION NUMBER: 60/082700  
35 PRIOR FILING DATE: 1998-04-22  
36 PRIOR APPLICATION NUMBER: 60/082797  
37 PRIOR FILING DATE: 1998-04-22  
38 PRIOR APPLICATION NUMBER: 60/082796  
39 PRIOR FILING DATE: 1998-04-23  
40 PRIOR APPLICATION NUMBER: 60/083336  
41 PRIOR FILING DATE: 1998-04-27  
42 PRIOR APPLICATION NUMBER: 60/083322  
43 PRIOR FILING DATE: 1998-04-28  
44 PRIOR APPLICATION NUMBER: 60/083392  
45 PRIOR FILING DATE: 1998-04-29  
46 PRIOR APPLICATION NUMBER: 60/083495  
47 PRIOR FILING DATE: 1998-04-29  
48 PRIOR APPLICATION NUMBER: 60/083496  
49 PRIOR FILING DATE: 1998-04-29  
50 PRIOR APPLICATION NUMBER: 60/083499  
51 PRIOR FILING DATE: 1998-04-29  
52 PRIOR APPLICATION NUMBER: 60/083545  
53 PRIOR FILING DATE: 1998-04-29  
54 PRIOR APPLICATION NUMBER: 60/083554  
55 PRIOR FILING DATE: 1998-04-29  
56 PRIOR APPLICATION NUMBER: 60/083558  
57 PRIOR FILING DATE: 1998-04-29  
58 PRIOR APPLICATION NUMBER: 60/083559  
59 PRIOR FILING DATE: 1998-04-29  
60 PRIOR APPLICATION NUMBER: 60/083500  
61 PRIOR FILING DATE: 1998-04-29  
62 PRIOR APPLICATION NUMBER: 60/083742  
63 PRIOR FILING DATE: 1998-04-30  
64 PRIOR APPLICATION NUMBER: 60/084366  
65 PRIOR FILING DATE: 1998-05-05  
66 PRIOR APPLICATION NUMBER: 60/084414  
67 PRIOR FILING DATE: 1998-05-06  
68 PRIOR APPLICATION NUMBER: 60/084441  
69 PRIOR FILING DATE: 1998-05-06  
70 PRIOR APPLICATION NUMBER: 60/084637  
71 PRIOR FILING DATE: 1998-05-07  
72 PRIOR APPLICATION NUMBER: 60/084639  
73 PRIOR FILING DATE: 1998-05-07

1 PRIOR APPLICATION NUMBER: 60/084640  
2 PRIOR FILING DATE: 1998-05-07  
3 PRIOR APPLICATION NUMBER: 60/084598  
4 PRIOR FILING DATE: 1998-05-07  
5 PRIOR APPLICATION NUMBER: 60/084600  
6 PRIOR FILING DATE: 1998-05-07  
7 PRIOR APPLICATION NUMBER: 60/084627  
8 PRIOR FILING DATE: 1998-05-07  
9 PRIOR APPLICATION NUMBER: 60/084643  
10 PRIOR FILING DATE: 1998-05-07  
11 PRIOR APPLICATION NUMBER: 60/085339  
12 PRIOR FILING DATE: 1998-05-13  
13 PRIOR APPLICATION NUMBER: 60/085338  
14 PRIOR FILING DATE: 1998-05-13  
15 PRIOR APPLICATION NUMBER: 60/085323  
16 PRIOR FILING DATE: 1998-05-13  
17 PRIOR APPLICATION NUMBER: 60/085582  
18 PRIOR FILING DATE: 1998-05-15  
19 PRIOR APPLICATION NUMBER: 60/085700  
20 PRIOR FILING DATE: 1998-05-15  
21 PRIOR APPLICATION NUMBER: 60/085689  
22 PRIOR FILING DATE: 1998-05-15  
23 PRIOR APPLICATION NUMBER: 60/085579  
24 PRIOR FILING DATE: 1998-05-15  
25 PRIOR APPLICATION NUMBER: 60/085580  
26 PRIOR FILING DATE: 1998-05-15  
27 PRIOR APPLICATION NUMBER: 60/085573  
28 PRIOR FILING DATE: 1998-05-15  
29 PRIOR APPLICATION NUMBER: 60/085704  
30 PRIOR FILING DATE: 1998-05-15  
31 PRIOR APPLICATION NUMBER: 60/085697

Query Match 62.0%; Score 914.2; DB 10; Length 2849;

Best Local Similarity 83.5%; Pred. No. 4.6e-296; Matches 1050; Conservative 0; Mismatches 203; Indels 4; Gaps 1;

QY 2 ACCTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGAAACTA 61  
Db 87 AACTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGAAACTA 146  
QY 62 CCCTGGAGTTCTGTCTCCAGAGCGGCGCAGAGGCTTCCACCGCAGGCGAGCTTTCCC 121  
Db 147 CCCTGGAGTTCTGTCTCCAGAGCGGCTCGGCGCTTCCACCGCAGGCGAGCTTTCCC 206  
QY 122 CGG----GCTGGGTGAGCCTTTGGAGTGTGAGTGTCTCCAGTGGCGCGGAGTGAGCC 177  
Db 207 TGGCGGTGTTGAAGAGACTCGGAGTGTGAGTGTCTCCAGTGGCGCGGAGTGAGCT 266  
QY 178 CTGCGCCAGTCAGCCAAATGCTCTCTCGGCTCTCTCTGCTGAGCATCTGCGCTGGCC 237  
Db 267 CTCACCCAGTCAGCCAAATGAGCCTCTTTCGGGCTTCTCTGCTGACATCTGCGCTGGCC 326  
QY 238 GGCACAAAGACGGGACTCGGGCTGAGTCCAACTGAGCAGCAGTTCAGCTCTCCAGC 297  
Db 327 GGCAGAGACAGGGACTCAGCGGATCCAACTGAGTAAATTCAGCTTTTCCAGC 386  
QY 298 GACAAAGAACAGAGCGGAGTCAAGATCCCGGATGAGAGAGTGTCTACTATCTGCT 357  
Db 387 AACAGGAACAGAGCGGAGTCAAGATCCCTCAGATGAGAGATTTATCTGTGCTACT 446  
QY 358 AATGGAGCATCCACAGCGGCGGAGTTCCTCATAGTACCCCAAGAAATATGCTGCTGG 417  
Db 447 AATGAAGTATTCACAGCGGCGGAGTTCCTCATAGTATTCCTCAAGAAATACCTGCTG 506  
QY 418 TGGAGATTAGTTGCAAGTAAATGTCGGATCCAGCTGACATTTGATGAGAGATTT 477  
Db 507 TGGAGATTAGTTGCAAGTAAATGTCGGATCCAGCTGACATTTGATGAGAGATTT 566  
QY 478 GGGCTGGAAGATCCAGAGAGCATATATGCAAGTATGATTTTGTAGAGTTGAGAGCCC 537  
Db 567 GGGCTGGAAGATCCAGAGAGCATATATGCAAGTATGATTTTGTAGAGTTGAGAGCCC 626  
QY 538 ACTGATGGAAGTGTGTTTGTAGGAGCGCTGGTGTGTTCTGGAGCTGTGCCAGGAGCAGACT 597

Db 627 AGTGATGAACTATATAGGCGCTGTGTGGTCTGTACTGTACAGGAAAACAGATT 686  
Qy TCTAAGGAAATCATATCAGGATAAGATTTGTATCTGATGAGTATTTTCCATCTGAACCC 657  
Db TCTAAGGAAATCAATAGGATAAGATTTGTATCTGATGAGTATTTTCCATCTGAACCA 746  
Qy GGATTTGCTATCTACAGTATATATGCGCAAGTACAGAAACCGAGTCTCTTCG 717  
Db GGGTTCTGCTATCTACAGTATATATGCGCAAGTACAGAAACCGAGTCTCTTCG 806  
Qy GTGTTGCCCCCTTCTATCTGCTATGCTGCTCAACATGCTGCTGCTGCTGCTGCT 777  
Db GTGCTACCCCCCTTCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 866  
Qy ACCTTGAAGAGCTGATTCGGTACTAGAGCAGATCGATGGAGGAGTGGAGCTTGGACAGC 837  
Db ACCTTGAAGAGCTTATTCGATATCTTGAACAGAGAGATGGAGTGGAGCTTGAAGAT 926  
Qy CTCTACAGGCAACATGCGAGCTTTTGGCAAGCTTTCTGTATGGGAAAAAAGCAAA 897  
Db CTATATAGGCAACTTGGCAACTTTTGGCAAGCTTTTGTGGAAGAAATCCAGA 986  
Qy GTGTGATATGAACTCTCTCAAGGAAAGATTAACCTTACAGCTGCAACCCCGAAC 957  
Db GTGTGATATGAACTCTCTCAAGGAAAGATTAACCTTACAGCTGCAACCCCGAAC 1046  
Qy TTCTCAGTGTCCATACGGAGAGCTTAAAGAGGACATACCATATTTCTGCCAGGTTGT 1017  
Db TTCTCAGTGTCCATACGGAGAGCTTAAAGAGGACATACCATATTTCTGCCAGGTTGT 1106  
Qy CTCTGCTGCAAGCTGTGGAGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1077  
Db CTCTGCTGCAAGCTGTGGAGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1166  
Qy CAGTGTGTCCACCTAAAGTTACAAAAGTACCATGAGTCTTCAAGTGTGAGACAAA 1137  
Db CAATGTGTCCCAAGAGTTTACAAAAGTACCATGAGTCTTCAAGTGTGAGACAAA 1226  
Qy ACTGAGTCAAGGATTCATAGTCACTCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1197  
Db ACCGTTGTGAGGATTCATAGTCACTCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1286  
Qy TGTGACTGTGTGTAGAGGAAACGCGAGGAGTAACTGAGCTTCTGCTGAGCAGC 1254  
Db TGTGACTGTGTGTAGAGGAAACGCGAGGAGTAACTGAGCTTCTGCTGAGCAGC 1343

## RESULT 10

US-09-978-192A-487

Sequence 487, Application US/09978192A

Patent No. US20020177553A1

## GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnovers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James;

APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC9  
CURRENT APPLICATION NUMBER: US/09/978,192A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004  
PRIOR FILING DATE: 1998-03-13  
PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078936  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078939  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079664  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079663  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079786  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079920  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/079923  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/080105  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080107  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080194  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080327  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080328  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080333



Db 627 AGTGATGGAATATATTAGGCGCTGGTGTCTCTGGTACTGTACACAGGAAACAGATT 686  
Qy 598 TCTAAAGAAATCATATACAGGATAGATTGTATCTGATAGTATTTTCCATCTGAACCC 657  
Db 687 TCTAAAGAAATCAAAATAGGATAGATTGTATCTGATGAATATTTTCTTCTGAACCA 746  
Qy 658 GGATTCTGCATCCACTACAGTATTATCATGCCACAAGTCACAGAAACACGAGTCTTCG 717  
Db 747 GGGTCTGCATCCACTACACATGTCTATGCCAATTCACAGAAGCTGTGAGTCCCTCA 806  
Qy 718 GTGTGCCCCCTTCATCTTTGTCAFTGGACCTGTCTCAACATGCTGTGACTGCCCTTCAGT 777  
Db 807 GTGCTACCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATGCTATAACTGCCCTTAGT 866  
Qy 778 ACCTTGGAGAGCTGATTTCGGTACCTAGACGACAGATCATGTCAGGTGGACTTGGACAGC 837  
Db 867 ACCTTGGAGAGCTTATTTCGATATCTTGAACACAGAGATGGCAGTTGACTTAGAAGT 926  
Qy 838 CTCTACAAAGCCAAACATGGCAGCTTTTGGCAAGGCTTTTCTGTATGGGAAAAAGCAAA 897  
Db 927 CTATATAGCCCACTTGGCAACTTCTTGGCAAGGCTTTTGTGTTGGAGAAATCCAGA 986  
Qy 898 GTGTGAATCTGAATCTCTCAAGGAGAGGTAAATCTACAGCTGCACACCCCGGAAC 957  
Db 987 GTGTGTGATCTGAACCTTCTTAAACAGAGGAGGTAAATATATACAGCTGCACACCTCGTAAC 1046  
Qy 958 TTCTCAGTGTCCATACGGGAGAGCTTAAAGAGGACAGATACCATATCTTGGCCAGGTGT 1017  
Db 1047 TTCTCAGTGTCCATNAGGAGAGAACTAAAGAACCGATACCATTTCTTGGCCAGGTGT 1106  
Qy 1018 CTCCTGGTCAAGCGCTGTGGAGAAATGTGCTGTCTTCTCCATAATTCGAATGAATGT 1077  
Db 1107 CTCCTGGTAAACGCTGTGGTGGAACTGTGCTGTCTTCTCCAAATTCGAATGAATGT 1166  
Qy 1078 CAGTGTGTCCACGTAAGTTACAAAAAGTACCAATGAGGTGCTTTCAGTTGAGACCAAAA 1137  
Db 1167 CAATGTGTCCCAAGCAAAAGTTACTAAAAAATACCAAGAGGTGCTTTCAGTTGAGACCAAG 1226  
Qy 1138 ACTGGAGTCAAGGATTCATTAAGTCACTCACTGATGTGGCTGTGGACACACAGAGAA 1197  
Db 1227 ACCGGTGCAGGGATTCACAAATCACTCCAGGAGTGGCCCTGGAGACCATGAGAG 1286  
Qy 1198 TGTGACTGTGTGTAGAGGAAACGAGGAGGTAACTGCAGCCTTCTGTAGCAGCAC 1254  
Db 1287 TGTGACTGTGTGCAGAGGAGGACAGAGAGTAGCCGATCACCACGAGCAGCTC 1343

## RESULT 11

US-09-999-832A-487  
; Sequence 487, Application US/09999832A  
; Publication No. US20020192706A1

## GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630PIC63  
; CURRENT APPLICATION NUMBER: US/09/999,832A  
; CURRENT FILING DATE: 2001-10-24  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/077450  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 60/077632  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077641  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077649  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077791  
; PRIOR FILING DATE: 1998-03-12  
; PRIOR APPLICATION NUMBER: 60/078004  
; PRIOR FILING DATE: 1998-03-13  
; PRIOR APPLICATION NUMBER: 60/078886  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078936  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078939  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079664  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079663  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079786  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079920  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 60/079923  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 60/080105  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080107  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080165  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080194  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080327  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080328  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080333



1 PRIOR FILING DATE: 1998-04-01  
2 PRIOR APPLICATION NUMBER: 60/080334  
3 PRIOR FILING DATE: 1998-04-01  
4 PRIOR APPLICATION NUMBER: 60/081070  
5 PRIOR FILING DATE: 1998-04-08  
6 PRIOR APPLICATION NUMBER: 60/081049  
7 PRIOR FILING DATE: 1998-04-08  
8 PRIOR APPLICATION NUMBER: 60/081071  
9 PRIOR FILING DATE: 1998-04-08  
10 PRIOR APPLICATION NUMBER: 60/081195  
11 PRIOR FILING DATE: 1998-04-08  
12 PRIOR APPLICATION NUMBER: 60/081203  
13 PRIOR FILING DATE: 1998-04-09  
14 PRIOR APPLICATION NUMBER: 60/081229  
15 PRIOR FILING DATE: 1998-04-09  
16 PRIOR APPLICATION NUMBER: 60/081955  
17 PRIOR FILING DATE: 1998-04-15  
18 PRIOR APPLICATION NUMBER: 60/081817  
19 PRIOR FILING DATE: 1998-04-15  
20 PRIOR APPLICATION NUMBER: 60/081819  
21 PRIOR FILING DATE: 1998-04-15  
22 PRIOR APPLICATION NUMBER: 60/081952  
23 PRIOR FILING DATE: 1998-04-15  
24 PRIOR APPLICATION NUMBER: 60/081838  
25 PRIOR FILING DATE: 1998-04-15  
26 PRIOR APPLICATION NUMBER: 60/082568  
27 PRIOR FILING DATE: 1998-04-21  
28 PRIOR APPLICATION NUMBER: 60/082569  
29 PRIOR FILING DATE: 1998-04-21  
30 PRIOR APPLICATION NUMBER: 60/082704  
31 PRIOR FILING DATE: 1998-04-22  
32 PRIOR APPLICATION NUMBER: 60/082804  
33 PRIOR FILING DATE: 1998-04-22  
34 PRIOR APPLICATION NUMBER: 60/082700  
35 PRIOR FILING DATE: 1998-04-22  
36 PRIOR APPLICATION NUMBER: 60/082797  
37 PRIOR FILING DATE: 1998-04-22  
38 PRIOR APPLICATION NUMBER: 60/082796  
39 PRIOR FILING DATE: 1998-04-23  
40 PRIOR APPLICATION NUMBER: 60/083336  
41 PRIOR FILING DATE: 1998-04-27  
42 PRIOR APPLICATION NUMBER: 60/083322  
43 PRIOR FILING DATE: 1998-04-28  
44 PRIOR APPLICATION NUMBER: 60/083392  
45 PRIOR FILING DATE: 1998-04-29  
46 PRIOR APPLICATION NUMBER: 60/083495  
47 PRIOR FILING DATE: 1998-04-29  
48 PRIOR APPLICATION NUMBER: 60/083496  
49 PRIOR FILING DATE: 1998-04-29  
50 PRIOR APPLICATION NUMBER: 60/083499  
51 PRIOR FILING DATE: 1998-04-29  
52 PRIOR APPLICATION NUMBER: 60/083545  
53 PRIOR FILING DATE: 1998-04-29  
54 PRIOR APPLICATION NUMBER: 60/083554  
55 PRIOR FILING DATE: 1998-04-29  
56 PRIOR APPLICATION NUMBER: 60/083558  
57 PRIOR FILING DATE: 1998-04-29  
58 PRIOR APPLICATION NUMBER: 60/083559  
59 PRIOR FILING DATE: 1998-04-29  
60 PRIOR APPLICATION NUMBER: 60/083500  
61 PRIOR FILING DATE: 1998-04-29  
62 PRIOR APPLICATION NUMBER: 60/083742  
63 PRIOR FILING DATE: 1998-04-30  
64 PRIOR APPLICATION NUMBER: 60/084366  
65 PRIOR FILING DATE: 1998-05-05  
66 PRIOR APPLICATION NUMBER: 60/084414  
67 PRIOR FILING DATE: 1998-05-06  
68 PRIOR APPLICATION NUMBER: 60/084441  
69 PRIOR FILING DATE: 1998-05-06  
70 PRIOR APPLICATION NUMBER: 60/084637  
71 PRIOR FILING DATE: 1998-05-07  
72 PRIOR APPLICATION NUMBER: 60/084639  
73 PRIOR FILING DATE: 1998-05-07

1 PRIOR APPLICATION NUMBER: 60/084640  
2 PRIOR FILING DATE: 1998-05-07  
3 PRIOR APPLICATION NUMBER: 60/084598  
4 PRIOR FILING DATE: 1998-05-07  
5 PRIOR APPLICATION NUMBER: 60/084600  
6 PRIOR FILING DATE: 1998-05-07  
7 PRIOR APPLICATION NUMBER: 60/084627  
8 PRIOR FILING DATE: 1998-05-07  
9 PRIOR APPLICATION NUMBER: 60/084643  
10 PRIOR FILING DATE: 1998-05-07  
11 PRIOR APPLICATION NUMBER: 60/085339  
12 PRIOR FILING DATE: 1998-05-13  
13 PRIOR APPLICATION NUMBER: 60/085338  
14 PRIOR FILING DATE: 1998-05-13  
15 PRIOR APPLICATION NUMBER: 60/085323  
16 PRIOR FILING DATE: 1998-05-13  
17 PRIOR APPLICATION NUMBER: 60/085582  
18 PRIOR FILING DATE: 1998-05-15  
19 PRIOR APPLICATION NUMBER: 60/085700  
20 PRIOR FILING DATE: 1998-05-15  
21 PRIOR APPLICATION NUMBER: 60/085689  
22 PRIOR FILING DATE: 1998-05-15  
23 PRIOR APPLICATION NUMBER: 60/085579  
24 PRIOR FILING DATE: 1998-05-15  
25 PRIOR APPLICATION NUMBER: 60/085580  
26 PRIOR FILING DATE: 1998-05-15  
27 PRIOR APPLICATION NUMBER: 60/085573  
28 PRIOR FILING DATE: 1998-05-15  
29 PRIOR APPLICATION NUMBER: 60/085704  
30 PRIOR FILING DATE: 1998-05-15  
31 PRIOR APPLICATION NUMBER: 60/085697

Query Match 62.0%; Score 914.2; DB 10; Length 2849;  
Best Local Similarity 83.5%; Pred. No. 4.6e-296;

Matches 1050; Conservative 0; Mismatches 203; Indels 4; Gaps 1;

QY 2 ACCTGGAGACACAGAGAGGGCTTAGGAAAAATTTTGGATGGGATTTATGTGGAACCTA 61  
DB 87 AACTGGAGACACAGAGAGGGCTTAGGAAAAATTTTGGATGGGATTTATGTGGAACCTA 146  
QY 62 CCTTGGATTCTCTGCTCCAGAGCGGGCAGGCGCTTCCACCGCAGCGCAGCTTTTCCC 121  
DB 147 CCTTGGATTCTCTGCTCCAGAGCGGGCTCGGCGCTTCCACCGCAGCTTTTCCC 206  
QY 122 CGG---GCTGGGCTGAGCTTGGAGTCGTGCTTCCCGAGTCCCGCGCGAGTGAGCC 177  
DB 207 TGGGGTGGTGAAGAGACTCGGGAGTCGTGCTTCCAAAGTCCCGCGCTGAGTGAGCT 266  
QY 178 CTGCGCCCGAGTCAGCCAAATGCTCTCTCGGCGCTTCTCTGCTGACATCTGCCCTGGCC 237  
DB 267 CTCACCCCGAGTCAGCCAAATGAGCCTCTTGGGCTTCTCTGCTGACATCTGCCCTGGCC 326  
QY 238 GGCCAAAGAACGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGAGCTCTCCAGC 297  
DB 327 GGCCAGAGACAGGGGACTCAGGCGGAATCCAACCTGAGTAGTAATTCAGTTTTCCAGC 386  
QY 298 CACAAGGAACAGAACGGAGTCCAGATCCCGGATGAGAGAGTGTCTACTATATCTGCT 357  
DB 387 AACAGGACAGACAGGAGTACAGATCTCAGATGAGAGATTTATTACTGTCTACT 446  
QY 358 AATGGGAGCATCCACAGCCCGAAGTTTCTCATAGTACCAAGAAATATGCTGCTGGTG 417  
DB 447 AATGGAAGTATTCACAGCCCAAGTTTCTCATACTTATCCAGAAATACGGTCTTGTA 506  
QY 418 TGGAGATTAGTTCAGTAGATGAAATGTGGGATCCAGCTGACATTTGATGAGAGATT 477  
DB 507 TGGAGATTAGTAGCAGTAGAGGAAATGATGAGTACAACTTACGTTTGAAGAAATT 566  
QY 478 GGGCTGGAAGATCCAGAGAGCATATATGAAATGATGATTTTGTAGAGTTGAGAGCCC 537  
DB 567 GGGCTTGAAGACCCAGAGAGTACATATGAAATGATGATTTTGTAGAGTTGAGAGCCC 626  
QY 538 AGTGATGGAAGTGTTTTAGGACGCTGGTGGTTCTGGGACTGTGCCAGGAAAGCAGACT 597





Db 627 AGTGATGGAATATATAGGCGCTGGTGTGTTCTGGTACTGTACCGAGAAAACAGATT 686  
Qy 598 TCTAAAGGAAATCATATCAGGATAAGATTGTTATCTGATGAGTATTTTCCATCTCAACCC 657  
Db 687 TCTAAAGGAAATCAATATAGGATAAGATTGTTATCTGATGATATTTTCTCTGACCA 746  
Qy 658 GGATTCTGCATCCATCAGTATATATCATGCCAACAGTCAAGAAACACGAGTCTCTGG 717  
Db 747 GGGTCTTGATCCACTACAACTTGTATGACCAATTCACAGAACTGTGAGTCTCTCA 806  
Qy 718 GTGTGCCCTTCACTTGTGATGAGCTTCTCAACAACTGCTCAACAACTGCTCACTCTCAGT 777  
Db 807 GTGCTACCCCTTCACTTGTGATGAGCTTCTCAACAACTGCTCAACAACTGCTCACTCTCAGT 866  
Qy 778 ACCTTGAAGAGCTGATTTGGTACCTAGAGCAGATCGATGCGAGTGGAGCTTGGACAGC 837  
Db 867 ACCTTGAAGAGCTTATTCGATATCTTGAACAGAGAGATGGCAGTTGACATAGAGAT 926  
Qy 838 CTCTAAGCCACATGCGAGCTTTTGGCAGGCTTCTCTGATGAGGAAAGAAAGCAAA 897  
Db 927 CTATATAGGCAACTTGGCACTTCTTGGCAAGCTTTTGTGTTTGAAGAAATCCAGA 986  
Qy 898 GTGGTGAATCTGAATCTCTCAAGGAGAGGTAAACTCTACAGCTGCAACCCCGGAC 957  
Db 987 GTGGTGAATCTGAATCTCTCAAGGAGAGGTAAAGATTTATACAGCTGCAACCTCTGTAAC 1046  
Qy 958 TTCTCAGTGTCCATAGGAGAGCTTAAAGAGAGAGATACCATATCTCTGAGGAGGTGT 1017  
Db 1047 TTCTCAGTGTCCATAGGAGAGCTTAAAGAGAGAGATACCATATCTCTGAGGAGGTGT 1106  
Qy 1018 CTCTGCTCAAGGCTGTGAGGAAATTTGCTGTTGTTCTCATATTTGCAATGAATGT 1077  
Db 1107 CTCTGCTTAAAGCTGTGGTGGAACTGTGCTGTTGTTCTCCAAATTTGCAATGAATGT 1166  
Qy 1078 CAGTGTGCTCAAGGCTGTGAGGAAATTTGCTGTTGTTCTCATATTTGCAATGAATGT 1137  
Db 1167 CAATGTGTCCCAAGAAATTTGCTGTTGTTCTCATATTTGCAATGAATGT 1226  
Qy 1138 ACTGGAGTCAAGGCTGTGAGGAAATTTGCTGTTGTTCTCATATTTGCAATGAATGT 1197  
Db 1227 ACCGTTGCTCAAGGCTGTGAGGAAATTTGCTGTTGTTCTCATATTTGCAATGAATGT 1286  
Qy 1198 TGTGACTGTGTGTGAGGAAATTTGCTGTTGTTCTCATATTTGCAATGAATGT 1254  
Db 1287 TGTGACTGTGTGTGAGGAAATTTGCTGTTGTTCTCATATTTGCAATGAATGT 1343

## RESULT 13

US-09-978-608A-487  
; Sequence 487, Application US/09978608A  
; Publication No. US20030045462A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas P.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C22  
; CURRENT APPLICATION NUMBER: US/09/978,608A  
; CURRENT FILING DATE: 2001-10-16  
; NUMBER OF SEQ ID NOS: 624  
; Prior Application removed - See File Wrapper or Palm  
; SEQ ID NO 487  
; LENGTH: 2849  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 2715  
; OTHER INFORMATION: unknown base  
US-09-978-608A-487

Query Match 62.0%; Score 914.2; DB 11; Length 2849;  
Best Local Similarity 83.5%; Pred. No. 4.6e-296;  
Matches 1050; Conservative 0; Mismatches 203; Indels 4; Gaps 1;  
Qy 2 ACCTGGAGACACAGAGAGGCTCTAGGAAAAATTTGGATGGGATATGTGGAACCTA 61  
Db 87 AACTGGAGACACAGAGAGGCTCTAGGAAAAATTTGGATGGGATATGTGGAACCTA 146  
Qy 62 CCCTGGGATTTCTCTGCGCAGAGCGCGCAGAGGCTTCCACCGCAGCGAGCTTTCCC 121  
Db 147 CCCTGGGATTTCTCTGCGCAGAGCGCGCAGAGGCTTCCACCGCAGCGAGCTTTCCC 206  
Qy 122 CGG---GCTGGGCTGAGGCTTTGAGTCTGCTTCCCGAGTGCCCGCGAGTGAGCC 177  
Db 207 TGGCGGTGGTGAAGAGACTCGGGAGTCTGCTTCCAAAGTGCCCGCGAGTGAGCT 266  
Qy 178 CTCGCCCGAGTCAGCCAAATGCTCTCTCTGGGCTCTCTCTGCTGATGATCTGCGCTGCC 237  
Db 267 CTCACCCCGAGTCAGCCAAATGAGCTCTCTCTGGGCTCTCTCTGCTGATGATCTGCGCTGCC 326  
Qy 238 GGCACAAAGAAAGCGGAGTCTCGGCTGAGTCCAACTGAGCAGCAAGTTGCGAGCTTCCAGC 297  
Db 327 GGCACAGACAGAGGAGTCTCGGCGGAATCCAACTGAGTAGTAATTTCCAGTTTCCAGC 386  
Qy 298 GACAAAGAAACAGAGGAGTCCAAAGATCCCGGCGATGAGAGAGTTGCTACTATCTGCT 357  
Db 397 AACAAAGAAACAGAGGAGTCCAAAGATCCCGGCGATGAGAGAGTTTACTGTGCTACT 446  
Qy 358 AATGGAGATCCACAGCGCGGAGTTCCTCTCATAGTACCGCAAGAAATATGCTGCTGCTG 417  
Db 447 AATGGAGATTCACAGCGCGGAGTTCCTCTCATAGTATTCACAGAAATACGCTTGGTA 506  
Qy 418 TGGAGATTAGTTCAGTAGATGAAAAATGTCGGGATCCAGCTGCAATTTGATGAGAGATT 477  
Db 507 TGGAGATTAGTTCAGTAGAGGAAAAATGATGGAATCAACTTACGTTTGTATGAGAGATT 566  
Qy 478 GGGCTGGAAGATCCAGAGAGGATATATGCAAGTATGATTTTGTAGAGTTGAGGAGCCC 537  
Db 567 GGGCTTGAAGACCCAGAGAGATGATATGCAAGTATGATTTTGTAGAGTTGAGGAGCCC 626  
Qy 538 AGTGATGGAAGTGTGTTTAGGACGCTGGTGTGGTTCTGGGACTGTGCGCAGGAAAGCAGACT 597  
Db 627 AGTGATGGAATCATATCAGGATAAGATTGATTTGATCTGATGAGTATTTTCCATCTGAACCC 686  
Qy 598 TCTAAAGGAAATCAATATCAGGATAAGATTGATTTGATCTGATGAGTATTTTCCATCTGAACCC 657  
Db 687 TCTAAAGGAAATCAATATCAGGATAAGATTGATTTGATCTGATGAGTATTTTCCATCTGAACCC 746  
Qy 658 GGATTTCTGATCCACTACAGTATTTATCATGCCCAAGTCAAGAAACACGAGTCTCTTCG 717

Db 747 GGGTCTGATCCACTACAACTTGTCTGATCCCACTTACAGAAAGCTGTGAGTCTTCA 806  
Qy 718 GTGTGCCCCCTTCATCTTTGTCTGATGGACCTGCTCAACAATGCTGTGACTGCTTCACT 777  
Db 807 GTGTGCCCCCTTCATCTTTGTCTGATGGACCTGCTCAACAATGCTGTGACTGCTTCACT 866  
Qy 778 ACCTTGAAGAGCTGTGATGCTTACCTAGAGCCAGATGCTGATGGAGGCTGTGAGCAGC 837  
Db 867 ACCTTGAAGAGCTGTGATGCTTACCTAGAGCCAGATGCTGATGGAGGCTGTGAGCAGC 926  
Qy 838 CTCTACAGGCAACATGCGACGCTTTTGGGCAAGGCTTCTGATGGAGGCAAAAGCAAA 897  
Db 927 CTATATAGGCAACTTGGCACTTCTTGGCAAGGCTTCTGATGGAGGCAAAAGCAAA 986  
Qy 898 GTGTGATCTGAATCTCTCAAGGAGAGGTTAAACTCTACAGCTGTCACACCCCGGAA 957  
Db 987 GTGTGATCTGAATCTCTCAAGGAGAGGTTAAACTCTACAGCTGTCACACCCCGGAA 1046  
Qy 958 TTCTCAGTGTCCATAGAGGAGGCTTAAAGAGGAGATACCATATTTCTGGCCAGGTTGT 1017  
Db 1047 TTCTCAGTGTCCATAGAGGAGGCTTAAAGAGGAGATACCATATTTCTGGCCAGGTTGT 1106  
Qy 1018 CTCTGCTCAAGGCTGTGAGGAAATTTGCTGCTGTGCTCTCATATTTGCAATGAATGT 1077  
Db 1107 CTCTGCTTAAACGCTGTGAGGAACTGTGCTGTGCTCTCATATTTGCAATGAATGT 1166  
Qy 1078 CAGTGTGTCCACGATGAAGTTACAAAAGATACCATGAGTCTTCTGAGTGAAGCCAAA 1137  
Db 1167 CAATGTGTCCACGATGAAGTTACAAAAGATACCATGAGTCTTCTGAGTGAAGCCAAA 1226  
Qy 1138 ACTGGAGTCAAGGATTTGCAATGATCACTCACTGATGTGGCTCTGGAACACACAGGAA 1197  
Db 1227 ACCGCTGTGAGGATTTGCAATGATCACTCACTGATGTGGCTCTGGAACACACAGGAA 1286  
Qy 1198 TGTGACTGTGTGTAGAGGAAAGCAGAGGAGTAACTGAGGCTTCTGAGCAGC 1254  
Db 1287 TGTGACTGTGTGTAGAGGAAAGCAGAGGAGTAACTGAGGCTTCTGAGCAGC 1343

## RESULT 14

US-09-978-585A-487  
; Sequence 487, Application US/09978585A  
; Publication No. US20030049633A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Flivaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C15  
; CURRENT APPLICATION NUMBER: US/09/978,585A  
; CURRENT FILING DATE: 2001-10-16  
; NUMBER OF SEQ ID NOS: 624  
; Prior Application removed - See File Wrapper or Palm  
; SEQ ID NO 487  
; LENGTH: 2849  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 2715  
; OTHER INFORMATION: unknown base  
; US-09-978-585A-487

Query Match 62.0%; Score 914.2; DB 11; Length 2849;  
Best Local Similarity 83.5%; Pred. No. 4.6e-296;  
Matches 1050; Conservative 0; Mismatches 203; Indels 4; Gaps 1;

Qy 2 ACCTGGAGACACACAGAGGGCTCTAGGAAAAATTTGGATGGGATTTATGTGGAACCTA 61  
Db 87 AACCTGGAGACACAGAGGGCTCTAGGAAAAATTTGGATGGGATTTATGTGGAACCTA 146  
Qy 62 CCCTGCGATTTCTCTGCTGCCAGAGCCGGCCAGAGGCTTCCACCCGACGAGCCTTTCCC 121  
Db 147 CCCTGCGATTTCTCTGCTGCCAGAGGCTCGGGCTTCCACCCGACGAGCCTTTCCC 206  
Qy 122 CGG----GCTGGGCTGAGCCTTGGAGTGTGCTTCCCGAGTCCCGCCGCGAGTGAGCC 177  
Db 207 TGGCGGTGGTGAAGAGACTCGGAGTGTGCTTCCAAAGTCCCGCGTGTGAGTGTGAGCT 266  
Qy 178 CTGCCCCCAGTCAGCCAAATGCTCTCTCGGCTCTCTCTGCTGATCTGCTGCTGCTGCTG 237  
Db 267 CTACCCCGAGTCAGCCAAATGAGGCTTCTCGGCTTCTCTGCTGATCTGCTGCTGCTG 326  
Qy 238 GGCACAAAGAACGGGAGTCTGGGCTGTAGTCCAACTGAGCAGCAAGTTGCAAGCTCTCCAGC 297  
Db 327 GGCACAGACAGGGGAGTCTGAGGGGAACTCAACCTGAGTAGTAAATTTCCAGTTTTCAGC 386  
Qy 298 GACAAGGAACAGAACGAGTGCAAGATCCCGGATGAGAGAGTTGTCACTATATCTGTT 357  
Db 387 AACAAAGAAACAGAACGAGTGCAAGATCCCTCAGCATGAGAGAAATTTACTGTCTACT 446  
Qy 358 AATGGAGCATTCACACGCCGAAAGTTTCTCATACGTATCCCAAGAAATATGTGTGCTG 417  
Db 447 AATGGAAGTATTTCACAGCCCAAGGTTTCTCTCATACTTTATCCAAAGAAATACGGTCTTGGTA 506  
Qy 418 TGGAGATTAGTTCAGTAGATGAAAATGTGCGGATCCAGCTGACATTTGATGAGAGATTT 477  
Db 507 TGGAGATTAGTTCAGTAGAGGAAATGTATGATACAACTTACGTTTGTATGAAAGATTT 566  
Qy 478 GGGCTGGAAGATCCAGAAAGCATATATGCAAGTATGATTTTGTAGAGTTGAGGAGCCC 537  
Db 567 GGGCTTGAAGACCCAGAAAGATGACATATGCAAGTATGATTTTGTAGAAAGTTGAGGAAACC 626  
Qy 538 AGTCATGGAAGTGTTTTAGGAGCTGTGTGTGTTCTGGGAGTGTGCGCAGGAAGAGAGCT 597  
Db 627 AGTCATGGAAGTGTTTTAGGAGCTGTGTGTGTTCTGGGAGTGTGCGCAGGAAGAGAGCT 686  
Qy 598 TCTAAAGGAATCATATCAGGATAAGATTTGTATCTGATGAGTATTTTCCATCTGAACCC 657  
Db 687 TCTAAAGGAATCAATTAGGATAAGATTTGTATCTGATGAGTATTTTCTCTCTGAACCA 746  
Qy 558 GGATTTGCTGATCTCAGTACAGTATTTATCATGCCACAGATCAAGAAACAGAGCTCTTCG 717  
Db 747 GGGTTCTGATCTCCACTACATTTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 806  
Qy 718 GTGTGCCCCCTTCTCATCTTTGTGATGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 777  
Db 807 GTGTGCCCCCTTCTCATCTTTGTGATGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 866  
Qy 778 ACCTTGAAGAGCTGTGATTCGGTACCTAGACCCAGATGCGAGGTGGAGCTTGGACAGC 837



;; PRIOR FILING DATE: 1998-04-15  
;; PRIOR APPLICATION NUMBER: 60/081817  
;; PRIOR FILING DATE: 1998-04-15  
;; PRIOR APPLICATION NUMBER: 60/081819  
;; PRIOR FILING DATE: 1998-04-15  
;; PRIOR APPLICATION NUMBER: 60/081952  
;; PRIOR FILING DATE: 1998-04-15  
;; PRIOR APPLICATION NUMBER: 60/081838  
;; PRIOR FILING DATE: 1998-04-15  
;; PRIOR APPLICATION NUMBER: 60/082568  
;; PRIOR FILING DATE: 1998-04-21  
;; PRIOR APPLICATION NUMBER: 60/082569  
;; PRIOR FILING DATE: 1998-04-21  
;; PRIOR APPLICATION NUMBER: 60/082704  
;; PRIOR FILING DATE: 1998-04-22  
;; PRIOR APPLICATION NUMBER: 60/082804  
;; PRIOR FILING DATE: 1998-04-22  
;; PRIOR APPLICATION NUMBER: 60/082700  
;; PRIOR FILING DATE: 1998-04-22  
;; PRIOR APPLICATION NUMBER: 60/082797  
;; PRIOR FILING DATE: 1998-04-22  
;; PRIOR APPLICATION NUMBER: 60/082796  
;; PRIOR FILING DATE: 1998-04-23  
;; PRIOR APPLICATION NUMBER: 60/083336  
;; PRIOR FILING DATE: 1998-04-27  
;; PRIOR APPLICATION NUMBER: 60/083322  
;; PRIOR FILING DATE: 1998-04-28  
;; PRIOR APPLICATION NUMBER: 60/083392  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083495  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083496  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083499  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083545  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083554  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083558  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083559  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083500  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083742  
;; PRIOR FILING DATE: 1998-04-30  
;; PRIOR APPLICATION NUMBER: 60/084366  
;; PRIOR FILING DATE: 1998-05-05  
;; PRIOR APPLICATION NUMBER: 60/084414  
;; PRIOR FILING DATE: 1998-05-06  
;; PRIOR APPLICATION NUMBER: 60/084441  
;; PRIOR FILING DATE: 1998-05-06  
;; PRIOR APPLICATION NUMBER: 60/084637  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/084639  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/084640  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/084598  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/084600  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/084627  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/084643  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/085339  
;; PRIOR FILING DATE: 1998-05-13  
;; PRIOR APPLICATION NUMBER: 60/085338  
;; PRIOR FILING DATE: 1998-05-13  
;; PRIOR APPLICATION NUMBER: 60/085323  
;; PRIOR FILING DATE: 1998-05-13

;; PRIOR APPLICATION NUMBER: 60/085582  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085700  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085689  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085579  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085580  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085573  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085704  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 29.0%; Score 914.2; DB 11; Length 2849;  
Best Local Similarity 83.5%; Pred. No. 4.6e-296;  
Matches 1050; Conservative 0; Mismatches 203; Indels 4; Gaps 1;

QY	2	ACCTGGACACACAGAGGGCTCTAGGAAAAATTTGGATGGGATATATGGAACCTA	61
Db	87	AACCTGGACACACAGAGGGCTCTAGGAAAAATTTGGATGGGATATATGGAACCTA	146
QY	62	CCCTGCGATTCTCTGCTGCCAGAGCCGGCCAGAGGCTTCCACCCGAGCAGCCTTCCC	121
Db	147	CCCTGCGATTCTCTGCTGCCAGAGAGGCTCGGGCGCTTCCACCCGAGCAGCCTTCCC	206
QY	122	CGG-----GCTGGGCTGAGCCTTGAGTCTGCTTCCCGAGTCCCGCGGAGTGAGCC	177
Db	207	TGGGGGCTGAGGAGCTCGGGAGTCTGCTTCCAAAGTCCCGCGGAGTGAGCT	266
QY	178	CTCGCCCGAGTCAGCCAAATGCTCTCTCGGCGCTCTCTCTGCTGACATCTGCCCTGGCC	237
Db	267	CTCACCCCGAGTCAGCCAAATGAGCTCTTGGGGCTTCTCTGCTGACATCTGCCCTGGCC	326
QY	238	GGCCAAAGAACGGGAGCTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCGAGCTCTCCAGC	297
Db	327	GGCCAGAGACAGGGGAGCTCAGGCGGAATCCAACTGAGTAGTAATATCCAGTTTCCAGC	386
QY	298	GACAGGAACAGACGGAGTCCAGATCCCGGCGATCAGAGAGTGTGACATATATCTGGT	357
Db	387	AACAGGAACAGACGGAGTCCAGATCCCGGCGATCAGAGAGTGTGACATATATCTGGT	446
QY	358	AATGGAGCATCCACAGCCCGAAGTTCTCTCATAGTACCAAGATCCCAAGAAATATGGTGGT	417
Db	447	AATGGAGTATTCACAGCCCAAGTTTCTCTCATAGTACCAAGATCCCAAGAAATATGGTGGT	506
QY	418	TGGAGATTAGTTCAGTAGATGAAATGTGGGATCCAGCTGACATTTGATGAGAGATT	477
Db	507	TGGAGATTAGTTCAGTAGAGAAATGTATGGATACACTTACGTTTGTATGAAAGATT	566
QY	478	GGGCTGGAAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAGTTGAGGAGCCC	537
Db	567	GGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTTGTAGAGTTGAGGAGCCC	626
QY	538	AGTGAATGAAGTGTGTTAGGAGCGTGGTGGTCTGGGCTGTCGAGGAAAGCAGACT	597
Db	627	AGTGAATGAAGTGTGTTAGGAGCGTGGTGGTCTGGGCTGTCGAGGAAAGCAGACT	686
QY	598	TCTAAAGGAAATCATATATCAGGATTAAGATTGTATCTGATGAGTATTTTCCATCTGAACCC	657
Db	687	TCTAAAGGAAATCAATATGAGTAAAGATTGTATCTGATGAATATTTTCTTCTGAACCA	746
QY	658	GGATTCTGATCCACTACAGTATTTATCATGCCACAGTCCAGAAACCAAGAGTCTCTCG	717
Db	747	GGTTCTGATCCACTACAGTATTTATCATGCCACAGTCCAGAAACCAAGAGTCTCTCG	806
QY	718	GTGTTGCCCTTCTCATCTTTGATGAGAGTCTGCTCAACAAATGTGTGATGCTGCTTCAGT	777
Db	807	GTGTTGCCCTTCTCATCTTTGATGAGAGTCTGCTCAACAAATGTGTGATGCTGCTTCAGT	866
QY	778	ACCTTGGAGAGCTGATTCGGTACCTAGAGCGGAGATCGAGGCGGTGGAGCTTGGACAGC	837

[illegible]

Search completed: November 26, 2003, 09:32:33  
Job time : 366.884 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 25, 2003, 23:55:21 ; Search time 3146.15 Seconds  
(without alignments)  
15537.553 Million cell updates/sec

Title: US-09-852-209A-6

Perfect score: 1474

Sequence: 1 cactcgagacacagaagag.....aatcacaagcactgcacg 1474

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 33363688 seqs, 16581889874 residues

Total number of hits satisfying chosen parameters: 66727376

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending\_Patents\_NA\_Main:\*

1: /cgn2\_6/ptodata/2/pna/PCTUS COMB.seq.\*  
2: /cgn2\_6/ptodata/2/pna/PCTUS COMB.seq.old.\*  
3: /cgn2\_6/ptodata/2/pna/US06 COMB.seq.\*  
4: /cgn2\_6/ptodata/2/pna/US07 COMB.seq.\*  
5: /cgn2\_6/ptodata/2/pna/US08 COMB.seq.\*  
6: /cgn2\_6/ptodata/2/pna/US081 COMB.seq.\*  
7: /cgn2\_6/ptodata/2/pna/US082 COMB.seq.\*  
8: /cgn2\_6/ptodata/2/pna/US083 COMB.seq.\*  
9: /cgn2\_6/ptodata/2/pna/US084 COMB.seq.\*  
10: /cgn2\_6/ptodata/2/pna/US085 COMB.seq.\*  
11: /cgn2\_6/ptodata/2/pna/US086 COMB.seq.\*  
12: /cgn2\_6/ptodata/2/pna/US087 COMB.seq.\*  
13: /cgn2\_6/ptodata/2/pna/US088 COMB.seq.\*  
14: /cgn2\_6/ptodata/2/pna/US089 COMB.seq.\*  
15: /cgn2\_6/ptodata/2/pna/US090 COMB.seq.\*  
16: /cgn2\_6/ptodata/2/pna/US091 COMB.seq.\*  
17: /cgn2\_6/ptodata/2/pna/US092A COMB.seq.\*  
18: /cgn2\_6/ptodata/2/pna/US092B COMB.seq.\*  
19: /cgn2\_6/ptodata/2/pna/US093A COMB.seq.\*  
20: /cgn2\_6/ptodata/2/pna/US093B COMB.seq.\*  
21: /cgn2\_6/ptodata/2/pna/US094 COMB.seq.\*  
22: /cgn2\_6/ptodata/2/pna/US095A COMB.seq.\*  
23: /cgn2\_6/ptodata/2/pna/US095B COMB.seq.\*  
24: /cgn2\_6/ptodata/2/pna/US095C COMB.seq.\*  
25: /cgn2\_6/ptodata/2/pna/US095D COMB.seq.\*  
26: /cgn2\_6/ptodata/2/pna/US096A COMB.seq.\*  
27: /cgn2\_6/ptodata/2/pna/US096B COMB.seq.\*  
28: /cgn2\_6/ptodata/2/pna/US096C COMB.seq.\*  
29: /cgn2\_6/ptodata/2/pna/US096D COMB.seq.\*  
30: /cgn2\_6/ptodata/2/pna/US096E COMB.seq.\*  
31: /cgn2\_6/ptodata/2/pna/US097A COMB.seq.\*  
32: /cgn2\_6/ptodata/2/pna/US097B COMB.seq.\*  
33: /cgn2\_6/ptodata/2/pna/US097C COMB.seq.\*  
34: /cgn2\_6/ptodata/2/pna/US098A COMB.seq.\*  
35: /cgn2\_6/ptodata/2/pna/US098B COMB.seq.\*  
36: /cgn2\_6/ptodata/2/pna/US098C COMB.seq.\*  
37: /cgn2\_6/ptodata/2/pna/US098D COMB.seq.\*  
38: /cgn2\_6/ptodata/2/pna/US099A COMB.seq.\*  
39: /cgn2\_6/ptodata/2/pna/US099B COMB.seq.\*  
40: /cgn2\_6/ptodata/2/pna/US099C COMB.seq.\*  
41: /cgn2\_6/ptodata/2/pna/US099D COMB.seq.\*  
42: /cgn2\_6/ptodata/2/pna/US099E COMB.seq.\*  
43: /cgn2\_6/ptodata/2/pna/US099F COMB.seq.\*

44: /cgn2\_6/ptodata/2/pna/US100A COMB.seq.\*  
45: /cgn2\_6/ptodata/2/pna/US100B COMB.seq.\*  
46: /cgn2\_6/ptodata/2/pna/US101A COMB.seq.\*  
47: /cgn2\_6/ptodata/2/pna/US101B COMB.seq.\*  
48: /cgn2\_6/ptodata/2/pna/US102A COMB.seq.\*  
49: /cgn2\_6/ptodata/2/pna/US102B COMB.seq.\*  
50: /cgn2\_6/ptodata/2/pna/US103A COMB.seq.\*  
51: /cgn2\_6/ptodata/2/pna/US103B COMB.seq.\*  
52: /cgn2\_6/ptodata/2/pna/US104A COMB.seq.\*  
53: /cgn2\_6/ptodata/2/pna/US104B COMB.seq.\*  
54: /cgn2\_6/ptodata/2/pna/US6000 COMB.seq.\*  
55: /cgn2\_6/ptodata/2/pna/US6001 COMB.seq.\*  
56: /cgn2\_6/ptodata/2/pna/US6002 COMB.seq.\*  
57: /cgn2\_6/ptodata/2/pna/US6003 COMB.seq.\*  
58: /cgn2\_6/ptodata/2/pna/US6004 COMB.seq.\*  
59: /cgn2\_6/ptodata/2/pna/US6005 COMB.seq.\*  
60: /cgn2\_6/ptodata/2/pna/US6006 COMB.seq.\*  
61: /cgn2\_6/ptodata/2/pna/US6007 COMB.seq.\*  
62: /cgn2\_6/ptodata/2/pna/US6008 COMB.seq.\*  
63: /cgn2\_6/ptodata/2/pna/US6009 COMB.seq.\*  
64: /cgn2\_6/ptodata/2/pna/US6010 COMB.seq.\*  
65: /cgn2\_6/ptodata/2/pna/US6011 COMB.seq.\*  
66: /cgn2\_6/ptodata/2/pna/US6012 COMB.seq.\*  
67: /cgn2\_6/ptodata/2/pna/US6013 COMB.seq.\*  
68: /cgn2\_6/ptodata/2/pna/US6014 COMB.seq.\*  
69: /cgn2\_6/ptodata/2/pna/US6015 COMB.seq.\*  
70: /cgn2\_6/ptodata/2/pna/US6016 COMB.seq.\*  
71: /cgn2\_6/ptodata/2/pna/US6017 COMB.seq.\*  
72: /cgn2\_6/ptodata/2/pna/US6018 COMB.seq.\*  
73: /cgn2\_6/ptodata/2/pna/US6019 COMB.seq.\*  
74: /cgn2\_6/ptodata/2/pna/US6020 COMB.seq.\*  
75: /cgn2\_6/ptodata/2/pna/US6021 COMB.seq.\*  
76: /cgn2\_6/ptodata/2/pna/US6022 COMB.seq.\*  
77: /cgn2\_6/ptodata/2/pna/US6023A COMB.seq.\*  
78: /cgn2\_6/ptodata/2/pna/US6023B COMB.seq.\*  
79: /cgn2\_6/ptodata/2/pna/US6024 COMB.seq.\*  
80: /cgn2\_6/ptodata/2/pna/US6025 COMB.seq.\*  
81: /cgn2\_6/ptodata/2/pna/US6026 COMB.seq.\*  
82: /cgn2\_6/ptodata/2/pna/US6027 COMB.seq.\*  
83: /cgn2\_6/ptodata/2/pna/US6028 COMB.seq.\*  
84: /cgn2\_6/ptodata/2/pna/US6029 COMB.seq.\*  
85: /cgn2\_6/ptodata/2/pna/US6030 COMB.seq.\*  
86: /cgn2\_6/ptodata/2/pna/US6031 COMB.seq.\*  
87: /cgn2\_6/ptodata/2/pna/US6032 COMB.seq.\*  
88: /cgn2\_6/ptodata/2/pna/US6033 COMB.seq.\*  
89: /cgn2\_6/ptodata/2/pna/US6034 COMB.seq.\*  
90: /cgn2\_6/ptodata/2/pna/US6035 COMB.seq.\*  
91: /cgn2\_6/ptodata/2/pna/US6036 COMB.seq.\*  
92: /cgn2\_6/ptodata/2/pna/US6037 COMB.seq.\*  
93: /cgn2\_6/ptodata/2/pna/US6038 COMB.seq.\*  
94: /cgn2\_6/ptodata/2/pna/US6039 COMB.seq.\*  
95: /cgn2\_6/ptodata/2/pna/US6040 COMB.seq.\*  
96: /cgn2\_6/ptodata/2/pna/US6041 COMB.seq.\*  
97: /cgn2\_6/ptodata/2/pna/US6042 COMB.seq.\*  
98: /cgn2\_6/ptodata/2/pna/US6043 COMB.seq.\*  
99: /cgn2\_6/ptodata/2/pna/US6044 COMB.seq.\*  
100: /cgn2\_6/ptodata/2/pna/US6045 COMB.seq.\*  
101: /cgn2\_6/ptodata/2/pna/US6046 COMB.seq.\*  
102: /cgn2\_6/ptodata/2/pna/US6047 COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1473	99.9	1474	1	PCT-US99-23668-6
2	1473	99.9	1474	2	PCT-US99-23668-6
3	1473	99.9	1474	21	US-09-410-349A-6
4	1473	99.9	1474	35	US-09-852-209-6

Sequence 6, Appli  
Sequence 6, Appli  
Sequence 6, Appli

5 1473 99.9 1474 35 US-09-852-209A-6  
6 1473 99.9 1474 46 US-10-131-600-6  
7 1473 99.9 1474 50 US-10-303-997B-6  
8 1444.8 98.0 3571 24 US-09-540-707-3  
9 1444.8 98.0 3571 24 US-09-541-752-42  
10 1444.8 98.0 3571 30 US-09-695-121-3  
11 1444.8 98.0 3571 31 US-09-706-968-42  
12 1444.8 98.0 3571 34 US-09-823-033-3  
13 1444.8 98.0 3571 46 US-10-139-583-42  
14 1444.8 98.0 3571 49 US-10-264-361-3  
15 1432.8 97.2 3573 19 US-09-304-216-34  
16 1154.4 78.3 2376 46 US-10-144-771-11108  
17 1154.4 78.3 2376 91 US-09-360-207-11108  
18 914.2 62.0 2878 82 US-09-278-258-1879  
19 914.2 62.0 2825 16 US-09-184-216-1  
20 914.2 62.0 2825 32 US-09-723-749-1  
21 914.2 62.0 2825 47 US-10-178-442-1  
22 914.2 62.0 2827 46 US-10-110-594-1  
23 914.2 62.0 2828 28 US-09-644-868-8135  
24 914.2 62.0 2828 28 US-09-652-353-9531  
25 914.2 62.0 2828 28 US-09-652-913-9239  
26 914.2 62.0 2828 28 US-09-652-916-8985  
27 914.2 62.0 2839 2 PCT-US99-31025-1  
28 914.2 62.0 2839 2 PCT-US99-31025-1  
29 914.2 62.0 2839 17 US-09-223-546-1  
30 914.2 62.0 2839 21 US-09-471-179-1  
31 914.2 62.0 2839 25 US-09-599-596-1  
32 914.2 62.0 2839 33 US-09-796-753-5  
33 914.2 62.0 2849 1 PCT-US01-43523-285  
34 914.2 62.0 2849 1 PCT-US02-24562-285  
35 914.2 62.0 2849 2 PCT-US01-43523-285  
36 914.2 62.0 2849 18 US-09-267-213-1  
37 914.2 62.0 2849 30 US-09-380-138-487  
38 914.2 62.0 2849 38 US-09-918-585A-487  
39 914.2 62.0 2849 39 US-09-929-404-1  
40 914.2 62.0 2849 42 US-09-978-187B-487  
41 914.2 62.0 2849 42 US-09-978-188A-487  
42 914.2 62.0 2849 42 US-09-978-189-487  
43 914.2 62.0 2849 42 US-09-978-191A-487  
44 914.2 62.0 2849 42 US-09-978-192-487  
45 914.2 62.0 2849 42 US-09-978-192A-487

## ALIGNMENTS

RESULT 1  
PCT-US99-22668-6  
; Sequence 6, Application PC/TUS9922668B  
; GENERAL INFORMATION:  
; APPLICANT: HELSINKI UNIVERSITY FOR CANCER RESEARCH  
; APPLICANT: LUDWIG INSTITUTE FOR CANCER RESEARCH  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C,  
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF  
; FILE REFERENCE: PCT/US99/22669-LUDWIG INST FOR CANCER  
; CURRENT APPLICATION NUMBER: PCT/US99/22668B  
; CURRENT FILING DATE: 1999-09-30  
; EARLIER APPLICATION NUMBER: 60/102,461  
; EARLIER FILING DATE: 1998-09-30  
; EARLIER APPLICATION NUMBER: 60/108,109  
; EARLIER FILING DATE: 1998-11-12  
; EARLIER APPLICATION NUMBER: 60/110,749  
; EARLIER FILING DATE: 1998-12-03  
; EARLIER APPLICATION NUMBER: 60/113,002  
; EARLIER FILING DATE: 1998-12-18  
; EARLIER APPLICATION NUMBER: 60/135,426  
; EARLIER FILING DATE: 1999-05-21  
; EARLIER APPLICATION NUMBER: 60/144,022  
; EARLIER FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 1474

; TYPE: DNA  
; ORGANISM: Murinae gen. sp.  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1447)  
; OTHER INFORMATION: a, c, g or t  
PCT-US99-22668-6  
  
Query Match 99.9%; Score 1473; DB 1; Length 1474;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CACCTGGAGACACAGAGAGGGCTCTAGGAAATTTTGGATGGGATTTATGGAACT 60  
DB 1 CACCTGGAGACACAGAGAGGGCTCTAGGAAATTTTGGATGGGATTTATGGAACT 60  
QY 61 ACCCTGGGATTTCTCTGCTGCCAGAGCGCGCTTCCACCGCAGCGAGCTTTTC 120  
DB 61 ACCCTGGGATTTCTCTGCTGCCAGAGCGCGCTTCCACCGCAGCGAGCTTTTC 120  
QY 121 CCGGGCTGGGCTGAGCCCTTGGAGTCGTGCTTCCCGAGTCCCGCCGCGAGTGGCCCTC 180  
DB 121 CCGGGCTGGGCTGAGCCCTTGGAGTCGTGCTTCCCGAGTCCCGCCGCGAGTGGCCCTC 180  
QY 181 GCCCAGTCAGCCAAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCCCTGGCCGCGC 240  
DB 181 GCCCAGTCAGCCAAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCCCTGGCCGCGC 240  
QY 241 CAAAGAACGGGAGCTCGGGCTGAGTCCAACTTGAGAGCAAGTTGCAAGTCTCCAGGAC 300  
DB 241 CAAAGAACGGGAGCTCGGGCTGAGTCCAACTTGAGAGCAAGTTGCAAGTCTCCAGGAC 300  
QY 301 AAGGAACAGAGCAGAGTGCAGATCCCGGCGATCAGAGAGTTGTCATATCTGGTAAT 360  
DB 301 AAGGAACAGAGCAGAGTGCAGATCCCGGCGATCAGAGAGTTGTCATATCTGGTAAT 360  
QY 361 GGGAGCATCCA CAGCCCGAGTTTCTCATACGTACCAAGAAATATGGTCTGGTGG 420  
DB 361 GGGAGCATCCA CAGCCCGAGTTTCTCATACGTACCAAGAAATATGGTCTGGTGG 420  
QY 421 AGATTAGTTCAGTAGATGAAATGCGGATCCAGCTGACATTTGATGAGAGATTTGGG 480  
DB 421 AGATTAGTTCAGTAGATGAAATGCGGATCCAGCTGACATTTGATGAGAGATTTGGG 480  
QY 481 CTGGAAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAGTTGAGGAGCCAGT 540  
DB 481 CTGGAAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAGTTGAGGAGCCAGT 540  
QY 541 GATGGAAGTGTGTTAGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
DB 541 GATGGAAGTGTGTTAGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
QY 601 AAAGGAATCATATCAGGATTAAGTGTATCTCATGAGTATTTTCCATCTGAACCCGGA 660  
DB 601 AAAGGAATCATATCAGGATTAAGTGTATCTCATGAGTATTTTCCATCTGAACCCGGA 660  
QY 661 TTTCGATCCATCAGTATTTATCATGCCCAAGTTCACAGAAACAGAGTCTTCGGTG 720  
DB 661 TTTCGATCCATCAGTATTTATCATGCCCAAGTTCACAGAAACAGAGTCTTCGGTG 720  
QY 721 TTGCCCCCTTCATCTTTGTCATTCGACCTGCTCAACAACTGCTGCTGCTGCTGCTGCT 780  
DB 721 TTGCCCCCTTCATCTTTGTCATTCGACCTGCTCAACAACTGCTGCTGCTGCTGCTGCT 780  
QY 781 TTGGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGGATCTGGACAGCTC 840  
DB 781 TTGGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGGATCTGGACAGCTC 840  
QY 841 TACAGCCCAACATGGCAGCTTTTGGGCAAGGCTTTTCCGTATGCGGAAAGAAAGAGTG 900  
DB 841 TACAGCCCAACATGGCAGCTTTTGGGCAAGGCTTTTCCGTATGCGGAAAGAAAGAGTG 900  
QY 901 GTGAATCTGAAATCTCTCCTCAGGAAAGAGTAAACTCTACAGCTGCACACCCCGGAATTC 960

Db 901 GTGAATCTGAATCTCTCAAGGAAGAGGTAAGAACTCTACAGCTGCACACCCCGAACTTC 960  
Qy 961 TCAGTGTCCATACAGGGAAGAGCTAAAGAGACAGATACCATATTTCTGGCCAGGTTGTCTC 1020  
Db 961 TCAGTGTCCATACAGGGAAGAGCTAAAGAGACAGATACCATATTTCTGGCCAGGTTGTCTC 1020  
Qy 1021 CTGTCGAAGCGCTGTGAGGAATTTGTCCTGTGTCTTCATTAATTCGAATGAATGTCAG 1080  
Db 1021 CTGTCGAAGCGCTGTGAGGAATTTGTCCTGTGTCTTCATTAATTCGAATGAATGTCAG 1080  
Qy 1081 TGTGTCCACGTAAAGTTACAAAAGTACCATGAGTCTTCCAGTTTGAGACCAAAAAC 1140  
Db 1081 TGTGTCCACGTAAAGTTACAAAAGTACCATGAGTCTTCCAGTTTGAGACCAAAAAC 1140  
Qy 1141 GGAGTCAAGGATTCGATAAGTCACTCACTGATGTGCTCTGGAAACACACGAGGAATGT 1200  
Db 1141 GGAGTCAAGGATTCGATAAGTCACTCACTGATGTGCTCTGGAAACACACGAGGAATGT 1200  
Qy 1201 GACTGTGTGTAGAGAAAGCGAGGAGGTAACTGAGGCTTCGTAGACGACACGTCG 1260  
Db 1201 GACTGTGTGTAGAGAAAGCGAGGAGGTAACTGAGGCTTCGTAGACGACACGTCG 1260  
Qy 1261 GCACTGTCATCTGTGTACCCCAACAGCAACCTTCATCCCAAGCGGTGGCCGACG 1320  
Db 1261 GCACTGTCATCTGTGTACCCCAACAGCAACCTTCATCCCAAGCGGTGGCCGACG 1320  
Qy 1321 GCTCTGAGTCTGATGCTGCTATGCTAAAGATCTTACTCTCCCAACCAATTTCTCA 1380  
Db 1321 GCTCTGAGTCTGATGCTGCTATGCTAAAGATCTTACTCTCCCAACCAATTTCTCA 1380  
Qy 1381 GTTCTGTCTCAATAGCTTCCCTGACGACTTCAAGTGTCTTAAAGACCAAGAG 1440  
Db 1381 GTTCTGTCTCAATAGCTTCCCTGACGACTTCAAGTGTCTTAAAGACCAAGAG 1440  
Qy 1441 CACCAANAGGAGTCAATCACAAGCACTGCACCG 1474  
Db 1441 CACCAANAGGAGTCAATCACAAGCACTGCACCG 1474

## RESULT 2

PCT-US99-22668-6  
; Sequence 6, Application PC/TUS9922668B  
; GENERAL INFORMATION:  
; APPLICANT: LUDWIG INSTITUTE FOR CANCER RESEARCH  
; APPLICANT: HELSINKI UNIVERSITY LICENSING LTD.  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING  
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF  
; FILE REFERENCE: PCT/US99/22669-LUDWIG INST FOR CANCER  
; CURRENT APPLICATION NUMBER: PCT/US99/22668B  
; CURRENT FILING DATE: 1998-09-30  
; EARLIER APPLICATION NUMBER: 60/102,461  
; EARLIER FILING DATE: 1998-09-30  
; EARLIER APPLICATION NUMBER: 60/108,109  
; EARLIER FILING DATE: 1998-11-12  
; EARLIER APPLICATION NUMBER: 60/110,749  
; EARLIER FILING DATE: 1998-12-03  
; EARLIER APPLICATION NUMBER: 60/113,002  
; EARLIER FILING DATE: 1998-12-18  
; EARLIER APPLICATION NUMBER: 60/135,426  
; EARLIER FILING DATE: 1999-05-21  
; EARLIER APPLICATION NUMBER: 60/144,022  
; EARLIER FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 1474  
; TYPE: DNA  
; ORGANISM: Murinae gen. sp.  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1447)  
; OTHER INFORMATION: a, c, g or t

PCT-US99-22668-6  
Query Match  
Best Local Similarity 99.9%; Score 1473; DB 2; Length 1474;  
Matches 1474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CACCTGGAGACACAGAGAGGGCTCTAGGAAATTTTGGATGGGATTTATGGAAC 60  
Db 1 CACCTGGAGACACAGAGAGGGCTCTAGGAAATTTTGGATGGGATTTATGGAAC 60  
Qy 61 ACCCTGGGATTTCTCTGCTGCGAGCGCGCGCTTCCACCGACGCGAGCCTTTCC 120  
Db 61 ACCCTGGGATTTCTCTGCTGCGAGCGCGCGCTTCCACCGACGCGAGCCTTTCC 120  
Qy 121 CCGGCTGGGCTGAGCCCTTGGAGTGTCTTCCAGTGTCCCGCCCGCGAGTGAACCTC 180  
Db 121 CCGGCTGGGCTGAGCCCTTGGAGTGTCTTCCAGTGTCCCGCCCGCGAGTGAACCTC 180  
Qy 181 GCCCAGTACGCCAAATGCTCTCTGCGCTCTCTCTGCTGATCATCTGCTTGGCCGC 240  
Db 181 GCCCAGTACGCCAAATGCTCTCTGCGCTCTCTCTGCTGATCATCTGCTTGGCCGC 240  
Qy 241 CAAAGAACGGGACTCGGGCTGAGTCAACTGAGCAGCAAGTTGCACTATCTGTAAT 300  
Db 241 CAAAGAACGGGACTCGGGCTGAGTCAACTGAGCAGCAAGTTGCACTATCTGTAAT 300  
Qy 301 AAGGAACAGACGAGTGCAGATCCCGGCTGAGAGAGTTGTCATATCTGTAAT 360  
Db 301 AAGGAACAGACGAGTGCAGATCCCGGCTGAGAGAGTTGTCATATCTGTAAT 360  
Qy 361 GGGAGCATCCACAGCCCGAAGTTTCTCTACATGATGATGATGATGATGATGATG 420  
Db 361 GGGAGCATCCACAGCCCGAAGTTTCTCTACATGATGATGATGATGATGATGATG 420  
Qy 421 AGATTAGTGTGAGTGAATGAAATGTCGGATCCAGCTGATGATGATGATGATGATG 480  
Db 421 AGATTAGTGTGAGTGAATGAAATGTCGGATCCAGCTGATGATGATGATGATGATG 480  
Qy 481 CTGGAAGATCCAGAGACGATATATGCAAGTATGATGATGATGATGATGATGATG 540  
Db 481 CTGGAAGATCCAGAGACGATATATGCAAGTATGATGATGATGATGATGATGATG 540  
Qy 541 GATGGAAGTGTGATGAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
Db 541 GATGGAAGTGTGATGAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
Qy 601 AAAGGAATCATATCAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
Db 601 AAAGGAATCATATCAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
Qy 661 TTCTGCATCCATCAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 720  
Db 661 TTCTGCATCCATCAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 720  
Qy 721 TTGCCCCCTTCTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 780  
Db 721 TTGCCCCCTTCTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 780  
Qy 781 TTGGAAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840  
Db 781 TTGGAAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840  
Qy 841 TACAGCCCAACATGCGAGCTTTTGGCAAGGCTTCTGATGATGATGATGATGATGATG 900  
Db 841 TACAGCCCAACATGCGAGCTTTTGGCAAGGCTTCTGATGATGATGATGATGATGATG 900  
Qy 901 GTGAATCTGAATCTCTCAAGGAAGAGTAAATCTTACAGCTGCACACCCCGAACTTC 960  
Db 901 GTGAATCTGAATCTCTCAAGGAAGAGTAAATCTTACAGCTGCACACCCCGAACTTC 960  
Qy 961 TCAGTGTCCATACCGGAGAGCTTAAAGAGGACAGATACCATATTTCTGGCCAGGTTGTCTC 1020  
Db 961 TCAGTGTCCATACCGGAGAGCTTAAAGAGGACAGATACCATATTTCTGGCCAGGTTGTCTC 1020

QY 1021 CTGCTCAAGCGCTGTGGAGAAATTTGGCTGTGTCTCATTAATTCGAATGATGTCAG 1080  
Db 1021 CTGCTCAAGCGCTGTGGAGAAATTTGGCTGTGTCTCATTAATTCGAATGATGTCAG 1080  
QY 1081 TGTGTCCACGTAAGATTACAAAAGAGTACCATGAGTCTTTCAGTTGAGACCAAAACT 1140  
Db 1081 TGTGTCCACGTAAGATTACAAAAGAGTACCATGAGTCTTTCAGTTGAGACCAAAACT 1140  
QY 1141 GGAGTCAAGGATTTGCATAGTCACTCACTGATGTGGCTCTGGAACACCAAGGAAATGT 1200  
Db 1141 GGAGTCAAGGATTTGCATAGTCACTCACTGATGTGGCTCTGGAACACCAAGGAAATGT 1200  
QY 1201 GACTGTGTGTAGAGAAACGAGAGGTAATCTGAGGCTTCGTAGAGCACACGTGA 1260  
Db 1201 GACTGTGTGTAGAGAAACGAGAGGTAATCTGAGGCTTCGTAGAGCACACGTGA 1260  
QY 1261 GCACTGGCATTTCTGTGTACCCCAAGCAACCTTCATCCCAAGCGTTGGCCGCGAG 1320  
Db 1261 GCACTGGCATTTCTGTGTACCCCAAGCAACCTTCATCCCAAGCGTTGGCCGCGAG 1320  
QY 1321 GCTCTCAGCTGT 1380  
Db 1321 GCTCTCAGCTGT 1380  
QY 1381 GTTGT 1440  
Db 1381 GTTGT 1440  
QY 1441 CACCAANAGAGTCAATCAAAAGAGTCAAAAGAGTCAAAAGAGTCAAAAGAGTCA 1474  
Db 1441 CACCAANAGAGTCAATCAAAAGAGTCAAAAGAGTCAAAAGAGTCAAAAGAGTCA 1474

## RESULT 3

US-09-410-349A-6  
; Sequence 6, Application US/09410349A  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: AASE, Karin  
; APPLICANT: LEE, Xuri  
; APPLICANT: PONTEN, Annika  
; APPLICANT: UUTELA, Marko  
; APPLICANT: ALITALO, Kari  
; APPLICANT: OESTMAN, Arne  
; APPLICANT: HELDIN, Carl-Henrik  
; APPLICANT: BETHSOLTZ, Christer  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING  
; FILE OF INVENTION: THEREFOR, AND USES THEREOF  
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740  
; CURRENT APPLICATION NUMBER: US/09/410,349A  
; PRIOR FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: 60/110,109  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: 60/110,749  
; PRIOR FILING DATE: 1998-12-03  
; PRIOR APPLICATION NUMBER: 60/113,002  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 60/135,426  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: 60/144,022  
; PRIOR FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 1474  
; TYPE: DNA  
; ORGANISM: Murinae gen. sp.  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1447)  
; OTHER INFORMATION: can be a, c, g or t  
US-09-410-349A-6

Query Match 99.9%; Score 1473; DB 21; Length 1474;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CACCTGGAGACACAGAGGGCTCTAGGAAATTTTGGATGGGATTTATGTGAAACT 60  
Db 1 CACCTGGAGACACAGAGGGCTCTAGGAAATTTTGGATGGGATTTATGTGAAACT 60  
QY 61 ACCCTGCGATTTCTCTGCTGCCAGAGCGCGCTTCCACCCGACGCGAGCTTTTC 120  
Db 61 ACCCTGCGATTTCTCTGCTGCCAGAGCGCGCTTCCACCCGACGCGAGCTTTTC 120  
QY 121 CGGGCTGGGTGAGCTTGGAGTGTGCTTCCCGAGTCCCGCGGAGTGAGCCCTC 180  
Db 121 CGGGCTGGGTGAGCTTGGAGTGTGCTTCCCGAGTCCCGCGGAGTGAGCCCTC 180  
QY 181 GCCCAGTCAACAAATCTCTCTCGGCTCTCTCTGCTGATCATCTGCCCTCGCGCGC 240  
Db 181 GCCCAGTCAACAAATCTCTCTCGGCTCTCTCTGCTGATCATCTGCCCTCGCGCGC 240  
QY 241 CAAAGAACGGGAGTCTGGGCTGAGTCCAACTGAGAGAGAGTTGCGAGCTCTCCAGCGAC 300  
Db 241 CAAAGAACGGGAGTCTGGGCTGAGTCCAACTGAGAGAGAGTTGCGAGCTCTCCAGCGAC 300  
QY 301 AAGGAACAGAGCGGAGTCCAAAGATCCCGGCTGAGAGAGTTGTCACTATATCTGTAAT 360  
Db 301 AAGGAACAGAGCGGAGTCCAAAGATCCCGGCTGAGAGAGTTGTCACTATATCTGTAAT 360  
QY 361 GGGAGCATCCAAGCGCGAGTTTCTCTCATACGTAACCAAGAAATATGCTGCTGGTGG 420  
Db 361 GGGAGCATCCAAGCGCGAGTTTCTCTCATACGTAACCAAGAAATATGCTGCTGGTGG 420  
QY 421 AGATTAGTTCAGTAGAGTAAATGTGGGATCCAGCTGACATTTGATGAGAGTTGGG 480  
Db 421 AGATTAGTTCAGTAGAGTAAATGTGGGATCCAGCTGACATTTGATGAGAGTTGGG 480  
QY 481 CTGGAAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAGTTGAGAGCGCCAGT 540  
Db 481 CTGGAAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAGTTGAGAGCGCCAGT 540  
QY 541 GATGGAAGTGTGTTAGGACGCTGTGGTGTCTGGGACTGTGCCAGGAAAGCAGACTTCT 600  
Db 541 GATGGAAGTGTGTTAGGACGCTGTGGTGTCTGGGACTGTGCCAGGAAAGCAGACTTCT 600  
QY 601 AAAGGAATCATATCAGGATTAATGATCTCATGAGTATTTTCCATCTGAACCCGGA 660  
Db 601 AAAGGAATCATATCAGGATTAATGATCTCATGAGTATTTTCCATCTGAACCCGGA 660  
QY 661 TTCTGATCCACTACAGTATTTATCATGCCCAAGTCAAGAAACCAAGAGTCTTCGGTG 720  
Db 661 TTCTGATCCACTACAGTATTTATCATGCCCAAGTCAAGAAACCAAGAGTCTTCGGTG 720  
QY 721 TTGCCCCCTTCATCTTTGTCAATTCGAGCTGTCAACATGCTGACTGCCCTTCAGTACC 780  
Db 721 TTGCCCCCTTCATCTTTGTCAATTCGAGCTGTCAACATGCTGACTGCCCTTCAGTACC 780  
QY 781 TTGGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTTGGACAGCTTC 840  
Db 781 TTGGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTTGGACAGCTTC 840  
QY 841 TACAAGCCCAATGGCAGCTTTTGGGCAAGCTTTCTGTATGGGAAAGAAAGAAAGTG 900  
Db 841 TACAAGCCCAATGGCAGCTTTTGGGCAAGCTTTCTGTATGGGAAAGAAAGAAAGTG 900  
QY 901 GTGAATCTGAATCTCTCAAGGAAGAGTAAACTCTACAGCTGCACACCCCGAACTTC 960  
Db 901 GTGAATCTGAATCTCTCAAGGAAGAGTAAACTCTACAGCTGCACACCCCGAACTTC 960  
QY 961 TCAGTGTCCATACCGGAAGAGCTTAAAGAGGACAGATACCATATTTCTGGCAGGTTGTCT 1020  
Db 961 TCAGTGTCCATACCGGAAGAGCTTAAAGAGGACAGATACCATATTTCTGGCAGGTTGTCT 1020

QY 1021 CTGGTCAAGCGCTGTGGAGAAATTTGCTCTCTCCATTAATGCAATGTCAG 1080  
DB |||||  
QY 1021 CTGGTCAAGCGCTGTGGAGAAATTTGCTCTCTCCATTAATGCAATGTCAG 1080  
DB |||||  
QY 1081 TGTGTCCCAACGCTAAAGTTTACAAAAGTACCATGAGTCTCTTCAAGTTGAGACCAAAAAT 1140  
DB |||||  
QY 1141 GGAGTCAAGGGAATTTGATTAAGTCACTCACTGATGAGTCTCTGGAACACACAGGAATGT 1200  
DB |||||  
QY 1201 GACTGTGTGTAGAGAAAACGAGAGAGGTAACTGACGCTTCTGAGCAGCACACGTGA 1260  
DB |||||  
QY 1261 GACTGTGTGTAGAGAAAACGAGAGAGGTAACTGACGCTTCTGAGCAGCACACGTGA 1320  
DB |||||  
QY 1321 GCTCTCAGCTGTGATGCTGGCTATGCTAAAGATCTTACTGCTCCCAACCAATTTCTCA 1380  
DB |||||  
QY 1381 GTTGTGCTTCAATAGCTTCCCTGCGAGACTTCAAGTGTCTTCTAAAGACCAAGG 1440  
DB |||||  
QY 1441 CACCAANAGAGTCAATCAAAAGCACTGCACG 1474  
DB |||||

## RESULT 4

US-09-852-209-6  
; Sequence 6: Application US/09852209  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, ULF  
; APPLICANT: AASE, Karin  
; APPLICANT: LEE, Xuri  
; APPLICANT: PONTEN, Annica  
; APPLICANT: UUTELA, Marko  
; APPLICANT: ALITALO, Kari  
; APPLICANT: OESTMAN, Arne  
; APPLICANT: HELDIN, Carl-Henrik  
; APPLICANT: BETHSHOLTZ, Christer  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING  
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740  
; CURRENT APPLICATION NUMBER: US/09/852,209  
; CURRENT FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: 09/410,349  
; PRIOR FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: 60/110,749  
; PRIOR FILING DATE: 1998-12-03  
; PRIOR APPLICATION NUMBER: 60/113,002  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 60/135,426  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: 60/144,022  
; PRIOR FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 1474  
; TYPE: DNA  
; ORGANISM: Murinae gen. sp.  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1447)  
; OTHER INFORMATION: can be a, c, g or t

Query Match 99.9%; Score 1473; DB 35; Length 1474;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CACCTGGAGACACAGAAAGAGGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGAAACT 60  
DB |||||  
QY 61 ACCCTGGATTTCTGTGTCAGAGCCGCGCAGCGCTTCCACCGCAGCGAGCTTTCC 120  
DB |||||  
QY 121 CCGGCTGGGCTGAGCTTTGGAGTCGTCTTCCAGTCGCTTCCCGAGTCGCGAGTCGAGCCCTC 180  
DB |||||  
QY 181 GCCCGAGTCAGCCAAATGCTCTCTCGGCTCTCTCTGTGACATCTGCTGCTGATCTGCTGCTTCC 240  
DB |||||  
QY 241 CAAGAACGGGAGCTCGGGCTGAGTCCAACTGAGCAGCAGTTCGAGCTCTCCAGCGAC 300  
DB |||||  
QY 301 AAGGAACAGAACGGAGTCAAGATCCCGGCGATGAGAGAGTTGTCACTATATCTGGTAAT 360  
DB |||||  
QY 361 GGGAGCATCCACAGCCCGAGTTTCTCTACGTAAGTCCCAAGAAATNTGGTCTGGTGTGG 420  
DB |||||  
QY 421 AGATTAGTTGCAATGATGAAATGTGGGATCCAGCTGACATTTGATGAGAGATTTGGG 480  
DB |||||  
QY 481 CTGGAAGTCCAGAAAGCAGATATATGCAAGTATGATTTGTAGAGTTGAGAGAGCCAGT 540  
DB |||||  
QY 541 GATGGAAGTGTTTAGGAGCGCTGGTGTCTGGGACTGTCGAGGAAAGCAGACTTCT 600  
DB |||||  
QY 601 AAAGGAATCATATCAGGATAAGATTTGTATCTGATGAGTATTTTCCATCTGAACCCGGA 660  
DB |||||  
QY 661 TTCTGCTCCACTACGATTTATCATGCCCAAGTCCAGGAAACAGAGTCTCTCGGTG 720  
DB |||||  
QY 721 TTGCCCCCTTCATCTTTGTCTATTGAGACTGTCTCAACATGCTGTGACTGCTTCAGTACC 780  
DB |||||  
QY 781 TTGGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGCGAGTGGATTTGGAAGCCTC 840  
DB |||||  
QY 841 TACAAGCCCAATCGGAGCTTTTGGGCAAGCTTTCTGTATGGGAAAAAAGCAAGATG 900  
DB |||||  
QY 901 GTGAATCTGAATCTCTCAAGGAAGAGGTAAATCTCTACAGCTGCACACCCCGGAATTC 960  
DB |||||  
QY 961 TCAGTGTCCATACGGGAGAGCTTAAGAGCAGATACCATTTCTGCGCAGGTTGTCTC 1020  
DB |||||  
QY 1021 CTGCTCAAGCGCTGTGGAGGAAATTTGTGCTGTGCTCCATTAATGCAATGTCAG 1080

Db 1021 CTGGTCAAGCGCTGTGGAGAAATTTGGCTGTGTCTCATTAATTCGAATGAATCTCAG 1080  
QY 1081 TGTGTCCACGTAAAGTTTCAAAAAAGTACCATGAGTCTTTCAGTTGAGACCAAAAACT 1140  
Db 1081 TGTGTCCACGTAAAGTTTCAAAAAAGTACCATGAGTCTTTCAGTTGAGACCAAAAACT 1140  
QY 1141 GGAGTCAAGGGATTTGATAGTCACTCACTGATGTGGCTGTGGAACAACACGAGGAATGT 1200  
Db 1141 GGAGTCAAGGGATTTGATAGTCACTCACTGATGTGGCTGTGGAACAACACGAGGAATGT 1200  
QY 1201 GACTGTGTGTAGAGAAACGAGGAGGTAACTGACGCTTCGTAGCAGCACAGTGA 1260  
Db 1201 GACTGTGTGTAGAGAAACGAGGAGGTAACTGACGCTTCGTAGCAGCACAGTGA 1260  
QY 1261 GCACTGGCAATCTGTGTACCCCAAGCAACCTTCATCCCAACGAGCGTTGGCCGCGAGG 1320  
Db 1261 GCACTGGCAATCTGTGTACCCCAAGCAACCTTCATCCCAACGAGCGTTGGCCGCGAGG 1320  
QY 1321 GCTCTCAGCTGTGATGCTGGCTATGTTAAAGATCTTACTGTCTCCAAACCAATTTCTCA 1380  
Db 1321 GCTCTCAGCTGTGATGCTGGCTATGTTAAAGATCTTACTGTCTCCAAACCAATTTCTCA 1380  
QY 1381 GTTGTGTTGCTTCAATAGCTTCCCTGTCAGGACTTCAAGTGTCTTCTAAAGACCAAGG 1440  
Db 1381 GTTGTGTTGCTTCAATAGCTTCCCTGTCAGGACTTCAAGTGTCTTCTAAAGACCAAGG 1440  
QY 1441 CACCAANAGGAGTCAATCACAAGCACTGCACCG 1474  
Db 1441 CACCAANAGGAGTCAATCACAAGCACTGCACCG 1474

RESULT 5

US-09-852-209A-6  
; Sequence 6, Application US/09852209A  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: AASE, Karin  
; APPLICANT: LEE, Xuri  
; APPLICANT: PONTEN, Annica  
; APPLICANT: UTELA, Marko  
; APPLICANT: ALITALO, Arne  
; APPLICANT: OESTMAN, Arne  
; APPLICANT: HELDIN, Carl-Henrik  
; APPLICANT: BETHSHOLTZ, Christer  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING  
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF  
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740  
; CURRENT APPLICATION NUMBER: US/09/852,209A  
; CURRENT FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: 09/410,349  
; PRIOR FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: 60/110,749  
; PRIOR FILING DATE: 1998-12-03  
; PRIOR APPLICATION NUMBER: 60/113,002  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 60/135,426  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: 60/144,022  
; PRIOR FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 1474  
; TYPE: DNA  
; ORGANISM: Murinae gen. sp.  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1447)  
; OTHER INFORMATION: can be a, c, g or t  
US-09-852-209A-6

Query Match 99.9%; Score 1473; DB 35; Length 1474;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CACCTGGACACACAGAGAGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGGAAC 60  
Db 1 CACCTGGACACACAGAGAGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGGAAC 60  
QY 61 ACCCTGCGAATCTCTGCTGCCAGAGCGCGCTTCCACCGCAGCGCAGCCTTTCC 120  
Db 61 ACCCTGCGAATCTCTGCTGCCAGAGCGCGCTTCCACCGCAGCGCAGCCTTTCC 120  
QY 121 CCGGGCTGGGCTGAGCGTTGGAGTGGTCCCTTCCCAAGTCCCGCGCGAGTGAGCCCTC 180  
Db 121 CCGGGCTGGGCTGAGCGTTGGAGTGGTCCCTTCCCAAGTCCCGCGCGAGTGAGCCCTC 180  
QY 181 GCCCGAGTCAGCCAAATGCTCTCCGCGCTCTCTGCTGACATCTGCCCTGGCGGC 240  
Db 181 GCCCGAGTCAGCCAAATGCTCTCCGCGCTCTCTGCTGACATCTGCCCTGGCGGC 240  
QY 241 CAAAGAACGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCGAGCTCTCCACGAC 300  
Db 241 CAAAGAACGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCGAGCTCTCCACGAC 300  
QY 301 AAGGAACAGAACGGAGTGCAGATCCCGCGCATGAGAGAGTGTCTATATCTGTGTAAT 360  
Db 301 AAGGAACAGAACGGAGTGCAGATCCCGCGCATGAGAGAGTGTCTATATCTGTGTAAT 360  
QY 361 GGGAGCATCCACAGCGCCGAAAGTTTCTCATAGTACCCCAAGAAATATGGTGTGGTGG 420  
Db 361 GGGAGCATCCACAGCGCCGAAAGTTTCTCATAGTACCCCAAGAAATATGGTGTGGTGG 420  
QY 421 AGATTAGTTGCAATAGATGAAAAATGTGGGATCCAGCTGACATTTGATGAGAGATTTGG 480  
Db 421 AGATTAGTTGCAATAGATGAAAAATGTGGGATCCAGCTGACATTTGATGAGAGATTTGG 480  
QY 481 CTGGAAGATCCAGAAAGACGATATATGCAAGTATGATTTGTAGAAAGTTGAGGAGCCAGT 540  
Db 481 CTGGAAGATCCAGAAAGACGATATATGCAAGTATGATTTGTAGAAAGTTGAGGAGCCAGT 540  
QY 541 GATGGAAGTGTGTTAGGAGCGTGGTGTGGTCTGGGACTGTGCCAGGAAAGCAGACTTCT 600  
Db 541 GATGGAAGTGTGTTAGGAGCGTGGTGTGGTCTGGGACTGTGCCAGGAAAGCAGACTTCT 600  
QY 601 AAAGAAATCATATCAGGATTAAGATTTGTATCTGATGAGTATTTTCCATCTGAAACCCGA 660  
Db 601 AAAGAAATCATATCAGGATTAAGATTTGTATCTGATGAGTATTTTCCATCTGAAACCCGA 660  
QY 661 TTCTGCATCCACTACGATTTATCATGCGCAAGTCAAGAAACCAAGTCCCTTGGGTG 720  
Db 661 TTCTGCATCCACTACGATTTATCATGCGCAAGTCAAGAAACCAAGTCCCTTGGGTG 720  
QY 721 TTGCCCCCTTCATCTTTGTCTATTTGGACCTGCTCAACATGCTGACCTTCAGTACC 780  
Db 721 TTGCCCCCTTCATCTTTGTCTATTTGGACCTGCTCAACATGCTGACCTTCAGTACC 780  
QY 781 TTGGAAGAGCTGATTCGGTACCTTAGAGCCAGATCGATGGCAGGTGGAATTTGGACAGCTC 840  
Db 781 TTGGAAGAGCTGATTCGGTACCTTAGAGCCAGATCGATGGCAGGTGGAATTTGGACAGCTC 840  
QY 841 TACAGCCCAACATGCGAGCTTTTGGGCAAGCTTTTCTGTATGGGAAAAAAGCAAGATG 900  
Db 841 TACAGCCCAACATGCGAGCTTTTGGGCAAGCTTTTCTGTATGGGAAAAAAGCAAGATG 900  
QY 901 GTGAATCTGAATCTCTCAAGGAGAGGTAAACTCTACAGCTGCACACCCCGGACTTC 960  
Db 901 GTGAATCTGAATCTCTCAAGGAGAGGTAAACTCTACAGCTGCACACCCCGGACTTC 960  
QY 961 TCAGTGTCCATACGGGAAGAGCTAAAGAGACAGATACCATATTCTGCGCAGGTGTCTC 1020  
Db 961 TCAGTGTCCATACGGGAAGAGCTAAAGAGACAGATACCATATTCTGCGCAGGTGTCTC 1020  
QY 1021 CTGGTCAAGCGCTGTGGAGAAATTTGGCTGTGTCTCCATATTTGCAATGATGTGAG 1080

Db 1021 CTGGTCAAGCGCTGTGGAGGAAATTGTGCTGTGTCTCCATAATTGCAATGAATGTCTCAG 1080  
QY TGTGTCCACGTAAGTTACAAAAAGTAGCATGAGGTCTTTCAGTTCAGACCAAAAACT 1140  
Db TGTGTCCACGTAAGTTACAAAAAGTAGCATGAGGTCTTTCAGTTCAGACCAAAAACT 1140  
QY GGAGTCAAGGGAATTGCATAAGTCACTCACTGATGTGGCTCTGGAACACCAAGGGAATGT 1200  
Db GGAGTCAAGGGAATTGCATAAGTCACTCACTGATGTGGCTCTGGAACACCAAGGGAATGT 1200  
QY GACTGTGTGTGTAGAGGAAACGAGGAGGTAACTGCGAGCCTTCGTAGCAGACACGTGA 1260  
Db GACTGTGTGTGTAGAGGAAACGAGGAGGTAACTGCGAGCCTTCGTAGCAGACACGTGA 1260  
QY GCAGTGGCAATCTGTGTACCCCAACCAAGCAACCTTCATCCCAACCAAGCGGTGGCCGAGG 1320  
Db GCAGTGGCAATCTGTGTACCCCAACCAAGCAACCTTCATCCCAACCAAGCGGTGGCCGAGG 1320  
QY GCTCTCAGCTGT 1380  
Db GCTCTCAGCTGT 1380  
QY GTTGTCTCTCAATAGCTTCCCTCTGCGAGGACTTCAAGTGTCTTCTAAAGACCCAGAGG 1440  
Db GTTGTCTCTCAATAGCTTCCCTCTGCGAGGACTTCAAGTGTCTTCTAAAGACCCAGAGG 1440  
QY CACCAANAGGAGTCAATCAACAAAGCACTGCACCG 1474  
Db CACCAANAGGAGTCAATCAACAAAGCACTGCACCG 1474

## RESULT 6

US-10-131-600-6  
; Sequence 6, Application US/10131600  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: AASE, Karin  
; APPLICANT: LEE, Xuri  
; APPLICANT: PONTEN, Annica  
; APPLICANT: UUTELA, Marko  
; APPLICANT: ALITALO, Kari  
; APPLICANT: OESTMAN, Arne  
; APPLICANT: HELDIN, Carl-Henrik  
; APPLICANT: BETHSOLTZ, Christer  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING  
; FILE REFERENCE: THEREFOR, AND USES THEREOF  
; CURRENT APPLICATION NUMBER: US/10131,600  
; CURRENT FILING DATE: 2002-04-25  
; PRIOR APPLICATION NUMBER: US/09/410,349  
; PRIOR FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: 60/108,109  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: 60/110,749  
; PRIOR FILING DATE: 1998-12-03  
; PRIOR APPLICATION NUMBER: 60/113,002  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 60/135,426  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: 60/144,022  
; PRIOR FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 1474  
; TYPE: DNA  
; ORGANISM: Murinae gen. sp.  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1447)  
; OTHER INFORMATION: can be a, c, g or t  
US-10-131-600-6

Query Match  
Best Local Similarity 99.9%; Score 1473; DB 46; Length 1474;  
Matches 1474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CACCTGGAGACACAGAGGGCTCTAGAAAAATTTTGGATGGGATTTATGTGAAACT 60  
Db 1 CACCTGGAGACACAGAGGGCTCTAGAAAAATTTTGGATGGGATTTATGTGAAACT 60  
QY 61 ACCCTGCCATCTCTGCTGCCAGAGCGCGGCGCTTCCACCGCAGCGAGCCTTCC 120  
Db 61 ACCCTGCCATCTCTGCTGCCAGAGCGCGGCGCTTCCACCGCAGCGAGCCTTCC 120  
QY 121 CCGGCTCGGCTGAGCCTTGGAGTCTGCTTCCCAAGTCCCGCGCGAGTGAGCCCTC 180  
Db 121 CCGGCTCGGCTGAGCCTTGGAGTCTGCTTCCCAAGTCCCGCGCGAGTGAGCCCTC 180  
QY 181 GCCCAGTTCAGCAAAATCTCTCTCGGCTCTCTCTGCTGACATCTGCTCCCTGCGCG 240  
Db 181 GCCCAGTTCAGCAAAATCTCTCTCGGCTCTCTCTGCTGACATCTGCTCCCTGCGCG 240  
QY 241 CAAGAAACGAGGAGTCCGGCTGAGTCCAACTGAGCAGCAAGTTCGAGCTCTCCAGCGAC 300  
Db 241 CAAGAAACGAGGAGTCCGGCTGAGTCCAACTGAGCAGCAAGTTCGAGCTCTCCAGCGAC 300  
QY 301 AAGGAAACGAGGAGTCCGGCTGAGTCCAACTGAGCAGCAAGTTCGACTATATCTGTAAT 360  
Db 301 AAGGAAACGAGGAGTCCGGCTGAGTCCAACTGAGCAGCAAGTTCGACTATATCTGTAAT 360  
QY 361 GGGAGCATCCACAGCCCGAAGTTCCTCATAGTACCAAGAAATATGCTGTGTGG 420  
Db 361 GGGAGCATCCACAGCCCGAAGTTCCTCATAGTACCAAGAAATATGCTGTGTGG 420  
QY 421 AGATTAGTTCAGTAGTAAATGTCGGATCCAGCTGACATTTGATGAGAGATTTGG 480  
Db 421 AGATTAGTTCAGTAGTAAATGTCGGATCCAGCTGACATTTGATGAGAGATTTGG 480  
QY 481 CTGGAAGATCCAGAGACGATATATGCAAGTATGATTTGTAGAAAGTTCAGAGCCAGT 540  
Db 481 CTGGAAGATCCAGAGACGATATATGCAAGTATGATTTGTAGAAAGTTCAGAGCCAGT 540  
QY 541 GATGGAAGTTCAGAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600  
Db 541 GATGGAAGTTCAGAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600  
QY 601 AAAGAAATCATATCAGGATAAGATTTCTATCTGATGAGTATTTTCCATCTGAACCCGA 660  
Db 601 AAAGAAATCATATCAGGATAAGATTTCTATCTGATGAGTATTTTCCATCTGAACCCGA 660  
QY 661 TTCTGCATCCACTACAGTATTTATCATGCCAAGTTCAGAGAAACCAAGAGTCTTTCGGTG 720  
Db 661 TTCTGCATCCACTACAGTATTTATCATGCCAAGTTCAGAGAAACCAAGAGTCTTTCGGTG 720  
QY 721 TTGCCCCCTTCATCTTTGTCAATTTGCACTGTCTCAACATGCTGACTGCTTCACTACC 780  
Db 721 TTGCCCCCTTCATCTTTGTCAATTTGCACTGTCTCAACATGCTGACTGCTTCACTACC 780  
QY 781 TTGGAAGAGTGAATTCGCTACCTAGAGCCAGATCGATGGCAGGTGGAATTGGACAGCCTC 840  
Db 781 TTGGAAGAGTGAATTCGCTACCTAGAGCCAGATCGATGGCAGGTGGAATTGGACAGCCTC 840  
QY 841 TACAAGCCACATGGCAGCTTTTGGCAAGGCTTTTCTGTATGGGAAAAAAGCAAGTG 900  
Db 841 TACAAGCCACATGGCAGCTTTTGGCAAGGCTTTTCTGTATGGGAAAAAAGCAAGTG 900  
QY 901 GTGAATCTGAATCTCTCAAGGAAGAGGTAAACTCTTACAGCTGCAACCCCGAATTC 960  
Db 901 GTGAATCTGAATCTCTCAAGGAAGAGGTAAACTCTTACAGCTGCAACCCCGAATTC 960  
QY 961 TCAGTGTCCATACGGGAGAGCTAAAGAGGACAGATACCATATTTCTGGCCAGGTGTCTC 1020  
Db 961 TCAGTGTCCATACGGGAGAGCTAAAGAGGACAGATACCATATTTCTGGCCAGGTGTCTC 1020  
QY 1021 CTGGTCAAGCGCTGTGGAGGAAATTTGCTGTGTGTCTCCATAATTGCAATGAATGTCTCAG 1080



Db 1021 CTGGTCAAGCGCTGTGGAGGAAATTTGCTGTGCTCTCCATAATTTGCAATGAATGTCTAG 1080  
Qy 1081 TGTGTCCCAAGTAAAGTTACAAAAGTACCAATGAGTGTCTTCAAGTTGAGACCAAAAAT 1140  
Db 1081 TGTGTCCCAAGTAAAGTTACAAAAGTACCAATGAGTGTCTTCAAGTTGAGACCAAAAAT 1140  
Qy 1141 GGAGTCAAGGATTCATTAAGTCACTCACTGATGTGGCTCTGGAACACCAAGCAATGT 1200  
Db 1141 GGAGTCAAGGATTCATTAAGTCACTCACTGATGTGGCTCTGGAACACCAAGCAATGT 1200  
Qy 1201 GACTGTGTGTAGAGGAAACGACGAGGGTAACTGACGCTTCGTAGCAGCACACGTGA 1260  
Db 1201 GACTGTGTGTAGAGGAAACGACGAGGGTAACTGACGCTTCGTAGCAGCACACGTGA 1260  
Qy 1261 GCACGTGGATTCGTGTACCCCAACAGCAACTTCATCCCAACAGCGTTGGCCGACG 1320  
Db 1261 GCACGTGGATTCGTGTACCCCAACAGCAACTTCATCCCAACAGCGTTGGCCGACG 1320  
Qy 1321 GCTCTCAGCTGTGATGTGGCTATGCTAAAGATCTTACTCTCTCCAAACCAATTTCTCA 1380  
Db 1321 GCTCTCAGCTGTGATGTGGCTATGCTAAAGATCTTACTCTCTCCAAACCAATTTCTCA 1380  
Qy 1381 GTTGTTCCTCAATAGCTTCCCTGACGAGCTTCAAGTGTCTTCTAAAGACCAAGG 1440  
Db 1381 GTTGTTCCTCAATAGCTTCCCTGACGAGCTTCAAGTGTCTTCTAAAGACCAAGG 1440  
Qy 1441 CACCAANAGGAGTCAATCACAAGCACTGCACCG 1474  
Db 1441 CACCAANAGGAGTCAATCACAAGCACTGCACCG 1474

## RESULT 7

US-10-303-997B-6  
; Sequence 6, Application US/10303997B  
; GENERAL INFORMATION:  
; APPLICANT: LI, Xuri  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: CARMELIET, Peter  
; APPLICANT: COLLUM, Desire  
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR MODULATING VASCULOGENESIS AND ANGIOGENESIS  
; FILE REFERENCE: 029065.447403  
; CURRENT APPLICATION NUMBER: US/10/303,997B  
; CURRENT FILING DATE: 2002-11-26  
; PRIOR APPLICATION NUMBER: US 09/410,349  
; PRIOR FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: US 60/102,461  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: US 60/108,109  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: US 60/110,749  
; PRIOR FILING DATE: 1998-12-03  
; PRIOR APPLICATION NUMBER: US 60/113,002  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: US 60/135,426  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: US 60/144,022  
; PRIOR FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 1474  
; TYPE: DNA  
; ORGANISM: Murinae gen. sp.  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1447)..(1447)  
; OTHER INFORMATION: can be any of a, c, g, or t

Query Match 99.9%; Score 1473; DB 50; Length 1474;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CACCTGGAGACACAGAGGGCTCTAGGAAAAATTTTGGATGGGATTTATCTGGAAACT 60  
Db 1 CACCTGGAGACACAGAGGGCTCTAGGAAAAATTTTGGATGGGATTTATCTGGAAACT 60  
Qy 61 ACCCTGGCATTCCTGTGTCAGAGCCGCGGCTTCCACCGCAGCGCAGCCTTTCC 120  
Db 61 ACCCTGGCATTCCTGTGTCAGAGCCGCGGCTTCCACCGCAGCGCAGCCTTTCC 120  
Qy 121 CCGGCTGGCTGAGCCCTTGAGAGTCGTGCTTCCAGTGCCTCCGCGGAGTGAGCCCTC 180  
Db 121 CCGGCTGGCTGAGCCCTTGAGAGTCGTGCTTCCAGTGCCTCCGCGGAGTGAGCCCTC 180  
Qy 181 GCCCAGTCAGCCAAATGCTCCTCGGCTCTCTGCTGACATCTGCTCCCTGCCCGC 240  
Db 181 GCCCAGTCAGCCAAATGCTCCTCGGCTCTCTGCTGACATCTGCTCCCTGCCCGC 240  
Qy 241 CAAAGAACGGGACCTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCTCCAGCGAC 300  
Db 241 CAAAGAACGGGACCTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCTCCAGCGAC 300  
Qy 301 AAGGAAACGAGAGTCAGATCCCGGCGATGAGAGTTGTCACTATATCTGTAAT 360  
Db 301 AAGGAAACGAGAGTCAGATCCCGGCGATGAGAGTTGTCACTATATCTGTAAT 360  
Qy 361 GGGACATCCACAGCCCGAAGTTTCTCATAGTACCCCAAGAAATATGCTGCTGTGG 420  
Db 361 GGGACATCCACAGCCCGAAGTTTCTCATAGTACCCCAAGAAATATGCTGCTGTGG 420  
Qy 421 AGATTAGTTGAGTAGATGAAAAATGTGGGATCCAGCTGACATTTGATGAGAGATTGGG 480  
Db 421 AGATTAGTTGAGTAGATGAAAAATGTGGGATCCAGCTGACATTTGATGAGAGATTGGG 480  
Qy 481 CTGGAAGATCCAGAGACGATATATGAAATGATGATTTTGTAGAGATTGAGAGCCACT 540  
Db 481 CTGGAAGATCCAGAGACGATATATGAAATGATGATTTTGTAGAGATTGAGAGCCACT 540  
Qy 541 GATGGAAGTGTTTTAGGACGCTGTGTGCTGCTGGGACTGTGCCAGGAAGCAGACTTCT 600  
Db 541 GATGGAAGTGTTTTAGGACGCTGTGTGCTGCTGGGACTGTGCCAGGAAGCAGACTTCT 600  
Qy 601 AAAGAAATCATATCAGGATAGATTTGTATCTGATGATTTTCCATCTGAAACCCGA 660  
Db 601 AAAGAAATCATATCAGGATAGATTTGTATCTGATGATTTTCCATCTGAAACCCGA 660  
Qy 661 TTGTCATCCACTACAGTATTTATGTCACCAAGTTCACAGAAACCAAGTCTTGGTG 720  
Db 661 TTGTCATCCACTACAGTATTTATGTCACCAAGTTCACAGAAACCAAGTCTTGGTG 720  
Qy 721 TTGCCCCCTTCATCTTTGCTGATGACCTGCTCAACAATGCTGCTGCTTCACTTAC 780  
Db 721 TTGCCCCCTTCATCTTTGCTGATGACCTGCTCAACAATGCTGCTGCTTCACTTAC 780  
Qy 781 TTGGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGAGCTTGGACAGC 840  
Db 781 TTGGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGAGCTTGGACAGC 840  
Qy 841 TACAGCCCAATGCGACCTTTTGGGCAAGCTTTCCTGTATGGGAAAAAAGCAAGTG 900  
Db 841 TACAGCCCAATGCGACCTTTTGGGCAAGCTTTCCTGTATGGGAAAAAAGCAAGTG 900  
Qy 901 GTGAATCTGAATCTCTCAAGGAGAGGTAAACTCTACAGTGCACACCCCGGAACTTC 960  
Db 901 GTGAATCTGAATCTCTCAAGGAGAGGTAAACTCTACAGTGCACACCCCGGAACTTC 960  
Qy 961 TCAGTGTCCATACCGGAAGAGCTAAAGAGGACAGATACCATATTTGCGCCAGTTGTCTC 1020  
Db 961 TCAGTGTCCATACCGGAAGAGCTAAAGAGGACAGATACCATATTTGCGCCAGTTGTCTC 1020  
Qy 1021 CTGCTCAAGCGCTGTGAGGAAATTTGCTGCTTGTCTCCATATTTGCAATGAATGTCTC 1080  
Db 1021 CTGCTCAAGCGCTGTGAGGAAATTTGCTGCTTGTCTCCATATTTGCAATGAATGTCTC 1080



```

QY 1081 TGTGTCCACGTAAGTTACAAAAGTACATGAGGTCCTTCAGTTGAGACCAAAACT 1140
DB 1081 TGTGTCCACGTAAGTTACAAAAGTACATGAGGTCCTTCAGTTGAGACCAAAACT 1140
QY 1141 GGAAGTCAAGGATTTGATAGTCACTCACTGATGAGGTCCTGGAACACCAAGGAAATGT 1200
DB 1141 GGAAGTCAAGGATTTGATAGTCACTCACTGATGAGGTCCTGGAACACCAAGGAAATGT 1200
QY 1201 GACTGTGTGTAGAGGAAGCGAGGAGGTAACCTGACAGCTTCGTAGCAGCACAGTGA 1260
DB 1201 GACTGTGTGTAGAGGAAGCGAGGAGGTAACCTGACAGCTTCGTAGCAGCACAGTGA 1260
QY 1261 GCACGTGGATTCGTGTATACCCCAAGCAACCTTCATCCCAAGGGTTGGCCGAGG 1320
DB 1261 GCACGTGGATTCGTGTATACCCCAAGCAACCTTCATCCCAAGGGTTGGCCGAGG 1320
QY 1321 GCTCTCAGCTGCTGATGCTGGCTATGTTAAAGATCTTACTGCTCCCAACCAAAATCTCA 1380
DB 1321 GCTCTCAGCTGCTGATGCTGGCTATGTTAAAGATCTTACTGCTCCCAACCAAAATCTCA 1380
QY 1381 GTTGTGTTCTCAATAGCTTCCCTGACAGGCTTCAAGTGTCTTCTAAAGACCAAGG 1440
DB 1381 GTTGTGTTCTCAATAGCTTCCCTGACAGGCTTCAAGTGTCTTCTAAAGACCAAGG 1440
QY 1441 CACCAANAGGATCAATCAAAAGGCTGACCG 1474
DB 1441 CACCAANAGGATCAATCAAAAGGCTGACCG 1474

RESULT 8
US-09-540-703-3
; Sequence 3, Application US/09540703
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE
; FILE REFERENCE: 00-12X
; CURRENT APPLICATION NUMBER: US/09/540, 703
; CURRENT FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 3571
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1049)...(2086)
US-09-540-703-3

Query Match 98.0%; Score 1444.8; DB 24; Length 3571;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1460; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 2 ACCTGGAGACACAGAGGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGAAACTA 61
DB 856 AACTGGAGACACAGAGGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGAAACTA 915
QY 62 CCCTGCGATTTCTGTGTCAGAGCGCGCCAGCGGCTTCCACCGCAGCGAGCGCTTTCCC 121
DB 916 CCCTGCGATTTCTGTGTCAGAGCGCGCGCCAGCGGCTTCCACCGCAGCGAGCGCTTTCCC 975
QY 122 CGGGCTGGGCTGAGCCTTTGGAGTCTGCTGCTTCCCAAGTGGCCCGCGAGTGAGCCCTCG 181
DB 976 C-GGCTGGGCTGAGCCTTTGGAGTCTGCTGCTTCCCAAGTGGCCCGCGAGTGAGCCCTCG 1034
QY 182 CCCAGTCCAGCAATCTCTCTCGGCTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 241
DB 1035 CCCAGTCCAGCAATCTCTCTCGGCTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1094
QY 242 AAAGAACGGGACTCGGCTGAGTCCAACTGAGCAGCAAGTTGAGCTTCCAGCGACA 301

```

```

DB 1095 AAGAAACGGGACTCGGCTGAGTCCAACTGAGCAGCAAGTTGACGCTCTCCAGCGACA 1154
QY 302 AGAAACGAAACGGAGTGCAGATCCCGCATGAGAGAGTGTGCTACATATCTGTTAATG 361
DB 1155 AGAAACGAAACGGAGTGCAGATCCCGCATGAGAGAGTGTGCTACATATCTGTTAATG 1214
QY 362 GAGAGCATCCACAGCCCGAAGTTTCTCATACGTATCCCAAGAAATATGCTGCTGTTGGA 421
DB 1215 GAGAGCATCCACAGCCCGAAGTTTCTCATACGTATCCCAAGAAATATGCTGCTGTTGGA 1274
QY 422 GATTAGTTGAGTATGAAATGTCGGATCCAGCTGACATTTGATGAGAGATTTGGGC 481
DB 1275 GATTAGTTGAGTATGAAATGTCGGATCCAGCTGACATTTGATGAGAGATTTGGGC 1334
QY 482 TGAAGATCCAGAAAGCATATATGCAAGATATGTTTGTAGAGTTGAGAGCCAGTG 541
DB 1335 TGAAGATCCAGAAAGCATATATGCAAGATATGTTTGTAGAGTTGAGAGCCAGTG 1394
QY 542 ATGAAAGTGTGTTTGAAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601
DB 1395 ATGAAAGTGTGTTTGAAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1454
QY 602 AAGGAATCATATCAGATTAAGATTTGATCTGATGATGATTTTCCATCTGAAACCCGAT 661
DB 1455 AAGGAATCATATCAGATTAAGATTTGATCTGATGATGATTTTCCATCTGAAACCCGAT 1514
QY 662 TCTGATTCATACAGTATTTATGTCACCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 721
DB 1515 TCTGATTCATACAGTATTTATGTCACCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1574
QY 722 TGCCCCCTTCATCTTTGTCATTTGATGACCTGCTCAAAATGCTGCTGCTGCTGCTGCTG 781
DB 1575 TGCCCCCTTCATCTTTGTCATTTGATGACCTGCTCAAAATGCTGCTGCTGCTGCTGCTG 1634
QY 782 TGAAGAGTGTGATTCGCTACCTAGCAGCAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 841
DB 1635 TGAAGAGTGTGATTCGCTACCTAGCAGCAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1694
QY 842 ACAAGCAACATCGCAGCTTTTGGGCAAGGCTTCTCTATGGAAGAAAAAGCAAGTGG 901
DB 1695 ACAAGCAACATCGCAGCTTTTGGGCAAGGCTTCTCTATGGAAGAAAAAGCAAGTGG 1754
QY 902 TGAATCTGAATCTCTCAAGGAAGAGTAAATCTCAGCTGACACACCCCGAATCTCT 961
DB 1755 TGAATCTGAATCTCTCAAGGAAGAGTAAATCTCAGCTGACACACCCCGAATCTCT 1814
QY 962 CAGTGTCCATACGGGAAGAGCTTAAAGAGGACAGATACCATATTTCTGCGCAGGTTGCTCC 1021
DB 1815 CAGTGTCCATACGGGAAGAGCTTAAAGAGGACAGATACCATATTTCTGCGCAGGTTGCTCC 1874
QY 1022 TGCTCAAGCGCTGTGAGGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1081
DB 1875 TGCTCAAGCGCTGTGAGGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1934
QY 1082 GTGTCCCACTAAAGTTTACAAAAAGTACCATGAGTCTCTTCAAGTTGAGACCAAAAACTG 1141
DB 1935 GTGTCCCACTAAAGTTTACAAAAAGTACCATGAGTCTCTTCAAGTTGAGACCAAAAACTG 1994
QY 1142 GAGTCAAGGAATTCATTAAGTCACTCATGATGTGGCTCTGGAACACACAGAGAAATGT 1201
DB 1995 GAGTCAAGGAATTCATTAAGTCACTCATGATGTGGCTCTGGAACACACAGAGAAATGT 2054
QY 1202 ACTGTGTGTAGAGAAACCGCAGGAGGTAACCTGACGCTTCTGAGCAGCACACGCTGAG 1261
DB 2055 ACTGTGTGTAGAGAAACCGCAGGAGGTAACCTGACGCTTCTGAGCAGCACACGCTGAG 2114
QY 1262 CACTGGCATTTCTGTGTACCCCAAGCAACTTCATCCCAAGGAGTGTGGCGAGGG 1321
DB 2115 CACTGGCATTTCTGTGTACCCCAAGCAACTTCATCCCAAGGAGTGTGGCGAGGG 2174
QY 1322 CTCTCAGCTCTGATGCTGGCTATGTTAAAGATCTTACTGCTCTCCAAACCAAAATCTCAG 1381
DB 2175 CTCTCAGCTCTGATGCTGGCTATGTTAAAGATCTTACTGCTCTCCAAACCAAAATCTCAG 2234

```

QY 1382 TTGTTTGCTTCAATAGACCTCCCTGAGGACTTCAAGTGTCTTCTTAAAGACAGAGGC 1441  
Db 2235 TTGTTTGCTTCAATAGACCTCCCTGAGGACTTCAAGTGTCTTCTTAAAGACAGAGGC 2294  
QY 1442 ACCAAGGAGTCAATCAAGAGCACTGC 1470  
Db 2295 ACCAAGGAGTCAATCAAGAGCACTGC 2323

## RESULT 9

US-09-541-752-42  
; Sequence 42, Application US/09541752  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60C1  
; CURRENT APPLICATION NUMBER: US/09/541,752  
; CURRENT FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 42  
; LENGTH: 3571  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1049)...(2086)  
US-09-541-752-42

Query Match 98.0%; Score 1444.8; DB 24; Length 3571;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 1460; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

QY 2 ACCTGGAGACAGAGAGGGCTTAGGAAATTTTGGATGGGATTTATGTGAAACTA 61  
Db 856 AACTGGAGACAGAGAGGGCTTAGGAAATTTTGGATGGGATTTATGTGAAACTA 915  
QY 62 CCTCTGCGATCTCTGTCGAGCGCGCGAGCGCTTCCACCGCAGCGAGCGCTTTCCC 121  
Db 916 CCTCTGCGATCTCTGTCGAGCGCGCGAGCGCTTCCACCGCAGCGAGCGCTTTCCC 975  
QY 122 CGGCTGGCTGAGCTTGGAGTCTGCTTCCCGAGTCCCGCGCGAGTGAGCCCTCG 181  
Db 976 C-GGCTGGGCTGAGCTTGGAGTCTGCTTCCCGAGTCCCGCGCGAGTGAGCCCTCG 1034  
QY 182 CCCAGTCAGCCAAATGCTCTCTCTCGGCTCTCTCTGACATCTGCCCCTGGCCGCGC 241  
Db 1035 CCCAGTCAGCCAAATGCTCTCTCTCGGCTCTCTCTGACATCTGCCCCTGGCCGCGC 1094  
QY 242 AAGAACGGGACTCGGCTGAGTCCACCTGAGCAGCAAGTTCAGCTCTCCAGCGACA 301  
Db 1095 AAGAACGGGACTCGGCTGAGTCCACCTGAGCAGCAAGTTCAGCTCTCCAGCGACA 1154  
QY 302 AGGAACAGAACGGAGTGAAGATCCCGGCGATGAGAGAGTGTCACTATATCTGTTAATG 361  
Db 1155 AGGAACAGAACGGAGTGAAGATCCCGGCGATGAGAGAGTGTCACTATATCTGTTAATG 1214  
QY 362 GGAGATCCAGACCGCGAAGTTCTCTCATAGTACCCAGAAATATGTTGCTGTGTGGA 421  
Db 1215 GGAGATCCAGACCGCGAAGTTCTCTCATACATACCCAGAAATATGTTGCTGTGTGGA 1274  
QY 422 GATTAGTTCAGTATGAAATGTGGATCCAGCTGACATTTGATGAGAGATTTGGGC 481  
Db 1275 GATTAGTTCAGTATGAAATGTGGATCCAGCTGACATTTGATGAGAGATTTGGGC 1334  
QY 482 TGGAAATCCAGAGACGATATATGCAAGTATGATTTTGTAGAGTTGAGGAGCCAGTG 541

## RESULT 10

US-09-695-121-3

; Sequence 3, Application US/09695121

; GENERAL INFORMATION:

; APPLICANT: Gilbertson, Debra G.

TITLE OF INVENTION: METHOD OF TREATING FIBROSIS

FILE REFERENCE: 00-53  
CURRENT APPLICATION NUMBER: US/09/695,121  
CURRENT FILING DATE: 2000-10-23  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 3  
LENGTH: 3571  
TYPE: DNA  
ORGANISM: Mus musculus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1049)...(2086)  
US-09-695-121-3

Query Match 98.0%; Score 1444.8; DB 30; Length 3571;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 1460; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  
QY 2 ACCTGGACACACAGAGAGGCTCTAGGAAAAATTTTGGATGGGATTAATGTGAAACTA 61  
DB AACTGGACACACAGAGAGGCTCTAGGAAAACTTTTGGATGGGATTAATGTGAAACTA 915  
QY 62 CCTCGGATTTCTGCTGCCAGAGCCGCGCCAGGCGCTTCCACCGAGCGAGCCTTTCC 121  
DB CCTCGGATTTCTGCTGCCAGAGCCGCGCCAGGCGCTTCCACCGAGCGAGCCTTTCC 975  
QY 122 CGGGCTGGGCTAGAGCTTGGAGTCTGCTTCCAGTGCCTCCGCGCGAGTGAGCCCTCG 181  
DB C-GGCTGGGCTAGAGCTTGGAGTCTGCTTCCAGTGCCTCCGCGCGAGTGAGCCCTCG 1034  
QY 182 CCCAGTCCAGCAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCCCTGGCGGCG 241  
DB CCCAGTCCAGCAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCCCTGGCGGCG 1094  
QY 242 AAAGAACGGGAGCTCGGGCTGAGTCAACCTGAGCAGCAAGTTGACGCTCTCCAGCGCA 301  
DB AAAGAACGGGAGCTCGGGCTGAGTCAACCTGAGCAGCAAGTTGACGCTCTCCAGCGCA 1154  
QY 302 AGGACACAGAGGAGTGCAGATCCCGGCGATGAGAGGTGTGCACTATCTGTTAATG 361  
DB AGGACACAGAGGAGTGCAGATCCCGGCGATGAGAGGTGTGCACTATCTGTTAATG 1214  
QY 362 GGAGCATCCACAGCCGAGTTTCTCTATACATGATCCCAAGAAATATGCTGCTGGA 421  
DB GGAGCATCCACAGCCGAGTTTCTCTATACATGATCCCAAGAAATATGCTGCTGGA 1274  
QY 422 GATTAGTCCAGTATGAAATGTCGGATCCAGCTGACATTTGATGAGAGTTTGGGC 481  
DB GATTAGTCCAGTATGAAATGTCGGATCCAGCTGACATTTGATGAGAGTTTGGGC 1334  
QY 482 TGAAGATCCAGAGCAGATATATGCAAGTATGATTTTGTAGAGTTGAGGAGCCAGTG 541  
DB TGAAGATCCAGAGCAGATATATGCAAGTATGATTTTGTAGAGTTGAGGAGCCAGTG 1394  
QY 542 ATGGAAGTGTTTTGAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTA 601  
DB ATGGAAGTGTTTTGAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTA 1454  
QY 602 AAGGAATCATATCAGATTAAGATTTGTATCTGATGAGTATTTCCATCTGAACCCGGAT 661  
DB AAGGAATCATATCAGATTAAGATTTGTATCTGATGAGTATTTCCATCTGAACCCGGAT 1514  
QY 662 TCTGCATCCACTACATGATTTATCATGCAAGTTCACAGAAACACAGAGTCTTCCGTTGT 721  
DB TCTGCATCCACTACATGATTTATCATGCAAGTTCACAGAAACACAGAGTCTTCCGTTGT 1574  
QY 722 TGCCCTTCTATCTTCTGATGAGCTGCTCAACATGCTGACCTTCCAGTACCT 781  
DB TGCCCTTCTATCTTGTCTGATGAGCTGCTCAACATGCTGACCTTCCAGTACCT 1634  
QY 782 TGAAGAGCTGATTCGGTACCTAGAGCCAGATCATGCGAGGTGGAGCTTGGACGCTCT 841  
DB TGAAGAGCTGATTCGGTACCTAGAGCCAGATCATGCGAGGTGGAGCTTGGACGCTCT

RESULT 11

US-09-706-968-42  
Sequence 42, Application US/09706968  
GENERAL INFORMATION:  
APPLICANT: Gao, Zeren  
APPLICANT: Hart, Charles E.  
APPLICANT: Piddington, Christopher S.  
APPLICANT: Sheppard, Paul O.  
APPLICANT: Shoemaker, Kimberly E.  
APPLICANT: Gilbertson, Debra G.  
APPLICANT: West, James W.  
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
FILE REFERENCE: 98-60C1  
CURRENT APPLICATION NUMBER: US/09/706,968  
CURRENT FILING DATE: 2000-11-06  
PRIOR APPLICATION NUMBER: US/09/541,752  
PRIOR FILING DATE: 2000-03-31  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 42  
LENGTH: 3571  
TYPE: DNA  
ORGANISM: Mus musculus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1049)...(2086)

DB 1635 TGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGCGAGTGGACTTGGACAGCTCT 1694  
QY 842 ACAAGCCAAACATGCGAGCTTTTGGCAAGGCTTCTGTATGGAAGAAAGCAAGTGG 901  
DB 1695 ACAAGCCAAACATGCGAGCTTTTGGCAAGGCTTCTGTATGGAAGAAAGCAAGTGG 1754  
QY 902 TGAATCTGAATCTCTCAAGAGAGGTAAACACTACAGCTGCACACCCCGGAATCTCT 961  
DB 1755 TGAATCTGAATCTCTCAAGAGAGGTAAACACTACAGCTGCACACCCCGGAATCTCT 1814  
QY 962 CAGTGTCCATACGGAAGAGCTAAAGAGGACAGATACCATATTTCTGGCAGGTTCTCTCC 1021  
DB 1815 CAGTGTCCATACGGAAGAGCTAAAGAGGACAGATACCATATTTCTGGCAGGTTCTCTCC 1874  
QY 1022 TGGTCAAGCGCTGTGGAGAAATTTGCTGTGTCTCCATTAATTTGCAATGATCTCAGT 1081  
DB 1875 TGGTCAAGCGCTGTGGAGAAATTTGCTGTGTCTCCATTAATTTGCAATGATCTCAGT 1934  
QY 1082 GTGTCCCAAGTAAAGTTACAAAAGTACCATGAGTCTCTCAGTTGAGACCAAAAAGTCTG 1141  
DB 1935 GTGTCCCAAGTAAAGTTACAAAAGTACCATGAGTCTCTCAGTTGAGACCAAAAAGTCTG 1994  
QY 1142 GAGTCAAGGATTTGCATAAGTCACTCACTGATGTGGCTCTGGAACACCAAGGAAATGTG 1201  
DB 1995 GAGTCAAGGATTTGCATAAGTCACTCACTGATGTGGCTCTGGAACACCAAGGAAATGTG 2054  
QY 1202 ACTGTGTGTAGAGGAAACGAGAGGATACTGAGGCTTCTGAGCAGTCTGAGCAGCAGT 1261  
DB 2055 ACTGTGTGTAGAGGAAACGAGAGGATACTGAGGCTTCTGAGCAGCAGTCTGAGCAGT 2114  
QY 1262 CACTGGCATTTCTGTATCCCAAGCAAGCAACCTTCATCCCAAGCAGGTTGGCCGAGG 1321  
DB 2115 CACTGGCATTTCTGTATCCCAAGCAAGCAACCTTCATCCCAAGCAGGTTGGCCGAGG 2174  
QY 1322 CACTGAGTCTGATGCTGCTGATGTAAGATCTTACTGCTCTCAACCAAAATTTCTCAG 1381  
DB 2175 CACTGAGTCTGATGCTGCTGATGTAAGATCTTACTGCTCTCAACCAAAATTTCTCAG 2234  
QY 1382 TTGTTTGTCTCAATAGCTTCCCTGAGGACTTCAAGTGTCTTCTAAAGACAGCAGGC 1441  
DB 2235 TTGTTTGTCTCAATAGCTTCCCTGAGGACTTCAAGTGTCTTCTAAAGACAGCAGGC 2294  
QY 1442 ACCAAGAGGATCAATCACAAGCACTGC 1470  
DB 2295 ACCAAGAGGATCAATCACAAGCACTGC 2323

[illegible]



```
Db 1215 GGAGCATCACAGCCCGAAGTTTCCTCATACATACCAAGAAATATGGTGTGTGGA 1274
Qy 422 GATTAGTTCAGTAGAATAATGTCCGGATCCAGCTGACATTTGATGAGAGATTTGGGC 481
Db 1275 GATTAGTTCAGTAGAATAATGTCCGGATCCAGCTGACATTTGATGAGAGATTTGGGC 1334
Qy 482 TGGAGATCCAGAGACGATATATCAAGTATGATTTTGTAGAAAGTTGAGAGCCAGTG 541
Db 1335 TGGAGATCCAGAGACGATATATCAAGTATGATTTTGTAGAAAGTTGAGAGCCAGTG 1394
Qy 542 ATGGAAGTGTTTTAGGACGCTGGTGTGTGTTCTGGACTGTGCGAGAAAGCAGACTTCTA 601
Db 1395 ATGGAAGTGTTTTAGGACGCTGGTGTGTGTTCTGGACTGTGCGAGAAAGCAGACTTCTA 1454
Qy 602 AAGGAATCATATCAGGATAGAGATTTGTATCTGATGAGTATTTTCCATCTGACCCGGAT 661
Db 1455 AAGGAATCATATCAGGATAGAGATTTGTATCTGATGAGTATTTTCCATCTGACCCGGAT 1514
Qy 662 TCTGCATCCACTACAGTATTTATCATGCCACAAGTTCAGAGAAACAGAGTCCCTTCGGTGT 721
Db 1515 TCTGCATCCACTACAGTATTTATCATGCCACAAGTTCAGAGAAACAGAGTCCCTTCGGTGT 1574
Qy 722 TGCCCCCTTCATTTTGTCAATGTGACCTGTCTCAACATGTGTGACTGTGACCTTCAGTACCT 781
Db 1575 TGCCCCCTTCATTTTGTCAATGTGACCTGTCTCAACATGTGTGACTGTGACCTTCAGTACCT 1634
Qy 782 TGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGGACTTGGACAGCCTCT 841
Db 1635 TGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGGACTTGGACAGCCTCT 1694
Qy 842 ACAAGCCAAATGGCAGCTTTTGGGCAAGGCTTTCCTGTATGGGAAAAAAGCAAGTGG 901
Db 1695 ACAAGCCAAATGGCAGCTTTTGGGCAAGGCTTTCCTGTATGGGAAAAAAGCAAGTGG 1754
Qy 902 TGAATCTGAATCTCTCAAGAGAGAGGTAAACTCTACAGCTGCAACCCCGGAATCTCT 961
Db 1755 TGAATCTGAATCTCTCAAGAGAGAGGTAAACTCTACAGCTGCAACCCCGGAATCTCT 1814
Qy 962 CAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACCATATTTCTGGCCAGGTTGTCTCC 1021
Db 1815 CAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACCATATTTCTGGCCAGGTTGTCTCC 1874
Qy 1022 TGCTCAAGCGCTGTGGAGGAAATTTGTCCTGTGTCTCCATAATTTGCAATGAATGTCACT 1081
Db 1875 TGCTCAAGCGCTGTGGAGGAAATTTGTCCTGTGTCTCCATAATTTGCAATGAATGTCACT 1934
Qy 1082 GTGTCCACGATAAGTTTACAAAAGTACCATGAGTCCCTTCAGTTGAGACCAAAACTG 1141
Db 1935 GTGTCCACGATAAGTTTACAAAAGTACCATGAGTCCCTTCAGTTGAGACCAAAACTG 1994
Qy 1142 GAGTCAAGGGATTGCATAAGTCACTCACTGATGTGGCTCTGGAACACACAGAGGAATGTG 1201
Db 1995 GAGTCAAGGGATTGCATAAGTCACTCACTGATGTGGCTCTGGAACACACAGAGGAATGTG 2054
Qy 1202 ACTGTGTGTAGAGGAAACGACAGGAGGTAACTGCAAGCTTTCGTAGAGCACAACGTGAG 1261
Db 2055 ACTGTGTGTGTAGAGGAAACGACAGGAGGTAACTGCAAGCTTTCGTAGAGCACAACGTGAG 2114
Qy 1262 CACTGGCATTCGTGTACCCCAACAGCAACTTCATCCCAACAGAGGTTGGCCGAGGG 1321
Db 2115 CACTGGCATTCGTGTGTACCCCAACAGCAACTTCATCCCAACAGAGGTTGGCCGAGGG 2174
Qy 1322 CTCTCAGCTGTGATGTGGCTATGGTAAAGATCTTACTCTCTCCAAACCAAAATCTCTCAG 1381
Db 2175 CTCTCAGCTGTGATGTGGCTATGGTAAAGATCTTACTCTCTCCAAACCAAAATCTCTCAG 2234
Qy 1382 TTGTTTGGTTCATATAGCTTCCCTCGCAGGACTTCAAGTGTCTTCTAAAGACACAGAGGC 1441
Db 2235 TTGTTTGGTTCATATAGCTTCCCTCGCAGGACTTCAAGTGTCTTCTAAAGACACAGAGGC 2294
Qy 1442 ACCAAGAGGTCAATCACAAGCACTGC 1470
Db 2295 ACCAAGAGGTCAATCACAAGCACTGC 2323
```

```
RESULT 14
US-10-264-361-3
; Sequence 3, Application US/10264361
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROSIS
; FILE REFERENCE: 00-53
; CURRENT APPLICATION NUMBER: US/10/264,361
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US/09/695,121
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 3571
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1049)...(2086)
US-10-264-361-3
```

```
Query Match 98.0%; Score 1444.8; DB 49; Length 3571;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1460; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

Qy 2 ACCTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGAAACTA 61
Db 856 AACTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGAAACTA 915
Qy 62 CCCTGGCATCTCTGCTGCCAGAGCGGCCAGCGCTTCCACCGCAGCGAGCCTTTTCCC 121
Db 916 CCCTGGCATCTCTGCTGCCAGAGCGGCCAGCGCTTCCACCGCAGCGAGCCTTTCCC 975
Qy 122 CGGGCTGGGTGAGCCTTTGGAGTGTGCTTCCCGAGTCCCGCGGAGTGAGCCCTCG 181
Db 976 C-GGCTGGGCTGAGCCTTTGGAGTGTGCTTCCCGAGTCCCGCGGAGTGAGCCCTCG 1034
Qy 182 CCCAGTTCAGCCAAATGCTCCTCTCGGCTCTCTCTGCTGACATCTGCCCTGCCGCGCC 241
Db 1035 CCCAGTTCAGCCAAATGCTCCTCTCGGCTCTCTCTGCTGACATCTGCCCTGCCGCGCC 1094
Qy 242 AAAGAACGGGACTTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCAGCTCTCCAGCGACA 301
Db 1095 AAAGAACGGGACTTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCAGCTCTCCAGCGACA 1154
Qy 302 AGGAACAGAACGGAGTCCAAAGATCCCGGCATGAGAGAGTTGTCACTATATCTGGTAATG 361
Db 1155 AGGAACAGAACGGAGTCCAAAGATCCCGGCATGAGAGAGTTGTCACTATATCTGGTAATG 1214
Qy 362 GGAGCATCCACAGCCCGAAGTTTCTCATAGTACCAAGAAATATGCTGCTGTGTGGA 421
Db 1215 GGAGCATCCACAGCCCGAAGTTTCTCATAGTACCAAGAAATATGCTGCTGTGTGGA 1274
Qy 422 GATTAGTTGCAGTAGATGAAAAATGTGCGGATCCAGCTGACATTTTGTAGAGAGATTTGGGC 481
Db 1275 GATTAGTTGCAGTAGATGAAAAATGTGCGGATCCAGCTGACATTTTGTAGAGAGATTTGGGC 1334
Qy 482 TGAAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAAAGTTGAGAGCCAGTG 541
Db 1335 TGAAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAAAGTTGAGAGCCAGTG 1394
Qy 542 ATGGAAGTGTTTTAGGACGCTGGTGTGTGTTCTGGACTGTGCGAGAAAGCAGACTTCTA 601
Db 1395 ATGGAAGTGTTTTAGGACGCTGGTGTGTGTTCTGGACTGTGCGAGAAAGCAGACTTCTA 1454
Qy 602 AAGGAATCATATCAGGATAGAGATTTTGTATCTGATGAGTATTTTCCATCTGGAACCCGGAT 661
Db 1455 AAGGAATCATATCAGGATAGAGATTTTGTATCTGATGAGTATTTTCCATCTGGAACCCGGAT 1514
Qy 662 TCTGCATCCACTACAGTATTTATCATGCCACAAGTTCAGAGAAACAGAGTCCCTTCGGTGT 721
```

```
Db 1515 TCTGATCACTACAGTATTATCATGCCACAAGTCACAGAAACCAGAGTCTTCGGTGT 1574
QY 722 TGGCCCTTCATCTTTGTCATTTGGACCTGCTCAACATGCTGTGACTGCTTCAGTACCT 781
Db 1575 TGGCCCTTCATCTTTGTCATTTGGACCTGCTCAACATGCTGTGACTGCTTCAGTACCT 1634
QY 782 TGGAGAGCTGATTCGGTACCTTAGACCCAGATCGATGGCAGTGGACTTTGGACAGCTCT 841
Db 1635 TGGAGAGCTGATTCGGTACCTTAGACCCAGATCGATGGCAGTGGACTTTGGACAGCTCT 1694
QY 842 ACAAGCCACATGCGAGCTTTTGGGCAAGGCTTTCTGTATGGAAAAAAGCAAGTGG 901
Db 1695 ACAAGCCACATGCGAGCTTTTGGGCAAGGCTTTCTGTATGGAAAAAAGCAAGTGG 1754
QY 902 TGAATCTGAATCTCTCAAGGAGAGGTAAACTCTACAGCTGCACACCCCGAATCTCT 961
Db 1755 TGAATCTGAATCTCTCAAGGAGAGGTAAACTCTACAGCTGCACACCCCGAATCTCT 1814
QY 962 CAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACCATATTTCTGGCCAGGTTGTCTCC 1021
Db 1815 CAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACCATATTTCTGGCCAGGTTGTCTCC 1874
QY 1022 TGGTCAAGCGCTGTGAGGAAATTTGGCTGTGCTTCTCCATTAATGCAATGAATGTCACT 1081
Db 1875 TGGTCAAGCGCTGTGAGGAAATTTGGCTGTGCTTCTCCATTAATGCAATGAATGTCACT 1934
QY 1082 GTGTCCCAAGTAAAGTTACAAAAAGTACCATGAGGTCTCTCAGTTTGAGACCAAAAGTGG 1141
Db 1935 GTGTCCCAAGTAAAGTTACAAAAAGTACCATGAGGTCTCTCAGTTTGAGACCAAAAGTGG 1994
QY 1142 GAGTCAAGGATTTGCATAAGTCACTCACTGATGGCTCTCGGAACACCAGGAAATGTG 1201
Db 1995 GAGTCAAGGATTTGCATAAGTCACTCACTGATGGCTCTCGGAACACCAGGAAATGTG 2054
QY 1202 ACTGTGTGTAGAGAAAGCGAGGAGGTAACTGAGCTTCGTAGCAGCACACGTGAG 1261
Db 2055 ACTGTGTGTAGAGAAAGCGAGGAGGTAACTGAGCTTCGTAGCAGCACACGTGAG 2114
QY 1262 CACTGGCATCTGTGTACCCCAAGCAACCTTCATCCCAAGGTTGGCGCAGGG 1321
Db 2115 CACTGGCATCTGTGTACCCCAAGCAACCTTCATCCCAAGGTTGGCGCAGGG 2174
QY 1322 CTCTCAGCTGCTGATGCTGCTATGGTAAAGATCTTACTGCTCTCAACCAAAATTTCTCAG 1381
Db 2175 CTCTCAGCTGCTGATGCTGCTATGGTAAAGATCTTACTGCTCTCAACCAAAATTTCTCAG 2234
QY 1382 TTGTTTGTCTCAATAGCTTCCCTGCGAGGACTTCAAGTGTCTTCTAAAGACGAGGC 1441
Db 2235 TTGTTTGTCTCAATAGCTTCCCTGCGAGGACTTCAAGTGTCTTCTAAAGACGAGGC 2294
QY 1442 ACCAANAGGAGTCAATCACAAGACACTGC 1470
Db 2295 ACCAAGAGGAGTCAATCACAAGACACTGC 2323
```

RESULT 15

```
US-09-104-216-34
; Sequence 34, Application US/09304216
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19X
; CURRENT APPLICATION NUMBER: US/09/304,216
; CURRENT FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 3571
; TYPE: DNA
; ORGANISM: Mus musculus
```

```
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1049) ... (2086)
US-09-304-216-34

Query Match 97.2%; Score 1432.8; DB 19; Length 3573;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1460; Conservative 0; Mismatches 8; Indels 3; Gaps 2;

QY 2 ACCTGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGAAACTA 61
Db 856 AACTGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGAAACTA 915
QY 62 CCCTGCGATTCTCTGCTGCCAGAGCGCGCCAGCGCTTCCACCGCAGCGAGCTTTTCCC 121
Db 916 CCCTGCGATTCTCTGCTGCCAGAGCGCGCCAGCGCTTCCACCGCAGCGAGCTTTTCCC 975
QY 122 CCGGCTGGGCTGAGCCCTTGGAGTCGTCTTCCCGAGTCCCGCGGAGTGAGCCCTCG 181
Db 976 C-GGCTGGGCTGAGCCCTTGGAGTCGTCTTCCCGAGTCCCGCGGAGTGAGCCCTCG 1034
QY 182 CCGCAGTCAGCCAAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCCCCGCGGCC 241
Db 1035 CCGCAGTCAGCCAAATGCTCTCTCTCGGCTCTCTCTGCTGACATCTGCCCCGCGGCC 1094
QY 242 AAAGAACCGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCGAGCTCTCCAGCGACA 301
Db 1095 AAAGAACCGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCGAGCTCTCCAGCGACA 1154
QY 302 AGGACAGAACCGGAGTGCAGATCCCGGCATGAGAGAGTTGTCACTATATCTGGTAATG 361
Db 1155 AGGACAGAACCGGAGTGCAGATCCCGGCATGAGAGAGTTGTCACTATATCTGGTAATG 1214
QY 362 GGAGCATCCACAGCCCGAAGTTTCCTCATACGTACCCAGAAATATGGTCTGTGTGGA 421
Db 1215 GGAGCATCCACAGCCCGAAGTTTCCTCATACGTACCCAGAAATATGGTCTGTGTGGA 1274
QY 422 GATTAGTTCAGTAAATGTAATGTCGGATCCAGCTGACATTTGATGAGAGTTTGGGC 481
Db 1275 GATTAGTTCAGTAAATGTAATGTCGGATCCAGCTGACATTTGATGAGAGTTTGGGC 1334
QY 482 TGGAAATCCAGAAAGCATATATGCAAGTATGATTTGTAGAGTTGAGAGCCAGTG 541
Db 1335 TGGAAATCCAGAAAGCATATATGCAAGTATGATTTGTAGAGTTTGTAGAGCCAGTG 1394
QY 542 ATGGAAGTGTTTTGGAGCGCTGTGTGTTCTGGACTGTGCGAGAAAGCAGACTTCTA 601
Db 1395 ATGGAAGTGTTTTGGAGCGCTGTGTGTTCTGGACTGTGCGAGAAAGCAGACTTCTA 1454
QY 602 AAGGAAATCATATCAGGATAAGATTGTATCTGATGAGTATTTTCCATCTGAAACCCGAT 661
Db 1455 AAGGAAATCATATCAGGATAAGATTGTATCTGATGAGTATTTTCCATCTGAAACCCGAT 1514
QY 662 TCTGCAATCCATACAGTATTTATCATGCCCAAGTCCAGAAACCAGGTCCTTCGGTGT 721
Db 1515 TCTGCAATCCATACAGTATTTATCATGCCCAAGTCCAGAAACCAGGTCCTTCGGTGT 1574
QY 722 TGCCCTTCATCTTTGTGCTCAATGCTCAACATGCTGTGACTGCTTCAGTACCT 781
Db 1575 TGCCCTTCATCTTTGTGCTCAATGCTCAACATGCTGTGACTGCTTCAGTACCT 1634
QY 782 TGGAGAGCTGATTCGGTACCTTAGAGCCAGATCGATGGCAGGTTGAGTGAAGCTCT 841
Db 1635 TGGAGAGCTGATTCGGTACCTTAGAGCCAGATCGATGGCAGGTTGAGTGAAGCTCT 1694
QY 842 ACAAGCCACATGCGAGCTTTTGGGCAAGGCTTTCTGTATGGAAAAAAGCAAGTGG 901
Db 1695 ACAAGCCACATGCGAGCTTTTGGGCAAGGCTTTCTGTATGGAAAAAAGCAAGTGG 1754
QY 902 TGAATCTGAATCTCTCAAGGAGAGGTAAACTCTACAGCTGCACACCCCGAATCTCT 961
Db 1755 TGAATCTGAATCTCTCAAGGAGAGGTAAACTCTACAGCTGCACACCCCGAATCTCT 1814
```



QY	962	CAGTGTCCATACGGGAAGACTAAAGAGACAGATACCATATTTCTGGCCAGGTTGTCTCC	1021
Db	1815		
QY	1022	TGGTCAAGCGCTGTGAGGAAATTTGCTGTCTCCATAATTTGCAATGAATGTCACT	1081
Db	1875		
QY	1082	GTGTCCCAAGTAAAGTTACAAAAGTACCATGAGTCTTTCAGTTGAGACCAAAACTG	1141
Db	1935		
QY	1142	GAGTCAAGGATTTGCATAAGTCACTCACTGATGTGGCTCTGGAACACACGAGGAATGTG	1201
Db	1995		
QY	1202	ACTGTGTGTAGAGGAAAGCGAGGAGGTAACTGCAGCCTTCGTAGCAGCACACGTGAG	1261
Db	2055		
QY	1262	CAGTGCATTCTGTACCCCC--ACAAGCAACCTTCATCCCCCACGAGCGTTGGCCGCGAG	1319
Db	2115		
QY	1320	GGCTCTCAGCTGTGATGTGGCTATGTTAAAGATCTTACTCGTCTCCAAACCAATTC	1379
Db	2175		
QY	1380	AGTTGTTTGGTTCAATAGCCTTCCCTGCAGGACTTCAAGTGTCTTCTAAAGACCCAGAG	1439
Db	2235		
QY	1440	GCACCAANAGGAGTCAATCAAAAGCACTGC	1470
Db	2295		

Search completed: November 26, 2003, 08:55:02  
Job time : 3152.15 secs



GenCore version 5.1.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 26, 2003, 00:11:41 ; Search time 272.739 Seconds  
(without alignments)  
9894.257 Million cell updates/sec

Title: US-09-852-209A-6  
Perfect score: 1474  
Sequence: 1 caccgtggagacacagaagag.....aatcacaaagcactgcacgc 1474

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2523179 seqs, 915383134 residues

Total number of hits satisfying chosen parameters: 5046358

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents\_NA.New.\*  
1: /cgn2\_6/prodata/1/pna/US06\_NEW\_COMB.seq.\*  
2: /cgn2\_6/prodata/1/pna/US07\_NEW\_COMB.seq.\*  
3: /cgn2\_6/prodata/1/pna/US08\_NEW\_COMB.seq.\*  
4: /cgn2\_6/prodata/1/pna/US09\_NEW\_COMB.seq.\*  
5: /cgn2\_6/prodata/1/pna/US10\_NEW\_COMB.seq.\*  
6: /cgn2\_6/prodata/1/pna/US11\_NEW\_COMB.seq.\*  
7: /cgn2\_6/prodata/1/pna/US12\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1444.8	98.0	3571	5	US-09-457-066-42
2	1444.8	98.0	3571	5	US-09-876-813-34
3	1444.8	98.0	3571	6	US-10-864-432-3
4	914.2	62.0	3007	1	PCT-US03-26491-58
5	914.2	62.0	3007	6	US-10-648-593-58
6	914.2	62.0	3007	7	US-60-507-511-2084
7	913.8	62.0	3007	7	US-60-487-610-231
8	913.8	62.0	3007	7	US-60-485-450-137
9	912.6	61.9	2779	5	US-09-830-320A-8
10	878.8	59.6	1760	5	US-09-457-066-1
11	878.8	59.6	1760	5	US-09-876-813-32
12	878.8	59.6	1760	6	US-10-664-432-1
13	745.8	50.6	1095	5	US-09-457-066-50
14	660.8	44.8	1035	5	US-09-457-066-6
15	519	35.2	918	1	PCT-US00-28803-6
16	221.8	15.0	221510	7	US-60-487-610-19346
17	221.8	15.0	221510	7	US-60-485-450-11913
18	175	11.9	1110	7	US-09-876-813-6
19	137.2	9.3	1113	6	US-10-321-962-7
20	137.2	9.3	1472	5	US-09-876-813-52
21	137.2	9.3	1472	6	US-10-606-055-3
22	124	8.4	1829	6	US-10-321-962-3
23	123.2	8.4	1882	5	US-09-457-066-36
24	123.2	8.4	1882	6	US-09-876-813-1
25	123.2	8.4	1882	6	US-10-606-055-1
26	119.2	8.1	1587	6	US-10-321-962-5

27	105.6	7.2	135	5	US-09-540-233D-96491	Sequence 96491, A
28	102.6	7.0	462	6	US-10-321-962-11	Sequence 11, Appl
29	84.4	5.7	201	7	US-60-487-610-5053	Sequence 5053, Ap
30	84.4	5.7	201	7	US-60-487-610-5074	Sequence 32074, A
31	84.4	5.7	201	7	US-60-485-450-3279	Sequence 3279, Ap
32	84.4	5.7	201	7	US-60-485-450-19018	Sequence 19018, A
33	82.2	5.6	898	6	US-10-321-962-9	Sequence 9, Appl
34	60.8	4.1	173	1	PCT-US03-26220-26739	Sequence 26739, A
35	40.4	2.7	1176	7	US-60-485-450-651	Sequence 651, App
36	40.4	2.7	14575	7	US-60-485-450-12172	Sequence 12172, A
37	39.6	2.7	201	7	US-60-487-610-5054	Sequence 5054, Ap
38	39.6	2.7	201	7	US-60-487-610-32070	Sequence 32070, A
39	39.6	2.7	201	7	US-60-485-450-3280	Sequence 3280, Ap
40	39.6	2.7	201	7	US-60-485-450-19014	Sequence 19014, A
41	39.6	2.7	415	6	US-10-321-962-13	Sequence 13, Appl
42	39.4	2.7	17493	7	US-60-485-450-12170	Sequence 12170, A
43	37.6	2.6	1789	7	US-60-507-511-593	Sequence 593, App
44	37.6	2.6	8591	6	US-10-221-714A-291	Sequence 291, App
45	37.2	2.5	1133	1	PCT-US03-21379-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1  
US-09-457-066-42  
; Sequence 42, Application US/09457066  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60  
; CURRENT APPLICATION NUMBER: US/09/457,066  
; CURRENT FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 42  
; LENGTH: 3571  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1049)...(2086)  
US-09-457-066-42

Query Match	98.0%	Score 1444.8;	DB 5;	Length 3571;
Best Local Similarity	99.4%;	Pred. No. 0;	Mismatches 1460;	Conservative 0;
Matches	1460;	Conservative 0;	Mismatches 8;	Indels 1;
Gaps	1;			
QY	2	ACTTGAGACACAGAGAGCGCTCTAGGAAAAATTTTGGATGGGATATGTGGAACCTA	61	
Db	856	AACCTGAGACACAGAGAGCGCTCTAGGAAAAATTTTGGATGGGATATGTGGAACCTA	915	
QY	62	CCCTGGATTCTCTGCTGCCAGAGCGCGCAGCGCTTCCACCGCAGCGAGCTTTTCCC	121	
Db	916	CCCTGGATTCTCTGCTGCCAGAGCGCGCAGCGCTTCCACCGCAGCGAGCTTTTCCC	975	
QY	122	CGGGCTGGGCTGAGCGCTTGGAGTCGTCGCTTCCCGAGTCCCGCGGAGTGAGCCCTCG	181	
Db	976	C-GGCTGGGCTGAGCGCTTGGAGTCGTCGCTTCCCGAGTCCCGCGGAGTGAGCCCTCG	1034	
QY	182	CCCACTGAGCMAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCTGCGCGGCC	241	
Db	1035	CCCACTGAGCMAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCTGCGCGGCC	1094	
QY	242	AAAGACGGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGACAGCTCTCCAGGACA	301	
Db	1095	AAAGACGGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGACAGCTCTCCAGGACA	1154	

302 AGGAACAGACGAGTGCAGATCCCGCATGAGAGAGTTGCTCACTATATCTGTTAATG 361  
1155 AGGAACAGACGAGTGCAGATCCCGCATGAGAGAGTTGCTCACTATATCTGTTAATG 1214  
362 GGAGATCCACAGCCGAGATTTCTCTACATACGTACCCAGAAATATGGTGGTGTGGA 421  
1215 GGAGATCCACAGCCGAGATTTCTCTACATACGTACCCAGAAATATGGTGGTGTGGA 1274  
422 GATTAGTCCAGTAGATGAATAATGTCCGGATCCAGCTGATGATGATGAGAGATTTGGGC 481  
1275 GATTAGTCCAGTAGATGAATAATGTCCGGATCCAGCTGATGATGATGAGAGATTTGGGC 1334  
482 TGGAGATCCAGAGACGATATATGCAAGTATGATTTGTAGAGTTGAGGAGCCAGTG 541  
1335 TGGAGATCCAGAGACGATATATGCAAGTATGATTTGTAGAGTTGAGGAGCCAGTG 1394  
542 ATGGAGTGTGTTAGACGCTGGTGTGTTCTGGGACTGTGCCAGAAAGCAGACTCTA 601  
1395 ATGGAGTGTGTTAGACGCTGGTGTGTTCTGGGACTGTGCCAGAAAGCAGACTCTA 1454  
602 AAGGAATCATATCAGGATAAGATTTGTATCTGATGATGATTTTCCATCTGAACCCGGAT 661  
1455 AAGGAATCATATCAGGATAAGATTTGTATCTGATGATGATTTTCCATCTGAACCCGGAT 1514  
662 TCTGCATCCACTACAGTATTATCATGCCACAAGTCAAGAAACACGAGTCTCTCGGTGT 721  
1515 TCTGCATCCACTACAGTATTATCATGCCACAAGTCAAGAAACACGAGTCTCTCGGTGT 1574  
722 TGCCCCCTTTCATCTTTGTCAATGGAGCTGTCTCAACAAATGTGTGACTGCTTCAGTACCT 781  
1575 TGCCCCCTTTCATCTTTGTCAATGGAGCTGTCTCAACAAATGTGTGACTGCTTCAGTACCT 1634  
782 TGGAGAGCTGATTCGGTACCTAGACCCAGATCGATGGCAGGTGGACTTGGACAGCTCT 841  
1635 TGGAGAGCTGATTCGGTACCTAGACCCAGATCGATGGCAGGTGGACTTGGACAGCTCT 1694  
842 ACAAGCCAAATGGCAGCTTTTGGGCAAGGCTTTCTGTATGGGAAAAAAGCAAGTGG 901  
1695 ACAAGCCAAATGGCAGCTTTTGGGCAAGGCTTTCTGTATGGGAAAAAAGCAAGTGG 1754  
902 TGAATCTGAATCTCTCAAGGAAAGAGTAAATCTTACAGCTGCAACCCCGGAATCTCT 961  
1755 TGAATCTGAATCTCTCAAGGAAAGAGTAAATCTTACAGCTGCAACCCCGGAATCTCT 1814  
962 CAGTGTCCATACCGGAGAGCTAAAGAGGACAGATACCATATTTCTGGCCAGGTTGCTCC 1021  
1815 CAGTGTCCATACCGGAGAGCTAAAGAGGACAGATACCATATTTCTGGCCAGGTTGCTCC 1874  
1022 TGGTCAAGCGCTGTGGAGGAAATTTGTCCTGTTGTCTCCATAATTCGAATGTGTCAGT 1081  
1875 TGGTCAAGCGCTGTGGAGGAAATTTGTCCTGTTGTCTCCATAATTCGAATGTGTCAGT 1934  
1082 GTGTCCACGATAAGTTTACAAAAGTACCATGAGTCTTTCAGTTGAGACCAAAACTG 1141  
1935 GTGTCCACGATAAGTTTACAAAAGTACCATGAGTCTTTCAGTTGAGACCAAAACTG 1994  
1142 GAGTCAAGGATTCGATAAGTCACTCACTGATGTGGCTCTGGAACACACGAGGAATGTG 1201  
1995 GAGTCAAGGATTCGATAAGTCACTCACTGATGTGGCTCTGGAACACACGAGGAATGTG 2054  
1202 ACTGTGTGTGTAGAGGAAACGACGAGGATTAATTCGAGCCTTTCGTAGCAGCACACGTGAG 1261  
2055 ACTGTGTGTGTAGAGGAAACGACGAGGATTAATTCGAGCCTTTCGTAGCAGCACACGTGAG 2114  
1262 CACTGGCATTCGTGTATCCCCCAACAAGCACTTCATCTCCACACAGGTTGGCCGAGGG 1321  
2115 CACTGGCATTCGTGTATCCCCCAACAAGCACTTCATCTCCACACAGGTTGGCCGAGGG 2174  
1322 CTCTCAGCTGTGATGCTGGTATGGTAAAGATCTTACTGCTCCCAACCAAAATCTCTCAG 1381  
2175 CTCTCAGCTGTGATGCTGGTATGGTAAAGATCTTACTGCTCTCCCAACCAAAATCTCTCAG 2234

1382 TTGTTTGTCTCAATAGCCTTCCCTGCAGAGCTTCAAGTGTCTTTAAAGACGAGGC 1441  
2235 TTGTTTGTCTCAATAGCCTTCCCTGCAGAGCTTCAAGTGTCTTTAAAGACGAGGC 2294  
1442 ACCAANAGAGTCAATCAACAAAGCACTGC 1470  
2295 ACCAAGAGGAGTCAATCAACAAAGCACTGC 2323

RESULT 2  
US-09-876-813-34  
; Sequence 34, Application US/09876813  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4  
; FILE REFERENCE: 99-19  
; CURRENT APPLICATION NUMBER: US/09/876,813  
; CURRENT FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: US/09/564,595  
; PRIOR FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: US/09/304,216  
; PRIOR FILING DATE: 1999-05-03  
; PRIOR APPLICATION NUMBER: US/60/164,463  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: US/60/180,169  
; PRIOR FILING DATE: 2000-02-04  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 34  
; LENGTH: 3571  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1049)...(2086)  
US-09-876-813-34

Query Match 98.0%; Score 1444.8; DB 5; Length 3571;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 1460; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 2 ACCTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGAAACTA 61  
DB 856 AACTGGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTTATGTGAAACTA 915  
QY 62 CCTGGGATTTCTGTGCCAGAGCCGGCCAGGGCTTCCACCGCAGCGAGCCTTTCCC 121  
DB 916 CCTGGGATTTCTGTGCCAGAGCCGGCCAGGGCTTCCACCGCAGCGAGCCTTTCCC 975  
QY 122 CGGGCTGGGCTGAGCCTTGGAGTCGTCTTCCAGTCCCGCGGAGTGAGCCCTCG 181  
DB 976 C-GGCTGGGCTGAGCCTTGGAGTCGTCTTCCAGTCCCGCGGAGTGAGCCCTCG 1034  
QY 182 CCCAGTTCAGCCAAATGCTCTCTCGGCTCTCTCTGTGACATCTGCCCTGCCCGGCC 241  
DB 1035 CCCAGTTCAGCCAAATGCTCTCTCGGCTCTCTCTGTGACATCTGCCCTGCCCGGCC 1094  
QY 242 AAAGACGGGAGCTCGGGCTGAGTCCAACTGAGCAGCAAGTTGAGCTCTCCAGCGACA 301  
DB 1095 AAAGACGGGAGCTCGGGCTGAGTCCAACTGAGCAGCAAGTTGAGCTCTCCAGCGACA 1154  
QY 302 AGGAACAGAACGGAGTCCCGGATCCCGCATGAGAGATTGTCACTATATCTGTTAATG 361  
DB 1155 AGGAACAGAACGGAGTCCCGGATCCCGCATGAGAGATTGTCACTATATCTGTTAATG 1214  
QY 362 GGAGCATCCACAGCCCGAAGTTTCTCATACGTACCCAGAAATATGGTGTGTGGA 421  
DB 1215 GGAGCATCCACAGCCCGAAGTTTCTCATACGTACCCAGAAATATGGTGTGTGGA 1274  
QY 422 GATTAGTTCAGTAGATGAATAATGTGGGATCCAGCTGACATTTGATGAGAGATTTGGGC 481



Query Match		62.0%; Score 914.2; DB 1; Length 3007;	
Best Local Similarity		83.5%; Pred. No. 6.6e-285;	
Matches 1050; Conservative		0; Mismatches 203; Indels 4; Gaps 1;	
QY	2	ACCTCGAGACACAGAAAGAGGCTCTAGGAAAAATTTTGGATGGGGATTATGTGGAAACTA	61
DB	294	AACCTGGAGACACAGAAAGAGGCTCTAGGAAAAATTTTGGATGGGGATTATGTGGAAACTA	353
QY	62	CCCTCGAATTCCTGCTGCCAGAGCCGGCTTCCACCGAGCGAGCTCTTCCC	121
DB	354	CCCTCGAATTCCTGCTGCCAGAGCCGGCTTCCACCGAGCGAGCTCTTCCC	413
QY	122	CGG----GCTGGGCTGAGGCTTGGAGTCGTCTGCTTCCCAGTCCCGCGGAGTGAGCC	177
DB	414	TGGCGGTGGTGAAGAGAGCTCGGGAGTCGTCTTCCAAAGTGGCCCGGTGAGTGAGCT	473
QY	178	CTCGCCCCAGTCAGCCAAATGCTCTCTCTCGGCTCTCTCTCTGCTGACATCTGCCCCCTGGCC	237
DB	474	CTACCCCCAGTCAGCCAAATGAGCCTCTTCCGGCTTCTCTGCTGACATCTGCCCCCTGGCC	533
QY	238	GGCCAAAGAACCGGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCGAGCTCTCCAGC	297
DB	534	GGCCAGAGACAGGGGACTCGGGGAAATCCAACTGAGTAGTAATTTCCAGTTTCCAGC	593
QY	298	GACAGGAACAGAAAGGAGTGCAGATCCCGGATGAGAGAGTTGCTACTATATCTGGT	357
DB	594	AACAAGGAACAGAAAGGAGTGCAGATCCCGGATGAGAGAGTTTACTGTGTCTACT	653
QY	358	AATGGAGCATCCACAGCCCGAAGTTTCTCATATGATACCAAGAAATATGGTCTGGTG	417
DB	654	AATGGAAGTATTCACAGCCCAAGTTTCTCATCTTATCCAGAAATACGGTCTTGTA	713
QY	418	TGAGATTAAGTTGCGAGTAGATGAAATGTGGGATCCAGCTGACATTTGATGAGAGATT	477
DB	714	TGAGATTAAGTAGCAGTAGAGGAATGTATGGATACAACTTACGTTTGTGAAAGATT	773
QY	478	GGGCTGGAAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAAAGTTGAGAGGCC	537
DB	774	GGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTTGTAGAAAGTTGAGAGAAC	833
QY	538	AGTGATGGAAGTGTTTTAGGACGCTGGTGGTCTGGGACTGTGCCAGGAAGCAGACT	597
DB	834	AGTGATGGAAGTGTATTTAGGGCGCTGGTGGTCTGGTCTGTATGAT	

Db 1314 CTCCTGGTTAAACGCTGTGGTGGAACTGTGCCCTGTGTCTCCCAATTCGAATGAATGT 1373  
Qy 1078 CAGTGTGTCCCAAGTAAAGTTACAAAAGTACCATGAGTCTCTCAGTTGAGACCAAAA 1137  
Db 1374 CAATGTGTCCCAAGCAAGTTACTAAAATATACACGAGTCTCTCAGTTGAGACCAAG 1433  
Qy 1138 ACTGGAGTCAAGGATGTCATAGTCACTCAGTGTGTCTGGAACACCAAGGAA 1197  
Db 1434 ACCGGTGTGAGGGGATGCAAAATCACTCAGCAGTGGCCCTGGAGCACCATGAGGAG 1493  
Qy 1198 TGTGACTGTGTGTAGAGAAACGAGAGGTAAGTCTCAGCCTTCGTAGCAGCAC 1254  
Db 1494 TGTGACTGTGTGTGACAGAGGAGACAGGAGGATAGCCGATCACCAACGAGCCTC 1550

RESULT 5  
US-10-648-593-58  
; Sequence 58, Application US/10648593  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT  
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR  
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS  
; FILE REFERENCE: D0273 NP  
; CURRENT APPLICATION NUMBER: US/10/648,593  
; CURRENT FILING DATE: 2003-08-26  
; PRIOR APPLICATION NUMBER: 60/406,385  
; PRIOR FILING DATE: 2002-08-27  
; NUMBER OF SEQ ID NOS: 557  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 58  
; LENGTH: 3007  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-648-593-58

Query Match 62.0%; Score 914.2; DB 6; Length 3007;  
Best Local Similarity 83.5%; Pred. No. 6.6e-285;  
Matches 1050; Conservative 0; Mismatches 203; Indels 4; Gaps 1;

Qy 2 ACCTGGAGACACAGAGAGGCTCTAGGAAAAATTTTGGATGGGATTTATGCGAACTA 61  
Db 294 AACTGGAGACACAGAGAGGCTCTAGGAAAAATTTTGGATGGGATTTATGCGAACTA 353  
Qy 62 CCTGCGATTCCTGCTGCCAGAGCGGCGCAGCGGCTTCCACCGCAGCGAGCCTTTCCC 121  
Db 354 CCTGCGATTCCTGCTGCCAGAGCGGCTCGCGGCTTCCACCGCAGCGAGCCTTTCCC 413  
Qy 122 CGG----GCTGGGCTGAGCCTTGGAGTGTGCTTCCCAAGTCCCGCGCGAGTGAGCC 177  
Db 414 TGGCGGTGTGTGAAGAGACTCGGGAGTGTGCTTCCAAAGTCCCGCGCGTGTGAGTGAGCT 473  
Qy 178 CTCGCCCCAGTACAGCAATAGCTCTCTCGGCTCTCTCTGTCGATCATGCGCCTGGCC 237  
Db 474 CTCACCCAGTACAGCAATAGAGCTCTTCGGGCTTCTCTGTCGATCATGCGCCTGGCC 533  
Qy 238 GGCAAAGAACCGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCAAGTCTCCAGC 297  
Db 534 GGCAGAGACAGGGGACTCAGGCGGAATCCAACTGAGTAGTAATTCAGATTTCCAGC 593  
Qy 298 GACAAGAACAGAACCGAGTGAAGATCCCGGATGAGAGGTTGTCTACTATATCTGGT 357  
Db 594 AACAAAGAACAGAACCGAGTGAAGATCCCTCAGCATGAGAGATTTACTGTGTCTACT 653  
Qy 358 AATGGGAGCATCCACAGCCGGAAGTTTCTCATACGTACCCAGAAATATGGTCTGGTG 417  
Db 654 AATGGAAGTATTCACAGCCCAAGTTTCTCTACTATTATCCAAAGAAATAGGCTTGGTA 713  
Qy 418 TGGAGATTAGTTGACGTAGATGAAATGTGCGGATCCAGCTGACATTTGATGAGATTT 477  
Db 714 TGGAGATTAGTACAGTAGAGGAATGTATGTGATACACTTACCTTACCTTGTGATGAAGATTT 773

Qy 478 GGCTCGAAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAAAGTTGAGAGCCC 537  
Db 774 GGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTTGTAGAAAGTTGAGAGCCC 833  
Qy 538 AGTGTGGAAGTCTTTTAGGACGCTGGTGTGGTCTTGGGACTGTGCCAGGAAACGAGACT 597  
Db 834 AGTGTGGAAGTCTTTTAGGCGCTGGTGTGGTCTTGGTACTGTACCAGGAAACGAGATT 893  
Qy 598 TCTAAAGGAAATCATATCAGGATAAGATTTGTATCTGATGAGTATTTTCCATCTGAACCC 657  
Db 894 TCTAAAGGAAATCAATTAGGATAAGATTTGTATCTGATGATATTTTCTTCTGAAACCA 953  
Qy 658 GGAATCTGCACTACACAGTATATCATGCCCAAGTCAAGAAACCAAGGATCTTCG 717  
Db 954 GGGTTCTGCACTACACAACTTGTCAATGCCCAATTCACAGAAAGCTGTGAGTCTTCA 1013  
Qy 718 GTCTTGGCCCTTCACTTTGTCTATTGGACCTCTCAACATGCTGTGACCTGCTTCAGT 777  
Db 1014 GTCTTACCCCTTTCAGCTTTGCCACTGGACCTGCTTAATATGCTATACCTGCTTTAGT 1073  
Qy 778 ACCTTGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGGACTTGGACAGC 837  
Db 1074 ACCTTGAAGACCTTATTCGATATCTTGAACAGAGAGATGGCAGTTGGACTTAGAAGAT 1133  
Qy 838 CTCTAAGCCCAACATGGCAGCTTTTGGGCAAGCTTCTCTGTATGGAAGAAAGCAAA 897  
Db 1134 CTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTGTTTGGAAAGAAATCCAGA 1193  
Qy 898 GTGGTGAATCTGAATCTCTCAAGGAGAGGTAAACTCTACAGCTGCACACCCGGAAC 957  
Db 1194 GTGGTGAATCTGAACCTTCTAACAGAGGAGGTAAAGATTATACAGCTGCACACCTCGTAAC 1253  
Qy 958 TTCTCAGTGTCCATACGGGAAGAGCTAAAGAGACAGATACCATATTTCTGCCCAGGTTGT 1017  
Db 1254 TTCTCAGTGTCCATTAAGGAGAGACTAAAGAGAACCGATACCATTTCTGCCCAGGTTGT 1313  
Qy 1018 CTCTGCTCAAGCTGTGTGAGGAAATGTGCTGTGTGTCTCCATAATTCGAATGAATGT 1077  
Db 1314 CTCTGCTTAAACGCTGTGTGGGAACTGTGCTGTGTCTCCACAAATTCGAATGAATGT 1373  
Qy 1078 CAGTGTGTCCACGTAAGTTACAAAAGTACCATGAGTCTTCAAGTTGAGACCAAAA 1137  
Db 1374 CAATGTGTCCCAAGCAAGGTTACTAAAAAATACACAGGCTCTTCAAGTTGAGACCAAAAG 1433  
Qy 1138 ACTGGAGTCAAGGATTCGATAGTCACTCAGTGTGCTCTGGAACACCAAGAGAA 1197  
Db 1434 ACCGGTGTGAGGGGATTCACAATCACTACCGAGCTGGGCTTGGAGCAACCATGAGAG 1493  
Qy 1198 TGTGACTGTGTGTAGAGAAACGAGGAGGTAATCTGAGGCTTCGTAGCAGCAC 1254  
Db 1494 TGTGACTGTGTGTGACAGAGGAGACAGGAGGATAGCCGATCACCAACGAGCCTC 1550

RESULT 6  
US-60-507-511-2084  
; Sequence 2084, Application US/60507511  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WI  
; FILE REFERENCE: AM 101081  
; CURRENT APPLICATION NUMBER: US/60/507,511  
; CURRENT FILING DATE: 2003-10-02  
; NUMBER OF SEQ ID NOS: 203623  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2084  
; LENGTH: 3007  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-507-511-2084

Query Match 62.0%; Score 914.2; DB 7; Length 3007;

Best Local Similarity 83.5%; Pred. No. 6.6e-285;  
Matches 1050; Conservative 0; Mismatches 203; Indels 4; Gaps 1;

QY 2 ACCTGGAGACACAGAGAGGGCTCTAGGAAATTTTGGATGGGATATGTGGAAACTA 61  
Db  
294 AACCTGGAGACACAGAGAGGGCTCTAGGAAATTTTGGATGGGATATGTGGAAACTA 353  
QY 62 CCCTGGCATTTCTGTCTGCAGAGCGCGCAGGCGCTTCCACCGCAGCGAGCTTTCCC 121  
Db  
354 CCCTGGCATTTCTGTCTGCAGAGCGCGCAGGCGCTTCCACCGCAGCGAGCTTTCCC 413  
QY 122 CGG----GCTGGGCTGAGCCTTGGAGTGTGCTTCCCAAGTGCCTGAGTACT 177  
Db  
414 TGGCGGTGGTGAAGAGACTCGGGAGTGTGCTTCCCAAGTGCCTGAGTACT 473  
QY 178 CTGCCCCAGTCAAGCAATAGCTCTCTCGGCTCTCTCTGCTGACATCTGCCCTGCC 237  
Db  
474 CTACCCCGTCAAGCAATAGCTCTCTCGGCTCTCTCTGCTGACATCTGCCCTGCC 533  
QY 238 GGCCAAAGAACGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCGACTCTCCAGC 297  
Db  
534 GGCCAGAGACAGGGACTCAGCGGAATCCACCTGAGTAGTAATTTCCAGTTTCCAGC 593  
QY 298 GACAAGAACAGAACCGAGTGAAGTCCCGGATCAGAGAGTTGTCACTATATCTGGT 357  
Db  
594 AACAAAGAACAGAACCGAGTGAAGTCCCGGATCAGAGAGTTGTCACTATATCTGGT 653  
QY 358 AATGGGAGATCCACAGCGCGGAGTTTCTCATACGTACCAAGAAATATGGTCTGGTG 417  
Db  
654 AATGGGAGATCCACAGCGCGGAGTTTCTCATACGTATCCAGAAATATGGTCTGGTG 713  
QY 418 TGGAGATTAGTTGAGTGAATGAAATGTGGGATCCAGCTGACATTTGATGAGATTT 477  
Db  
714 TGGAGATTAGTTGAGTGAATGAAATGTGGGATCCAGCTGACATTTGATGAGATTT 773  
QY 478 GGGCTGAAGATCCAGAGAGATATATGCAAGTATGATTTGTAGAGTTGAGAGCCC 537  
Db  
774 GGGCTGAAGATCCAGAGAGATATATGCAAGTATGATTTGTAGAGTTGAGAGACC 833  
QY 538 AGTGTGAAGATGTTTGTAGGACGCTGTGTGGTCTCGGATGTGCCAGGAAGCAGACT 597  
Db  
834 AGTGTGAAGATGTTTGTAGGACGCTGTGTGGTCTCGGATGTGCCAGGAAGCAGACT 893  
QY 598 TCTAAAGGAATCATATCAGGATTAAGATTTGTATCTGATGATATTTTCCATCTGAACCC 657  
Db  
894 TCTAAAGGAATCATATCAGGATTAAGATTTGTATCTGATGATATTTTCCATCTGAACCA 953  
QY 658 GGATTTGCTACCTACAGTATTTATCATGCCAAGTCCAGAGAACCAAGAGTCTCTCG 717  
Db  
954 GGGTTCTGCACTCACTCAACATTTGTATCTGATGATATTTTCCATCTGAACCA 1013  
QY 718 GTGTGGCCCCCTTCTATCTGATGAGCTGCTCAACATGCTGTGACTGCTGCTTCAGT 777  
Db  
1014 GTGTACCCCCCTTCTGCTTGGCACTGGAATGCTTAATATGCTAATCTGCTTTAGT 1073  
QY 778 ACCTTGAAGAGCTGATTTGGTATCCTAGAGCCAGATCGATGGCAGGTGGACTTGGACAGC 837  
Db  
1074 ACCTTGAAGAGCTGATTTGGTATCCTTGAACAGAGAGATGGCAGTTGGACTTGAAGAT 1133  
QY 838 CTCTAAGGCCAATCGGAGCTTTTGGGCAAGCTTTCTGTATGAGGAAAGAAAGCAAA 897  
Db  
1134 CTATATAGGCCAATCGGAGCTTTTGGGCAAGCTTTTGGTATGAGGAAAGAAATCCAGA 1193  
QY 898 GTGTGATCTGAATCTCTCAAGGAAGAGTAAATCTTACAGCTGCACACCCCGGAAC 957  
Db  
1194 GTGTGATCTGAATCTCTCAAGGAAGAGTAAATCTTACAGCTGCACACCCCGGAAC 1253  
QY 958 TTCTCAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACATATTTCTGCCAGGTGT 1017  
Db  
1254 TTCTCAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACATATTTCTGCCAGGTGT 1313  
QY 1018 CTCTGTGTCAAGCGCTGTGGAGAAATTTGTCTCTGTTGCTCCATATTTGCAATGAATGT 1077

Db 1314 CTCTGTGTTAAACGCTGTGGTGGAACTGTGCTGTTGTCTCCACAAATTTGCAATGAATGT 1373  
QY 1078 CAGTGTGTCCACGTAAGTTACAAAAGTACCATGAGTTCCTTTCAGTTGAGACCAAAA 1137  
Db 1374 CAATGTGTCCCAAGCAAGTTTACTTAAAAAATACCACGAGGTCTTTCAGTTGAGACCAAA 1433  
QY 1138 ACTGGAGTCAAGGATTTGCAATAGTCACTCACTGATGTGGCTTGGAAACCAACGAGGAA 1197  
Db 1434 ACCGTGTCAAGGATTTGCAATAGTCACTCACTGATGTGGCTTGGAAACCAACGAGGAG 1493  
QY 1198 TGTGACTGTGTGTAGAGAAACGAGGAGGTAACTGAGAGCTTGTGAGCAGC 1254  
Db 1494 TGTGACTGTGTGTAGAGGAGCAGAGGAGTAGCGCATCATCCACGAGCTC 1550

RESULT 7  
US-60-487-610-231  
; Sequence 231, Application US/60487610  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; APPLICANT: HUANG, Hongjin  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,  
; FILE REFERENCE: CL001469  
; CURRENT APPLICATION NUMBER: US/60/487,610  
; CURRENT FILING DATE: 2003-07-17  
; NUMBER OF SEQ ID NOS: 97101  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 231  
; LENGTH: 3007  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-487-610-231

Query Match 62.0%; Score 913.8; DB 7; Length 3007;  
Best Local Similarity 83.5%; Pred. No. 9e-285;  
Matches 1049; Conservative 1; Mismatches 203; Indels 4; Gaps 1;

QY 2 ACCTGGAGACACAGAGGGCTCTAGGAAATTTTGGATGGGATATGTGGAAACTA 61  
Db 294 AACCTGGAGACACAGAGGGCTCTAGGAAATTTTGGATGGGATATGTGGAAACTA 353  
QY 62 CCCTGGCATTTCTGTCTGCAGAGCGCGCAGGCGCTTCCACCGCAGCGAGCTTTCCC 121  
Db 354 CCCTGGCATTTCTGTCTGCAGAGCGCGCAGGCGCTTCCACCGCAGCGAGCTTTCCC 413  
QY 122 CGG----GCTGGGCTGAGCCTTGGAGTGTGCTTCCCAAGTGCCTGAGTACT 177  
Db 414 TGGCGGTGGTGAAGAGACTCGGGAGTGTGCTTCCCAAGTGCCTGAGTACT 473  
QY 178 CTGCCCCAGTCAAGCAATAGCTCTCTCGGCTCTCTCTGCTGACATCTGCCCTGCC 237  
Db 474 CTACCCCGTCAAGCAATAGCTCTCTCGGCTCTCTCTGCTGACATCTGCCCTGCC 533  
QY 238 GGCCAAAGAACGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCGACTCTCCAGC 297  
Db 534 GGCCAGAGACAGGGACTCAGCGGAATCCACCTGAGTAGTAATTTCCAGTTTCCAGC 593  
QY 298 GACAAGAACAGAACCGAGTGAAGTCCCGGATCAGAGAGTTGTCACTATATCTGGT 357  
Db 594 AACAAAGAACAGAACCGAGTGAAGTCCCGGATCAGAGAGTTGTCACTATATCTGGT 653  
QY 358 AATGGGAGATCCACAGCGCGGAGTTTCTCATACGTACCAAGAAATATGGTCTGGTG 417  
Db 654 AATGGGAGATCCACAGCGCGGAGTTTCTCATACGTATCCAGAAATATGGTCTGGTG 713  
QY 418 TGGAGATTAGTTGAGTGAATGAAATGTGGGATCCAGCTGACATTTGATGAGATTT 477  
Db 714 TGGAGATTAGTTGAGTGAATGAAATGTGGGATCCAGCTGACATTTGATGAGATTT 773  
QY 478 GGGCTGAAGATCCAGAGAGATATATGCAAGTATGATTTGTAGAGTTGAGAGCCC 537

Db 774 GGCTTTGAGACCCAGAGATGATATGCAATGATATGTTTGTAGAGTTGAGGAACCC 833  
QY 538 AGTGTAGGAAGTGTCTTTAGGACCTCGTGTGGTCTGGGACTGTGCCAGGAAAGCAGACT 597  
Db 834 AGTGTAGGAACATATAGGGCGCTGGTGTGGTCTGGTACTGTACCGAGGAACAGATT 893  
QY 598 TCTAAAGGAATCATATCAGGATAGATTGTGTATCTGTATGTAGTATTTTCCATCTGAACCC 657  
Db 894 TCTAAAGGAATCAATATAGGATAGATTGTGTATCTGTATGTAGTATTTTCCATCTGAACCA 953  
QY 658 GGATCTGCATCCACTACAGTATATATGSCCAAGTACAGAAACACAGAGTCTCTCG 717  
Db 954 GGTTCTGCATCCACTACAACTGTATGTCATCCCAATTCACAGAGCTGTGAGTCTCTCA 1013  
QY 718 GTTTGCCCTTCATCTTTGTCAATGGACCTGCTCAACAAATGCTGTGATGCTCCTCAGT 777  
Db 1014 GTGTACCCCTTCAGCTTTGGCACTGGACCTGTTAAATGCTATTAATGCTTGTAGT 1073  
QY 778 ACCTTGGAGAGCTGATTTGGTACCTTAGAGCCAGATCGATGGCAGGTGGACTTTGGACAGC 837  
Db 1074 ACCTTGGAGAGCTTATTCGATATCTTGAACCGAGAGATGGCAGTTGGACTTTAGAAGAT 1133  
QY 838 CTCTAAGCAACATGCGCAGCTTTTGGGCAAGCTTTTCTGTATGGGAAAGAAACGAAA 897  
Db 1134 CTATATAGGCAACTTGGCACTTCTTGGCAAGCTTTTGTGTTTGGAGAAATCCAGA 1193  
QY 898 GTGTGAATCTGAATCTCTCTCAAGGAGAGGTAAACTCTACAGCTGCACACCCCGAAC 957  
Db 1194 GTGTGGAATCTGAACCTTCTAACAGAGGAGGTAAAGATTATACAGCTGCACACCTCGTAAC 1253  
QY 958 TTCTCAGTGCATACGGGAGAGCTTAAAGAGGACAGATACCATATTTCTGCCAGGTGTG 1017  
Db 1254 TTCTCAGTGCATACGGGAGAGCTTAAAGAGGAGGTAAAGATTATACAGCTGCACACCTCGTAAC 1313  
QY 1018 CTCTCAGTGCATACGGGAGAGCTTAAAGAGGAGGTAAAGATTATACAGCTGCACACCTCGTAAC 1077  
Db 1314 CTCTCAGTGCATACGGGAGAGCTTAAAGAGGAGGTAAAGATTATACAGCTGCACACCTCGTAAC 1373  
QY 1078 CAGTGTGCTCCAGTAAAGTTCAAAAAGTACATGAGTCTTTCAGTTGAGACCAAAA 1137  
Db 1374 CAATGTGCTCCAGCAAGTTACTAAAAAATACAGAGGTCTTTCAGTTGAGACCAAAAG 1433  
QY 1138 ACTGGAGTCAAGGATGATAGTACCTACCTGATGCTGTGGACTGTGGAACACAGAGGAA 1197  
Db 1434 ACCGGTGTGAGGGGATGACAAATCACTACCGAGTGGCCCTGGAGCACCATGAGGAG 1493  
QY 1198 TGTGACTGTGTGTAGAGAAACGAGGAGGTAACTGAGGCTTCTGAGCAGCAC 1254  
Db 1494 TGTGACTGTGTGTGAGAGGAGCAGAGGAGTACCGGATACCGCATCACACAGCAGCTC 1550

## RESULT 8

US-60-485-450-137  
; Sequence 137, Application US/60485450  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; APPLICANT: CHANG, Sheng-yung  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C  
; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001470  
; CURRENT APPLICATION NUMBER: US/60/485, 450  
; CURRENT FILING DATE: 2003-07-09  
; NUMBER OF SEQ ID NOS: 47859  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 137  
; LENGTH: 3007  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-485-450-137

Query Match

62.0%; Score 913.8; DB 7; Length 3007;

Best Local Similarity 83.5%; Pred. No. 9e-285;  
Matches 1049; Conservative 1; Mismatches 203; Indels 4; Gaps 1;  
QY 2 ACCTGAGACACAGAGGGCTCTAGGAAAAATTTTGGATGGGATTATGTGGAACCTA 61  
Db 294 AACTGAGACACAGAGAGGGCTCTAGGAAAAATTTTGGATGGGATTATGTGGAACCTA 353  
QY 62 CCCTGGATTTCTCTGCTGCCAGAGCCGGCAGGCTTCCACCGCAGCGAGCTTTCCC 121  
Db 354 CCCTGCGATTTCTCTGCTGCCAGAGAGGCTTCCACCGCAGCGAGCTTTCCC 413  
QY 122 CGG----GCTGGGCTGAGCCTTGGAGTCTGCTTCCAGTGCCTCCGCGAGTGAAC 177  
Db 414 TGGCGGTGGTGAAGAGACTCGGGAGTCTGCTTCCAAAGTGCCTCGTGTGAGCT 473  
QY 178 CTGCCCCAGTCAAGCAAAATGCTCTCTCGGCTCTCTCTGCTGCTGACATCGCCCTGGCC 237  
Db 474 CTACCCCGCTCAGCAAAATGAGCTCTCTCGGCTCTCTCTGCTGACATCGCCCTGGCC 533  
QY 238 GGCCAAAGAACGGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCGACTTCCAGC 297  
Db 534 GGCCAGAGACAGGGACTCAGGCGGAATCCAACTGAGTAGTAAATTTCCAGTTTCCAGC 593  
QY 298 GACAAGGAACAGAACGGAGTGAAGATCCCGGATGAGAGAGTTGTCTATATCTGCT 357  
Db 594 AACAGGAACAGAACGGAGTGAAGATCCCTCAGCATGAGAGAAATTTACTGTGTCTACT 653  
QY 358 AATGGAGAGCATCCACAGCCGGAAGTTTCTCATAGTACCCCAAGAAATATGGTCTGCTG 417  
Db 654 AATGGAGATTTTCCAGAGCCCAAGTTTCTCATATCTTATCCAAAGAAATAGCGTCTGTA 713  
QY 418 TGGAGATTAGTTGCTGAGTAGTAAATGTGCGGATCCAGCTGACATTTTGTATGAGAGATT 477  
Db 714 TGGAGATTAGTAGCAGTAGAGGAAATGTATGATACAACTTAGCTTTGATGAAGATT 773  
QY 478 GGCTGGAAGATCCAGAGAGATATATGCAAGTATGATTTTGTAGAGTTGAGGAGCCC 537  
Db 774 GGCTTGAAGACCCAGAGATGATATGCAAGTATGATTTTGTAGAGTTGAGGAGCCC 833  
QY 538 AGTGTAGGAAGTGTGTTAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 597  
Db 834 AGTGTAGGAAGTGTGTTAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 893  
QY 598 TCTAAAGGAATCATATCAGGATTAAGATTTGTATCTGATGAGTATTTTCCATCTGAACCC 657  
Db 894 TCTAAAGGAATCAAATTAGATAAGATTTGTATCTGATGAATATTTTCTTCTGAACCA 953  
QY 658 GGATTTCTGATCCACTACAGTATATATGCTCCAGAGTTCACAGAAACCAAGTCTCTCG 717  
Db 954 GGCTTCTGATCCACTACAGTATATGCTCCAGAGTTCACAGAAATTCAGAGAGCTGTGAGTCTCTCA 1013  
QY 718 GTGTGCCCTTCATCTTTGTCTATGGACCTGCTCAACAAATGCTGCTGCTGCTGCTGCT 777  
Db 1014 GTGTACCCCTTCAGCTTTGGCACTGGACCTGCTTAAATGCTATTAATGCTTGTAGT 1073  
QY 778 ACCTTGGAGAGCTGATTCGGTACCTTAGAGCCAGATCGATGGCAGGTGGACTTTGGACAGC 837  
Db 1074 ACCTTGGAGAGCTTATTCGATATCTTGAACACAGAGATGGCAGTTGGACTTTAGAAGAT 1133  
QY 838 CTCTAAGGCAACATGCGCAGCTTTTGGGCAAGCTTTCTGTATGGGAAAAAAGCAAA 897  
Db 1134 CTATATAGGCCCACTTGGCAACTTCTTGGCAAGCTTTTGTGTTTGGAGAAATCCAGA 1193  
QY 898 GTGGTGAATCTGAATCTCTCTCAAGGAAGAGGTAAACTCTACAGCTGCACACCCCGAAC 957  
Db 1194 GTGGTGAATCTGAACCTTCTAAGAGAGGAGGTAAAGATTATACAGCTGCACACCTCGTAAC 1253  
QY 958 TTCTCAGTGCATACGGGAGAGCTTAAAGAGGACAGATACCATATTTCTGCCAGGTGTG 1017  
Db 1254 TTCTCAGTGCATACGGGAGAGCTTAAAGAGGAGGTAAAGATTATACAGCTGCACACCTCGTAAC 1313  
QY 1018 CTCTCAGTGCATACGGGAGAGGTAAAGAGGAGGTAAAGATTATACAGCTGCACACCTCGTAAC 1077



Db	1314	CTCCTGTTTAAACGCTCTGTGTGGGAACTGTGCGCTTGTGTCTCCACAATTCGAATGAATGT	1373
Qy	1078	CAGTGTCTCCACGCTAAAGTTACAAAAAAGTACCATCAGGTCTCTCAGTTTGAGACCAAAA	1137
Db	1374	CAATGTCTCCAGCAAAAGTTACTTAAAAATACCACGAGGTCTTCAGTTGAGACCAAG	1433
Qy	1138	ACTGGAGTCAAGGGATTGCATACTCACTGATGTGGCTCTGGAACACCACGAGGAA	1197
Db	1434	ACCGGTGTCAAGGGATTGCATAATCACTACCGACGTGGCCCTGGAGCACCATGAGGAG	1493
Qy	1198	TGTGACTGTGTGTAGAGGAAACGCAAGGAGGTAACTGCAGCCTTCGTAGCAGCAC	1254
Db	1494	TGTGACTGTGTGTACAGGAGGACACAGGAGGATAGCGGATCAACCAACCAAGCAGCTC	1550

RESIST. T. 9

```

US-09-830-320A-8
; Sequence 8, Application US/09830320A
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: TANG, Y. Tom
; APPLICANT: YUE, Henry
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: CORLEY, Neil C.
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: AU-YOUNG, Janice K.
; TITLE OF INVENTION: GROWTH FACTOR RELATED MOLECULES
; FILE REFERENCE: PF-0627 USN
; CURRENT APPLICATION NUMBER: US/09/830,320A
; PRIORITY FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: PCT/US99/25458
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 60/183,024
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 60/155,216
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/172,233
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 8
; LENGTH: 2779
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No.: 4163378CB1
US-09-830-320A-8

```

Query Match	61.9%;	Score 912.6;	DB 5;	Length 2779;
Best Local Similarity	83.5%;	Pred. No. 2.1e-284;		
Matches 1049;	Conservative 0;	Mismatches 204;	Indels 4;	Gaps 1;
Qy	2	ACCTGGAGACACAGAGAGGCTCTAGGAAAAATTTTGGATGGGGATATCTGGAACCTA	61	
Db	60	AAC TGGAGACACAGAGAGGCTCTAGAAAAAGTTTGGATGGGATATGTGGAACCTA	119	
Qy	62	CCCTGCCATTCTCTGCTGCCAGAGCGCCGACGGCGCTTCCACCCAGCGAGCCTTTCCC	121	
Db	120	CCCTGCCATTCTCTGCTGCCAGAGCGCTCGGCGCTTCCACCCAGTGCAGSCCTTCCCC	179	
Qy	122	CGG----GCTGGGCTGAGCCTTGAGATGCTGCTCTCCCGAGTCCCGCGAGTGAGCC	177	
Db	180	TGGCGTGGTGAAGAGACTCGGAGTCTGCTGCTTCCAAAGTGCCTCGTGGTGAAGCT	239	
Qy	178	CTCGCCCGAGTCAGCCAAATGCTCCTCTCGGCTCCTCTCTGCTGACATCTGCCCTGACC	237	
Db	240	CTCACCCGAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCTGCTGACATCTGCCCTGACC	299	
Qy	238	GGCCAAAGACGGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCAGCTCTCCAGC	297	
Db	300	GGCCAGAGACAGGGGACTCAGGGCGGAATCCAACTGAGTGAATAATTCAGTTTTCCAGC	359	

Qy	298	GACAAAGAAACAGAAACGGAGTGCAGAGTCCCGCGCATGACAGAGAGTTGTCACTATATCTGGT	357
Db	360	AACAAGAAACAGTACGGAGTACAAAGATCCTCAGCATGAGAGAAATATTACTGTGTCTACT	419
Qy	358	AATGGGAGCATCCACAGCCCGAGTTCCTCATACGTACCACAGAAATATGGTGCTGGTG	417
Db	420	AATGGGAAGTATCCACAGCCCAAGGTTCTCTACACTTATCCAGAAATACGGTCTTGGTA	479
Qy	418	TGCAGATTAGTTCGACGTAGATGAAATGTGCGGATCCAGCTGCATTTGATGAGAGATTT	477
Db	480	TGGAGATTAGTACGACGTAGAGAAATGATGATGATACAACTTACGTTTGTATGAAGATTT	539
Qy	478	GGGCTGGAAGATCCAGAAAGCATATATGCAAGTATGATTTTGTAGAGTTGAGGAGCCC	537
Db	540	GGGCTTGAAGACCCAGAAGATGACATATGCAAGTATGATTTGTAGAAAGTTGAGGAACCC	599
Qy	538	AGTGATGGAAAGTGTTTTAGGACGCTGGTGTTCTGGGACTGTGCCAGAGAAAGCAGACT	597
Db	600	AGTGATGGAAACTATATTAGGGCCGCTGGTGGTCTGGTACTGTACCGAGAAACAGATT	659
Qy	598	TCTAAAGGAAATCATATCAGGATAAGATTTGTATCTGATGAGTATTTTCCATCTGAACCC	657
Db	660	TCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCTTCTGAACCA	719
Qy	658	GGATTCGTGATCCACTACAGTATATCATGCCACAAGTCAACAGAAACCAAGTGCCTTCG	717
Db	720	GGGTTCTGCATCCCACTACAAATTTGTATGCCACAAATTCACAGAAGCTGTGAGTCCCTCA	779
Qy	718	GTGTGCCCCCTTCATCTTTGTCTATGGACCTGCTCAACAACTGCTGACGCTGCCTTCAGT	777
Db	780	GTGCTACCCGCTTCAGCTTTGCCACTGGACCTGCTTAATGCTATTAATGCTTTAGT	839
Qy	778	ACCTTGGAAAGCTGATTCGTTTACCTAGAGCCAGATCGATGGCAGGTGGACTTGGACAGC	837
Db	840	ACCTTGGGAAGCCTTATTCGATATCTTGAACACAGAGAGATGGCAGTTTGAAGAT	899
Qy	838	CTCTACAGCCAACTGCGAGCTTTTGGCGAAGGCTTTCTGTATGGGAAAAAAGCAAA	897
Db	900	CTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTGTTTGTGGAAAGAAATCCAGA	959
Qy	898	GTGCTGAATCTGAATCTCTCAAGGAGAGGTAAAACTCTACAGCTGCACACCCCGGAAC	957
Db	960	GTGCTGATCTGAACCTTCTAAACAGAGAGGTAAAGATTATACAGCTGCACACCTCGTAAC	1019
Qy	958	TTCTCAGTGTCCATACGGGAAGACTAAAGAGACACAGATACCATATTTCTGGCCAGGTTGT	1017
Db	1020	TTCTCAGTGTCCATAGGGAAGAACTAAAGAGAACCGATACCACTTTTCTGGCCAGGTTGT	1079
Qy	1018	CTCTGTGTCAAGCGCTGTGAGAGAAATTGTGCGCTGTGTCTCATAATTTGCAATGAATGT	1077
Db	1080	CTCTGTGTAAACGCCTGTGTGTGGAACTGTGCGCTGTGTCTCCACAAATTCGAATGAATGT	1139
Qy	1078	CAGTGTGTCCACGTTAAAGTTTACAAAAAAGTACCATGAGTCTCTCAGTTTGAGACCAAAA	1137
Db	1140	CAATGTGTCCAGCAAAAGTTACTTAAAAAATACACAGAGTCTCTCAGTTGAGACCAAG	1199
Qy	1138	ACTGGAGTCAAGGGAATTGCATAAGTCACTCACTGATGTGGCTCTCGGAACACCGAGGAA	1197
Db	1200	ACCGTGTCCAGGGAATTGCACAAATCACTCACCGAGTGGCCCTGGAGCACCATGAGGAG	1259
Qy	1198	TGTGACTGTGTGTAGAGGAAACGCAAGGAGGTAACTGCAAGCCTTCGTAGAGACAC	1254
Db	1260	TGTGACTGTGTGTGACAGGAGGACACAGGAGGATAGCCGATCACCAACGACAGCTC	1316

```

RESULT 10
US-09-457-066-1
; Sequence 1, Application US/09457066
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.

```





```
QY 107 AGCGAGCCTTTCCCGG-----GCTGGCTGAGCCTTGGAGTGGTCTGCTCCCGAGTGCC 162
Db 61 AGTGCAGCCTTCCCTGGCGGTGGTGAAGAGACTCGGAGTGGTCTTCCAAAGTGCC 120
QY 163 CGCGGAGTGAGCCTTCGCCCGCAGTCCAGCAAAATGCTCTCTCTGGCCCTCTCTGCTG 222
Db 121 CGCGGTGAGTGAGCTCTCAACCCAGTCCAGCAAAATGAGCCTCTCTGGGCTTCTCTGCTG 180
QY 223 ACATCTGCTGCTGGCGGCAAGAAACGGGAGCTCGGCTGAGTCCCAACCTGAGCAGCAAG 282
Db 181 ACATCTGCTGCTGGCGGCAAGAGACAGAGGAGCTCAGCGGAATCCAACTGAGTAGTAA 240
QY 283 TTGCAGCTCTCCAGCAACAAGGACAGAACGGAGTCCAGATCCCGGCGATGAGAGATT 342
Db 241 TTCCAGTTTCCAGCAACAAGGACAGAACGGAGTCAAGATCTCAGCATGAGAGATT 300
QY 343 GTCACTATATCTGGTAATGGAGATCCACAGCCCGAAGTTTCTCTCATATGATCCCAAGA 402
Db 301 ATTACTGTGTCTACTAATGGAAGTAATTCACAGCCCAAGTTTCTCTCATATTTATCCAAGA 360
QY 403 AATATGCTGCTGGTGGAGATAGTTGTCAGTAGATCAAAATGTCGGATCCAGCTGACA 462
Db 361 AATACGGTCTGGTATGGAAGTATAGTAGCAGTAGAGGAAATGTATGATACACTTACG 420
QY 463 TTTGATGAGAGATTTTGGGCTGGAAGATCCAGAGACATATATGCAAGTATGATTTTGTGA 522
Db 421 TTTGATGAAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTTGTGA 480
QY 523 GAAGTTGAGAGCCAGTATGGAAGTGTATAGGACGCTGGTGTGTTCTGGAGCTGTG 582
Db 481 GAAGTTGAGAGCCAGTATGGAAGTATATAGGCGCTGGTGTGTTCTGGTACTGTGA 540
QY 583 CCAGGAAAGCAGACTTCTAAAGGAAATCAATCAGGATAAGATTTGATCTGATGAGTAT 642
Db 541 CCAGGAAAGCAGATTCTAAAGGAAATCAATTAGGATAGATTTGATCTGATGATAT 600
QY 643 TTTCCATCTGAACCCGAGTTCTGCATCCATACAGTATTAATGACCAAGTACAGAA 702
Db 601 TTTCCCTTCTGAACCCAGGTTCTGCATCCATCAACATTTGTCATGCCAATTCACAGAA 660
QY 703 ACCAGAGCTCTTCGGTGTGCCCCCTTCATCTTTGTCATTGGACCTGCTCAACATGCT 762
Db 661 GCTGTGAGTCTTCAGTGCTACCCCTTCAGCTTTGCTGCTGACCTGCTTAATATGCT 720
QY 763 GTGACTGCTCTCAGTACCTTTGGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAG 822
Db 721 ATAATGCTCTTAGTACCTTTGGAAGACCTTATTCGATATCTTGAACCCAGAGATGGCAG 780
QY 823 GTGGACTTGACAGCCTCTACAGCCAAATGGCAGCTTTTGGCAAGGCTTTCTCTGTAT 882
Db 781 TTGGACTTAGAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTGTTTT 840
QY 883 GGGAAAAAGCAAGTGGTGAATCTCAATCTCTCAAGGAAGAGGTAAACTCTACAGC 942
Db 841 GGAAGAAAAATCCAGATGGTGGATCTGAACCTTCTAAACAGGAGGTAAATATATACGC 900
QY 943 TGCAACCCCGGAATTTCTCAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACCATA 1002
Db 901 TGCACACTCTGTAACCTTCTCAGTGTCCATTAAGGGAAGAACTAAAGAGAACCGATACCATT 960
QY 1003 TTTGGCCAGGTTGTCTCTGGTCAAGCGCTGTGGAGAAATGTGTGCTGTGTCTCCAT 1062
Db 961 TTTGGCCAGGTTGTCTCTGGTAAACCGCTGTGGTGGAACTGTGTGCTGTGTCTCCAC 1020
QY 1063 AATTGCAATCAATGCTAGTGTGCTCCACGTAAGTTTACAAAAAGTACCATGAGTCCCTT 1122
Db 1021 AATTGCAATCAATGCTAGTGTGCTCCACGTAAGTTTACTAAAAAATCCAGAGGTCCTT 1080
QY 1123 CAGTTGAGACCAAAAACTGGAGTCAAGGGATTTGCATAAGTCACTCACTGATGTGGCTGTG 1182
Db 1081 CAGTTGAGACCAAAAGCCGGTGTGAGGGGATTCACAAATCACTCACCGACGTGGCCCTG 1140
QY 1183 GAACACCAGGGAATGTGACTGTGTGTGTAGAGGAAACCGAGAGGGTAACTGTGACGCT 1242
```

```
Db 1141 GAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGCAAGAGGATAGCCGATCAC 1200
QY 1243 TCGTAGCAGCAC 1254
Db 1201 CACCAGCAGCTC 1212

RESULT 12
US-10-664-432-1
; Sequence 1, Application US/10664432
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE
; FILE REFERENCE: 00-12
; CURRENT APPLICATION NUMBER: US/10/664,432
; CURRENT FILING DATE: 2003-09-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1760
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (154)...(1191)
US-10-664-432-1

Query Match 59.6%; Score 878.8; DB 6; Length 1760;
Best Local Similarity 83.4%; Pred. No. 1.5e-273;
Matches 1011; Conservative 0; Mismatches 197; Indels 4; Gaps 1;

QY 47 ATTATGTGGAACATACCTCGGATTTCTCTGTCGAGCGCGCCAGCGGCTTCCACGC 106
Db 1 ATTATGTGGAACATACCTCGGATTTCTCTGTCGAGCAGCGGCTCGGCGCTTCCACCCC 60
QY 107 AGCGAGCCTTTCCCGG-----GCTGGCTGAGCCTTGGAGTGGTCTGCTCCCGAGTGCC 162
Db 61 AGTGCAGCCTTCCCTGGCGGTGGTGAAGAGACTCGGAGTGGTCTTCCAAAGTGCC 120
QY 163 CGCGGAGTGAGCCTTCGCCCGCAGTCCAGCAAAATGCTCTCTCTGGCCCTCTCTGCTG 222
Db 121 CGCGGTGAGTGAGCTCTCAACCCAGTCCAGCAAAATGAGCCTTCTCGGCTTCTCTGCTG 180
QY 223 ACATCTGCTGCTGGCGGCAAGAAACGGGAGCTCGGCTGAGTCCCAACCTGAGCAGCAAG 282
Db 181 ACATCTGCTGCTGGCGGCAAGAGACAGAGGAGCTCAGCGGAATCCAACTGAGTAGTAA 240
QY 283 TTGCAGCTCTCCAGCAACAAGGACAGAACGGAGTCAAGATCCCGGCGATGAGAGATT 342
Db 241 TTCCAGTTTCCAGCAACAAGGACAGAACGGAGTCAAGATCTCAGCATGAGAGATT 300
QY 343 GTCACTATATCTGGTAATGGAGATCCACAGCCCGAAGTTTCTCTCATATGATCCCAAGA 402
Db 301 ATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGTTTCTCTCATATTTATCCAAGA 360
QY 403 AATATGCTGCTGGTGGAGATAGTTGTCAGTAGATGAAATGTGCGGATCCAGCTGACA 462
Db 361 AATACGGTCTGGTATGGAAGTATAGTAGCAGTAGAGGAAATGTATGATACACTTACG 420
QY 463 TTTGATGAGAGATTTTGGGCTGGAAGATCCAGAGACATATATGCAAGTATGATTTTGTGA 522
Db 421 TTTGATGAAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTTGTGA 480
QY 523 GAAGTTGAGAGCCAGTATGGAAGTGTATAGGACGCTGGTGTGTTCTGGAGCTGTG 582
Db 481 GAAGTTGAGAGCCAGTATGGAAGTATATAGGCGCTGGTGTGTTCTGGTACTGTGA 540
QY 583 CCAGGAAAGCAGACTTCTAAAGGAAATCAATCAGGATAAGATTTGATCTGATGAGTAT 642
Db 541 CCAGGAAAGCAGATTTCTAAAGGAAATCAATTAGGATAGATTTGATCTGATGATAT 600
```

QY 643 TTTCCATCTGAACCGGANTCTGCATCCACTACAGTATTATCATGCCCAAGTCCAGAA 702  
Db |||||  
QY 601 TTTCCCTCTGAACCGAGGTTCTGCATCCACTACAACTTGTCTATGCCCAATTCACAGAA 660  
Db |||||  
QY 703 ACCAGAGTCTCGTGTTCGCCCTTCATCTTTGTCTATTGGACCTCTCAACATGCT 762  
Db |||||  
QY 661 GCTGTAGTCTCTCAGTGTCTACCCCTTCAGCTTTGCCACTGGACCTCTTAATAATGCT 720  
QY 763 GTGACTGCTTCAGTACCTTCGGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAG 822  
Db |||||  
QY 721 ATAATGCTTTAGTACCTTCGGAAGACTTATTCGATATCTTGAACACAGAGATGGCG 780  
QY 823 GTGACTTGGACAGCTCTCAAGCCACATGGCAGCTTTTGGGCAAGGCTTTCTGTAT 882  
Db |||||  
QY 781 TTGGAATTTAGAGATCTATATAGGCCCACTTTGGCAACTTTCTTGGCAAGGCTTTTGT 840  
QY 883 GGGAAAAAACAAGTGTGAATCTGAATCTCTCAAGGAGAGGTAAACTCTACAGC 942  
Db |||||  
QY 841 GGAAGAAAATCCAGAGTGTGTGATCTGAACCTTTAAACAGAGGAGGTAAAGATTATACAGC 900  
QY 943 TGCACACCCCGAACTTCTCAGTGTCCATACCGGAAGAGCTTAAAGAGACAGATACCATA 1002  
Db |||||  
QY 901 TGCACACCTCGTAACCTTCTCAGTGTCCATAGGGAAGAACTTAAAGAGAACCGATACCAAT 960  
QY 1003 TTCTGGCCAGGTTCTCTCTGTCAGCGCTGTGGAGGAAATTTGTCTGTCTCCAT 1062  
Db |||||  
QY 961 TTCTGGCCAGGTTCTCTCTGTTAAACGCTGTGTGGGAACTGTGCTGTCTCCAC 1020  
QY 1063 AATTGCAATGAATCTCAGTGTGTCCAGTAAAGTTTACAAAAGTACCAATGAGTCTCT 1122  
Db |||||  
QY 1021 AATTGCAATGAATCTCAATGTGTCCAGCAAAAGTTTACTAAAAAATACCAAGGTCCT 1080  
QY 1123 CAGTTGAGACCAAAACTGGAGTCAAGGATTCAGTCACTCACTGATGTGGCTGT 1182  
Db |||||  
QY 1081 CAGTTGAGACCAAAAGCCGGTGTGAGGGAATGCACAAATCACTCACCGAGTGGCCCTG 1140  
QY 1183 GAACACCAAGGATGTGACTGTGTGTAGAGGAAACCGAGAGGTAATCTCGAGCT 1242  
Db |||||  
QY 1141 GAGCACCAGGAGTGTGATGTGTGTCAGAGGAGCACAGGAGGATAGCCGCATCAC 1200  
QY 1243 TCGTAGCAGCAC 1254  
Db |||||  
QY 1201 CACCAGCAGCTC 1212

RESULT 13  
US-09-457-066-50  
; Sequence 50, Application US/09457066  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60  
; CURRENT APPLICATION NUMBER: US/09/457,066  
; CURRENT FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 50  
; LENGTH: 1095  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fused DNA  
US-09-457-066-50

Query Match 50.6%; Score 745.8; DB 5; Length 1095;  
Best Local Similarity 84.3%; Pred. No. 1.4e-230;

Matches 840; Conservative 0; Mismatches 157; Indels 0; Gaps 0;  
QY 236 CCGGCCAAAGAACGGGACTCGGGCTGAGTCCAACTGAGCAGCAGAGTTGCGACTCTCCA 295  
Db |||||  
QY 80 CCGGCCAGAGACAGGGGACTCAGGCGAATCCAACTGAGTAGTAATTTCCAGTTTCCA 139  
Db |||||  
QY 296 CGCAACAAGGAACAGAACGGAGTGCAGATCCCCGGCATGAGAGAGTTGTCTATATCTG 355  
Db |||||  
QY 140 GCAACAAGGAACAGAACGGAGTGCAGATCCCCGGCATGAGAGAGTTGTCTATCTCTA 199  
QY 356 GTATGGGAGCATCCACAGCCCGAAGTTTCTCATAGTACCCAGAAATATGTGCTGG 415  
Db |||||  
QY 200 CTAATGGGAATTTACAGACCCCAAGTTTCTCTCATCTTATCCAAAGAAATACGGTCTGG 259  
QY 416 TGTGAGATTTAGTTGAGTGTAGTGAATGTCGCGATCCAGCTGACATTTGATGAGAGAT 475  
Db |||||  
QY 260 TATGGAGTTAGTAGCAGTAGAGGAAATGATGGATACAACTTACGTTTGTATGAAGAT 319  
QY 476 TTGGCTGGAAAGATCCAGAACCATATATCAAGATATGATTTGTAGAGTTGAGGAGC 535  
Db |||||  
QY 320 TTGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTGTAGAGTTGAGGAAC 379  
QY 536 CCAGTGTGGAGTGTGTTTGGAGCGCTGGTGTGTTCTGGGACTGTGCCAGGAAAGCAGA 595  
Db |||||  
QY 380 CCAGTGTGGAACTATATTAGGGCGCTGGTGTGTTCTGGTACTGTACCCAGGAAAACAGA 439  
QY 596 CTTCTAAAGGAAATCATATCAGGATTAAGTTTGTATCTGATGAGTATTTTCCATCTGAAC 655  
Db |||||  
QY 440 TTTCTAAAGGAAATCAATTAGGATTAAGTTTGTATCTGATGAATATTTTCTCTGAAC 499  
QY 656 CCGGATTTGCACTCCACTACAGTATTATCATGCCCAAGTCCAGAAACACAGAGTCTCT 715  
Db |||||  
QY 500 CAGGTTCTGCATCCACTACAACTTGTCTGCCACAAATTCACAGAGCTGTGAGTCTCT 559  
QY 716 CGGTTTGGCCCTTCTCTTGTCTATTTGAGCTGTCTCAACAACTGTGAGTCTCTCA 775  
Db |||||  
QY 560 CAGTGTACCCCTTCTGCTTTGCCACTGGACCTGCTTAATATGCTATACTGCTCTTA 619  
QY 776 GTACCTTTGGAAGAGCTGATTCGGTACCTAGAGCCAGATCGAGTGGAGTGGACA 835  
Db |||||  
QY 620 GTACCTTTGGAAGAGCTTATTCGATATCTTGAACAGAGAGATGGCAGTTGAGCTTAGAAG 679  
QY 836 GCCTCTCAAGCCCAACATGGCAGCTTTTGGGCAAGGCTTTCTGTATGGGAAAAAAGCA 895  
Db |||||  
QY 680 ATCTATATAGSCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTTTTGGAGAAATCCA 739  
QY 896 AAGTGGTGAATCTGAATCTCTCAAGGAAGAGGTAAACTCTACAGCTGCACACCCCGGA 955  
Db |||||  
QY 740 GAGTGGTGGATCTGAACCTTCTAAACAGAGGAGGTAAAGTATATACAGCTGCACACCTCGTA 799  
QY 956 ACTTCTCAGTGTCCATACGGGAAGAGCTTAAAGAGGACAGATACCATATTTCTGGCCAGTT 1015  
Db |||||  
QY 800 ACTTCTCAGTGTCCATTAAGGAGAACTTAAAGAGAACCGATACCATTTCTGGCCAGTT 859  
QY 1016 GTCTCTGTGCAAGCGCTGTGGAGGAAATTTGCTGTGTCTCCATAAATTTGCAATGAAT 1075  
Db |||||  
QY 860 GTCTCTGTGTTAAACGCTGTGGTGGGAACTGTGCTGTGTCTCCACAAATTTGCAATGAAT 919  
QY 1076 GTGAGTGTGTCACGCTTAAAGTTTACAAAAGTACCAATGAGTGTCTCTCAGTTGAGACCA 1135  
Db |||||  
QY 920 GTCAATGTGTCACCAAGCAAAAGTTTACTAAAAGTATACCAAGGAGGCTCTTCTCAGTTGAGACCA 979  
QY 1136 AAACTGGAGTCAAGGGGATTCATAAGTCACTCACTGATGTGGCTCTGGAACACACACAGG 1195  
Db |||||  
QY 980 AGACCGGTGTACGGGATTTGCAAAATCACTCACCGACGTGGCCCTGGAGCACCATGAGG 1039  
QY 1196 AATGTGACTGTGTGTAGAGGAAACCGCAGAGGGTA 1232  
Db |||||  
QY 1040 AGTGTGACTGTGTGTCAGAGGAGGACACAGAGGATA 1076

RESULT 14  
US-09-457-066-6



Db 121 GTACAAGATCCTAGCATGAGAGAAATTATTACTGTGTCTACTAATGGAAAGTATTTCACAGC 180  
Qy 376 CCGAAGTTTTCCTCATACGTACCCAGAAATATGGTGTGTGGAGATTAGTTGCCAGTA 435  
Db 181 CCAAGTTTCTCTCATACTTATCCAAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTA 240  
Qy 436 GATGAAATATGGCGGATCCAGCTGACATTTGATGAGAGATTGGGCTGGAAAGATCCAGAA 495  
Db 241 GAGGAAATATGATGGATACAACTTACGTTTGTGAAAGATTGGGCTTGAAGACCCAGAA 300  
Qy 496 GACGATATATGCAAGTATGATTTTGTAGAAGTTGAGGAGCCAGTGTGGAGTGTGTTTA 555  
Db 301 GATCACATATGCAAGTATGATTTTGTAGAAGTTGAGGAAACCCAGTGTGGAACCTATATTA 360  
Qy 556 GGACGCTGGTGTGGTCTTCTGGGACTGTGCCAGGAAAGCAGACTTCTAAAGGAAATCATATC 615  
Db 361 GGGGCTGGTGTGTCTTCTGGTACTGTACCAGGAAACAGATTCTTAAGGAAATCAATT 420  
Qy 616 AGGATAAGATTGTATCTGTGATGAGTATTTTCCATCTGAAACCGGATTTGATCCACTAC 675  
Db 421 AGGATAAGATTGTATCTGTGATGAATATTTTCTTCTGAACACAGGGTTCTGCATCCACTAC 480  
Qy 676 AGTATTATCATGCCCACAAAGTCACAGAAACACAGAGTCTCTCGGTGTGCCCCCTTCATCT 735  
Db 481 AACTTGTCTATGCCACCAATTCACAGAGCTGTGAGTCTTCACTACCTTGGAGAGCTGATT 540  
Qy 736 TTGTCAATGGACCTGTCTCAACAATGCTGTGACTGCTTCACTACCTTGGAGAGAGCTGATT 795  
Db 541 TTGCCACTGGACCTGTCTTAATAATGCTATAACTGCCTTTAGTACCTTGGAGAGACCTTATT 600  
Qy 796 CGGTACCTAGAGCCAGATCGATGGCAGGTGGACTTGGACAGCCTCTACAAGCCAAACATGG 855  
Db 601 CGATATCTTGAACACAGAGATGGCAGTTGGACTTGAAGATCTATATAGGCCAACTTGG 660  
Qy 856 CAGCTTTTGGCAAGGCTTTCTCTGTATGGGAAAAAAGCAAAGTGTGAAT 906  
Db 661 CAACTTCTTGGCAAGGCTTTTGTGTTTGGAGAAAAATCCAGAGGAGATAAT 711

Search completed: November 26, 2003, 09:11:10  
Job time : 275.739 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 25, 2003, 23:39:26 ; Search time 2150.81 Seconds  
(without alignments)  
16656.442 Million cell updates/sec

Title: US-09-852-209A-6

Perfect score: 1474

Sequence: 1 caccctggagacacagaag.....aatcacaaagcactgcaccc 1474

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estnu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_hcti:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_hct:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_mam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_pbg:\*

27: em\_gss\_vri:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1444.8	98.0	2765	11 AK052947	AK052947 Mus muscu
2	1444.8	98.0	3244	11 AK033734	AK033734 Mus muscu
3	1444.8	98.0	3405	11 AK042767	AK042767 Mus muscu
4	1366.2	92.7	2893	11 BC029099	BC029099 Mus muscu

5	873.6	59.3	902	13	BUS17879	BUS17879 AGENCOURT
6	865.4	58.7	2502	11	AK081347	AK081347 Mus muscu
7	840	57.0	2826	11	BC041783	BC041783 Homo sapi
8	809	54.9	823	13	BU614825	BU614825 UI-M-EVO-
9	757.6	51.4	2655	11	BC051876	BC051876 Homo sapi
10	707	48.0	901	13	BQ957838	BQ957838 AGENCOURT
11	616.4	41.8	999	13	BQ068266	BQ068266 AGENCOURT
12	597.6	40.5	910	10	BG243001	BG243001 602355974
13	595.6	40.4	877	10	BF137533	BF137533 601780532
14	595	40.4	712	12	BI693338	BI693338 603343666
15	562.2	38.1	677	10	BB662450	BB662450 BB662450
16	559	37.9	559	12	BM053896	BM053896 idg9c11.y
17	551.8	37.4	584	10	BF151355	BF151355 uz15b12.y
18	534.2	36.2	994	13	BUS54214	BUS54214 AGENCOURT
19	531	36.0	811	10	BG185961	BG185961 RST4916 A
20	519.8	35.3	523	10	BF021679	BF021679 uy50f05.y
21	511	34.7	511	9	AW210331	AW210331 ul53f09.y
22	497.2	33.7	721	13	BQ443526	BQ443526 UI-M-EVO-
23	456.2	30.9	609	10	BF133918	BF133918 601779154
24	448.4	30.4	695	12	BI668022	BI668022 603295848
25	446.6	30.3	478	12	BM022835	BM022835 id62e12.y
26	445.4	30.2	447	10	BF011835	BF011835 us37d10.y
27	441.2	29.9	902	10	BF163629	BF163629 601769732
28	440.2	29.9	770	12	BI556877	BI556877 6032339918
29	439	29.8	789	12	BI911795	BI911795 603065222
30	434.2	29.5	982	13	BU459467	BU459467 603368015
31	432.6	29.3	567	12	BM827309	BM827309 K-EST0099
32	415.4	28.2	1029	10	BG173847	BG173847 602333906
33	413.6	28.1	676	13	BU259419	BU259419 603415593
34	406.6	27.6	562	9	AU280428	AU280428 AU280428
35	405	27.5	521	10	BE374398	BE374398 601227568
36	404.4	27.4	408	10	BE304156	BE304156 601085830
37	400	27.1	400	9	AL364180	AL364180 AL364180
38	392.8	26.6	864	10	BF137524	BF137524 601780523
39	389.4	26.4	423	14	CB797465	CB797465 AMGNNUC:S
40	388.8	26.4	1142	10	BG681390	BG681390 602627750
41	382.2	25.9	411	14	CB802513	CB802513 AMGNNUC:S
42	379.6	25.8	980	13	BUS27807	BUS27807 AGENCOURT
43	374.2	25.4	399	13	BY018563	BY018563 BY018563
44	371.6	25.2	556	10	BG609411	BG609411 323251 MA
45	357.4	24.2	769	14	CB309471	CB309471 AGENCOURT

#### ALIGNMENTS

RESULT 1	AK052947	AK052947	2765 bp	mRNA	linear	HTC 05-DEC-2002
LOCUS	AK052947	Mus musculus	15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930001M08	product:platelet-derived growth factor, C polypeptide, full insert sequence.		
DEFINITION	AK052947	AK052947	GI:26343118			
ACCESSION	AK052947	AK052947	GI:26343118			
VERSION	AK052947.1	AK052947.1	GI:26343118			
KEYWORDS	HTC; CAP trapper.					
SOURCE	Mus musculus (house mouse)					
ORGANISM	Mus musculus					
REFERENCE	1	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
AUTHORS	1	Carninci, P. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning					
JOURNAL	99279253					
MEDLINE	99279253					
PUBMED	10349636					
REFERENCE	2	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
AUTHORS	2	Carninci, P. and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes					
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)					
MEDLINE	20499374					
PUBMED	11042159					

REFERENCE AUTHORS	3	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Oneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Koyada, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE		RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL MEDLINE PUBMED		Genome Res. 10 (11), 1757-1771 (2000)
REFERENCE AUTHORS	4	20530913 11076861
REFERENCE AUTHORS	4	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Sato, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, M., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, I., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Hoffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, J., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wyshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.
TITLE		Functional annotation of a full-length mouse cDNA collection
JOURNAL MEDLINE PUBMED		Nature 409 (6821), 685-690 (2001)
REFERENCE AUTHORS	5	21085660 11217851
REFERENCE AUTHORS	5	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE		Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL MEDLINE PUBMED		Nature 420, 563-573 (2002)
REFERENCE AUTHORS	6	(bases 1 to 2765)
REFERENCE AUTHORS	6	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Inotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE		Direct Submission
JOURNAL		Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT		cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
FEATURES		Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/ Location/Qualifiers

source	1..2765	/organism="Mus musculus"
		/mol_type="mRNA"
		/strain="C57BL/6J"
		/db_xref="PANTOM DB:D930001M08"
		/db_xref="taxon:10090"
		/clone="D930001M08"
		/tissue_type="head"
		/clone_lib="RIKEN full-length enriched mouse cDNA library"
		/dev_stage="15 days embryo"
CDS	274..1311	
		/note="unnamed protein product; platelet-derived growth factor, C polypeptide (MGD) [MG1:1859631, GB NM_019971, evidence: BLASTN, 99%, match=2691]"
		putative"
		/codon_start=1
		/protein_id="BAC35216.1"
		/db_xref="GI:26343119"
		/translation="MLLGLLLLSALAGQRTGTRAEENLSKQLQSSDKQNGVDDP RHERVTISNGSIHSPKPHYPRNVLVWRLVADENVRILQTFDERFGLDEDD ICKYDFVEVERPSDGVLCGSGTVPGKOTSGNIRIRFVSDEYFSPBFGCIHY SIIMPOVETTSPLSPSSLSLLNNAVTAFSLLELIRYLEPDRMOWDLSLYKP TWOLLGKAFYKKSQKVNINLLKEVKLYSCTPENFSVIREELKRTDTIIFWPGCLL VRCGNCACLLHNCNECQVPRVKYKXHEVLQRPKTGVKGLKLSLTDALEHHE CDCVCRGNAGG"
		2738..2743
		/note="putative"
		2765
		/note="putative"
polyA_signal	766 a	593 c 635 g 771 t
polyA_site		
BASE COUNT	766 a	593 c 635 g 771 t
ORIGIN		
		Query Match 98.0%; Score 1444.8; DB 11; Length 2765;
		Best Local Similarity 99.4%; Pred. No. 0;
		Matches 1460; Conservative 0; Mismatches 8; Indels 1; Gaps 1;
QY	2	ACCTGGAGACACAGAGAGGGCTCTAGAGAAAATTTTGGATGGGGATTATGTGAAACTA 61
Db	81	AACTGGAGACACAGAGAGGGCTCTAGAGAAAATTTTGGATGGGGATTATGTGAAACTA 140
QY	62	CCCTGGATTCTCTGTCGACAGCGCGCTTCCACCGCAGCGCAGCCTTTTCCC 121
Db	141	CCCTGGATTCTCTGTCGACAGCGCGCTTCCACCGCAGCGCAGCCTTTTCCC 200
QY	122	CGGGCTGGGCTGAGCGCTTGGAGTCTGCTGCCAGTCCCGCCGCGAGTGGAGCCTCG 181
Db	201	C-GGCTGGGCTGAGCGCTTGGAGTCTGCTGCCAGTCCCGCCGCGAGTGGAGCCTCG 259
QY	182	CCCCAGTTCAGCAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCCCTGGCCGCC 241
Db	260	CCCCAGTTCAGCAATGCTCTCTCGGCTCTCTCTGCTGACATCTGCCCTGGCCGCC 319
QY	242	AAAGAACGGGACTCGGGCTGAGTCCCACTGAGCAGCAAGTTGACAGTCTCCAGCGACA 301
Db	320	AAAGAACGGGACTCGGGCTGAGTCCCACTGAGCAGCAAGTTGACAGTCTCCAGCGACA 379
QY	302	AGGAACAGAACGGAGTCAAGATCCCGCGCATGAGAGAGTTGTCACTATATCTGTAATG 361
Db	380	AGGAACAGAACGGAGTCAAGATCCCGCGCATGAGAGAGTTGTCACTATATCTGTAATG 439
QY	362	GGAGCATCCACAGCGCGAGTTTCTCATAGTACCAAGAAATATGGTGTGCTGTGGA 421
Db	440	GGAGCATCCACAGCGCGAGTTTCTCATAGTACCAAGAAATATGGTGTGCTGTGGA 499
QY	422	GATTAGTTCAGTACAGTAAATGTCGGATCCAGCTGACATTTGATGAGAGATTTGGGC 481
Db	500	GATTAGTTCAGTACAGTAAATGTCGGATCCAGCTGACATTTGATGAGAGATTTGGGC 559
QY	482	TGGAAGATCCAGAACGATATATGCAAGTATGATTTTGTAGAGTTGAGGAGCCAGTG 541
Db	560	TGGAAGATCCAGAACGATATATGCAAGTATGATTTTGTAGAGTTGAGGAGCCAGTG 619
QY	542	ATGGAAGTCTTTAGACGCTGCTGTTCTGGGACTCTGCCAGGAAAGCAGACTCTTA 601

Db 620 ATGGAAGTGTATTAGACGCTGGTGTGTTCTGGGACTGTGCAGGAAAGCAGACTCTTA 679  
QY 602 RAGGAAATCATATCAGGATAAGATTGTATCTGATCAGTATTTTCATCTGAACCGGAT 661  
Db 680 AAGGAAATCATATCAGGATAAGATTGTATCTGATCAGTATTTTCATCTGAACCGGAT 739  
QY 662 TCTGCATCCACTACAGTATTATCATGCCACAAGTCACAGAAACCCAGAGTCTTCCGGTGT 721  
Db 740 TCTGCATCCACTACAGTATTATCATGCCACAAGTCACAGAAACCCAGAGTCTTCCGGTGT 799  
QY 722 TSCCCCTTCATCTTGTCTATGGACCTGCTCAACATGCTGTGACTGCTTCAGTACCT 781  
Db 800 TGCCCCCTTCATCTTGTCTATGGACCTGCTCAACATGCTGTGACTGCTTCAGTACCT 859  
QY 782 TGAAGAGCTGATTTCGGTACCTAGACCCAGATCGATGGCAGGTGGACTTGGACAGCCTCT 841  
Db 860 TGAAGAGCTGATTTCGGTACCTAGACCCAGATCGATGGCAGGTGGACTTGGACAGCCTCT 919  
QY 842 ACAAGCAACATGGCAGCTTTTGGGCAAGCTTTCTGTATGGAAAAAAGCAAGTGG 901  
Db 920 ACAAGCAACATGGCAGCTTTTGGGCAAGCTTTCTGTATGGAAAAAAGCAAGTGG 979  
QY 902 TGAATCTGAATCTCTCAGGAGAGGTAAACTCTACAGCTGCACACCCCGGAATTCT 961  
Db 980 TGAATCTGAATCTCTCAGGAGAGGTAAACTCTACAGCTGCACACCCCGGAATTCT 1039  
QY 962 CAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACCATATTCTGGCAGGTTGTCTCC 1021  
Db 1040 CAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACCATATTCTGGCAGGTTGTCTCC 1099  
QY 1022 TGGTCAAGCGCTGTGGAGAAATTTGTCCTGTGTCTCCATATTCCAATGAATGTCAGT 1081  
Db 1100 TGGTCAAGCGCTGTGGAGAAATTTGTCCTGTGTCTCCATATTCCAATGAATGTCAGT 1159  
QY 1082 GTGTCCCGCTAAAGTTACAAAAGTACCATGAGTCTCTCAGTGTGAGACCAAACTG 1141  
Db 1160 GTGTCCCGCTAAAGTTACAAAAGTACCATGAGTCTCTCAGTGTGAGACCAAACTG 1219  
QY 1142 GAGTCAAGGGATTGCATAAGTCACTCACTGATGTGGCTCTGGAACACCCAGGGAATGTG 1201  
Db 1220 GAGTCAAGGGATTGCATAAGTCACTCACTGATGTGGCTCTGGAACACCCAGGGAATGTG 1279  
QY 1202 ACTGTGTGTAGAGAAACGACGAGGGTAATCTGACGCTTCGTAGCAGCACACTGAG 1261  
Db 1280 ACTGTGTGTAGAGAAACGACGAGGGTAATCTGACGCTTCGTAGCAGCACACTGAG 1339  
QY 1262 CACTGCATTCTGTGTACCCCAAGCAACCTTCATCCCAAGCGTTGGCCGAGG 1321  
Db 1340 CACTGCATTCTGTGTACCCCAAGCAACCTTCATCCCAAGCGTTGGCCGAGG 1399  
QY 1322 CTCTCAGCTGCTGATGCTGGCTATGTTAAGATCTTTACTGCTCCCAACCAAAATTCCTAG 1381  
Db 1400 CTCTCAGCTGCTGATGCTGGCTATGTTAAGATCTTTACTGCTCCCAACCAAAATTCCTAG 1459  
QY 1382 TTGTTTGTCTCAATAGCTTCCCTCGAGGACTTCAAGTGTCTTCTAAAGACCAAGGC 1441  
Db 1460 TTGTTTGTCTCAATAGCTTCCCTCGAGGACTTCAAGTGTCTTCTAAAGACCAAGGC 1519  
QY 1442 ACCAAGAGGATCAATCACAAGCACTGC 1470  
Db 1520 ACCAAGAGGATCAATCACAAGCACTGC 1548

RESULT 2  
AK0333734  
LOCUS  
DEFINITION Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130403008 product:platelet-derived growth factor, C polypeptide, full insert sequence.  
ACCESSION AK0333734  
VERSION AK0333734.1 GI:26329432  
KEYWORDS HTC; CAP trapper.

SOURCE ORGANISM  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS Carninci, P. and Hayashizaki, Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE 99279253  
PUBMED 10349636  
REFERENCE  
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE 20499374  
PUBMED 11042159  
REFERENCE  
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Chata, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
MEDLINE 20530913  
PUBMED 11076861  
REFERENCE  
AUTHORS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Maeda, H., Ashburner, M., Batalov, S., Casavant, R., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staudli, P., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Anon, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bona, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, I., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombarts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, J., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.  
TITLE Functional annotation of a full-length mouse cDNA collection  
JOURNAL Nature 409 (6821), 685-690 (2001)  
MEDLINE 21085660  
PUBMED 11217851  
REFERENCE  
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
JOURNAL Nature 420, 563-573 (2002)  
MEDLINE 1217851  
PUBMED 1217851  
REFERENCE  
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,



TITLE JOURNAL	Muramatsu, M. and Hayashizaki, Y.		Db		797	AAAGAAACGGGAGCTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCGAGCTCTCCAGCGACA		856
	Direct Submission		QY		302	AGGAACAGAACGGAGTGCAGATCCCGCATGAGAGAGTGTGTCACTATATCTGGTAATG		361
COMMENT	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)		Db		857	AGGAACAGAACGGAGTGCAGATCCCGCATGAGAGAGTGTGTCACTATATCTGGTAATG		916
	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.		QY		362	GGAGCATCCACAGCCGAGTTCCTCATACATCCCAAGAAATATGGTGTGGTGGGA		421
FEATURES	Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://phantom.gsc.riken.go.jp/.		Db		917	GGAGCATCCACAGCCGAGTTCCTCATACATCCCAAGAAATATGGTGTGGTGGGA		976
	Location/Qualifiers		QY		422	GATTAGTTCAGTAGATGAAATATGCGGATCCAGCTGACATTTGATGAGAGATTTGGGC		481
source	1. .3244		Db		977	GATTAGTTCAGTAGATGAAATATGCGGATCCAGCTGACATTTGATGAGAGATTTGGGC		1036
	/organism="Mus musculus"		QY		482	TGGAGATCCACAGACGATATATGCAAGTATGATTTCTAGAAATTTGAGGAGCCAGTG		541
CDS	/mol_type="mRNA"		Db		1037	TGGAGATCCACAGACGATATATGCAAGTATGATTTCTAGAAATTTGAGGAGCCAGTG		1096
	/strain="C57BL/6J"		QY		542	ATGGAAGTGTTCAGGACGCTGGTGTGGTTCCTGGGACTGTGCCAGAAAGCAGACTCTA		601
	/db_xref="FANTOM DB:9130403008"		Db		1097	ATGGAAGTGTTCAGGACGCTGGTGTGGTTCCTGGGACTGTGCCAGAAAGCAGACTCTA		1156
	/db_xref="taxon:10090"		QY		602	AAGGAATCATATCAGGATTAAGATTTGTATCTGATGAGTATTTCCATCTGAACCCGGAT		661
	/clone="9130403008"		Db		1157	AAGGAATCATATCAGGATTAAGATTTGTATCTGATGAGTATTTCCATCTGAACCCGGAT		1216
	/sex="male"		QY		662	TCTGCATCCACTACAGTATTTATCATGCCACAAAGTACAGAAACACGAGTCTTCGGTGT		721
	/tissue type="cecum"		Db		1217	TCTGCATCCACTACAGTATTTATCATGCCACAAAGTACAGAAACACGAGTCTTCGGTGT		1276
	/clone_lib="RIKEN full-length enriched mouse cDNA library"		QY		722	TGCCTCCCTTCATCTTTGTCTATTCAGGACCTGCTCAACAAATGCTGTGACTGCCTTCAGTACCT		781
	/note="unnamed protein product; platelet-derived growth factor, C polypeptide (MGI:1859631, GB NM_019971, evidence: BLASTN, 99%, match=2691)"		Db		1277	TGCCTCCCTTCATCTTTGTCTATTCAGGACCTGCTCAACAAATGCTGTGACTGCCTTCAGTACCT		1336
	/codon_start=1		QY		782	TGGAGAGCTGATTCGGTACCTAGACCCAGATCGATGGAGGTGGACTTGGACAGCTCT		841
	/protein_id="BAC28455.1"		Db		1337	TGGAGAGCTGATTCGGTACCTAGACCCAGATCGATGGAGGTGGACTTGGACAGCTCT		1396
	/gb_xref="GI:26329433"		QY		842	ACAAGCAACATGCGAGCTTTTGGGCAAGCTTTCTGTATGGGAAAAAAGCAAGTGG		901
	/translation="MLLLGLLITLALAGRTGTAEISLSSKQLSSDKQNGVDPRIHVVITIGNSIHSHPKPTVPRNMLVRLVAVDENVRVQLTFDRFGLDPRDDICKYDVEEESDGLVRCWGSVPKQKSGNHIRIRFVSDVFPSEPCFCHYSTIMPVTTTSPSVLPSPSLDLNNVAFSTLEIRLVLEPRRWQVLDLSLYKPTWLLGKFLYKSKVNLNLEKVKLYSCPTNFVSIRBELKRTDTTFWPGCLLVRCGNCACCLHNCQCPKRVTKYKHYELQLRPKTVGKVLHSLTDVALEHHECDCVCRGNAGG"		Db		1397	ACAAGCAACATGCGAGCTTTTGGGCAAGCTTTCTGTATGGGAAAAAAGCAAGTGG		1456
	3216..3221		QY		902	TGAATCTGAATCTCTCAAGGAGAGGTAAACTCTACAGTGCACACCCCGGAACTTCT		961
polyA_signal	/note="putative"		Db		1457	TGAATCTGAATCTCTCAAGGAGAGGTAAACTCTACAGTGCACACCCCGGAACTTCT		1516
	3244		QY		962	CAGTGTCCATACGGGAGAGCTAAAGAGGACAGATACCATTTCTGSCCAGGTTGTCTCC		1021
polyA_site	/note="putative"		Db		1517	CAGTGTCCATACGGGAGAGCTAAAGAGGACAGATACCATTTCTGSCCAGGTTGTCTCC		1576
	821 a 810 c 763 g 850 t		QY		1022	TGTCAAGCGCTGTGGAGGAAATTTGCTGTTGTCTCCATAATTCGAATGCAATGTCAGT		1081
BASE COUNT	Query Match 98.0%; Score 1444.8; DB 11; Length 3244;		Db		1577	TGTCAAGCGCTGTGGAGGAAATTTGCTGTTGTCTCCATAATTCGAATGCAATGTCAGT		1636
	Best Local Similarity 99.4%; Pred. No. 0;		QY		1082	GTGTCCTCCAGTAAAGTTACAAAAGTACCATGAGGTCTTTCAGTTGAGACCAAAACTG		1141
ORIGIN	Matches 1460; Conservative 0; Mismatches 8; Indels 1; Gaps 1;		Db		1637	GTGTCCTCCAGTAAAGTTACAAAAGTACCATGAGGTCTTTCAGTTGAGACCAAAACTG		1696
	2 ACCTGAGACACAGAAGCGCTCTAGGAAAAATTTTGGATGGGATTATGTGAAACTA 61		QY		1142	GAGTCAAGGATTTGCATTAAGTCACTCACTGATGTGCTCTGGAAACACCAAGGAATGTG		1201
	558 AACTGAGACACAGAAGCGCTCTAGGAAAAATTTTGGATGGGATTATGTGAAACTA 617		Db		1697	GAGTCAAGGATTTGCATTAAGTCACTCACTGATGTGCTCTGGAAACACCAAGGAATGTG		1756
	62 CCTCGGATTTCTGTCGAGACCGCGCAGCGGCTTCCACCGCAGCGAGCTTTCCC 121		QY		1202	ACTGTGTGTAGAGGAAACCGCAGGAGGTAACTGACGCTTCTGTAGCAGCACACGCTGAG		1261
	618 CCTCGGATTTCTGTCGAGACCGCGCAGCGGCTTCCACCGCAGCGAGCTTTCCC 677		Db		1757	ACTGTGTGTAGAGGAAACCGCAGGAGGTAACTGACGCTTCTGTAGCAGCACACGCTGAG		1816
	122 CGGCTGGGCTGAGCCTTGAGTCTGCTTCCCGAGTCCCGCGAGTGAGCCCTCG 181		QY		1262	CACTGCAATTTGTGTATACCCGCAAGCAACCTTATCCCGCAGCGGTTGGCGCAGGG		1321
	678 C-GGCTGGGCTGAGCCTTGAGTCTGCTTCCCGAGTCCCGCGAGTGAGCCCTCG 736		Db		1817	CACTGCAATTTGTGTATACCCGCAAGCAACCTTATCCCGCAGCGGTTGGCGCAGGG		1876
	182 CCCAGTCAGCAAAATGCTCTCTCGGCTCTCTCTCTGTCGATCTGCTCCAGCAAAATTTCTCAG 241		QY		1322	CTCTCAGCTGCTGATCTGCTATGCTAAGATCTTACTGCTCTCCAAACCAAAATTTCTCAG		1381
	737 CCCAGTCAGCAAAATGCTCTCTCGGCTCTCTCTCTGTCGATCTGCTCCAGCAAAATTTCTCAG 796		Db		1877	CTCTCAGCTGCTGATCTGCTATGCTAAGATCTTACTGCTCTCCAAACCAAAATTTCTCAG		1936
	242 AAGAAGGGGACTCGGCTGAGTCCAACTGAGCAGCAAGTTGCGACTCTCCAGCGACA 301		QY					

QY	1382	TTGTTTCTTCAATAGCCTTCCCTGACGAGCTTCAAGTGTCTTCTTAAAGACCGAGGC	1441
Db	1937	TTGTTTCTTCAATAGCCTTCCCTGACGAGCTTCAAGTGTCTTCTTAAAGACCGAGGC	1996
QY	1442	ACCAAGAGGAGTCATCAAGACACTGC	1470
Db	1997	ACCAAGAGGAGTCATCAAGACACTGC	2025
RESULT 3			
AK042767			
LOCUS			
DEFINITION	AK042767	3405 bp mRNA linear	HTC 05-DSC-2002
		Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length	
		enriched library, clone:A730022G11	product:platelet-derived growth
		factor, C polypeptide, full insert sequence.	
ACCESSION	AK042767		
VERSION	AK042767.1	GI:26335314	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE			
AUTHORS	Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBLISHED	10349636		
REFERENCE			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,		
	Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to		
	prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20493374		
PUBLISHED	11042159		
REFERENCE			
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,		
	Konno, H., Akiyama, J., Nishi, K., Kitsuami, T., Tashiro, H., Itoh, M.,		
	Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,		
	Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,		
	Fujwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,		
	Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,		
	Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format		
	sequencing pipeline with 384 multipillar sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
MEDLINE	20530913		
PUBLISHED	11076861		
REFERENCE			
AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,		
	Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,		
	Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,		
	Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,		
	Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,		
	Fleischmann, W., Gaasterland, T., Giesi, C., King, B., Kochiwa, H.,		
	Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G.,		
	Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M.,		
	Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,		
	Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,		
	Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C.,		
	Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,		
	Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,		
	Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,		
	Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,		
	Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H.,		
	Toyo-oka, K., Wang, K. H., Weitz, C., Whitaker, C., Wilming, L.,		
	Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohsaki, S.		
	and Hayashizaki, Y.		
TITLE	Functional annotation of a full-length mouse cDNA collection		
JOURNAL	Nature 409 (6821), 685-690 (2001)		
MEDLINE	21085660		
11217851			
5			
REFERENCE	The FANTOM Consortium and the RIKEN Genome Exploration Research		
AUTHORS	Group Phase I & II Team.		
TITLE	Analysis of the mouse transcriptome based on functional annotation		
	of 60,770 full-length cDNAs		
JOURNAL	Nature 420, 563-573 (2002)		
REFERENCE	6 (bases 1 to 3405)		
AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,		
	Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,		
	Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,		
	Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,		
	Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,		
	Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,		
	Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,		
	Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,		
	Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,		
	Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akaira, S.,		
	Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,		
	Muramatsu, M. and Hayashizaki, Y.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of		
	Physical and Chemical Research (RIKEN), Laboratory for Genome		
	Exploration Research Group, RIKEN Genomic Sciences Center (GSC),		
	RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama,		
	Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp,		
	URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,		
	Fax: 81-45-503-9216)		
COMMENT	cDNA library was prepared and sequenced in Mouse Genome		
	Encyclopedia Project of Genome Exploration Research Group in Riken		
	Genomic Sciences Center and Genome Science Laboratory in RIKEN.		
	Division of Experimental Animal Research in Riken contributed to		
	prepare mouse tissues.		
	Please visit our web site for further details.		
	URL: http://genome.gsc.riken.go.jp/		
	URL: http://fantom.gsc.riken.go.jp/.		
FEATURES	Location/Qualifiers		
source	1. .3405		
	/organism="Mus musculus"		
	/mol_type="mRNA"		
	/strain="C57BL/6J"		
	/db_xref="FANTOM DB:A730022G11"		
	/db_xref="taxon:10090"		
	/clone="A730022G11"		
	/cisse_type="cerebellum"		
	/clone_lib="RIKEN full-length enriched mouse cDNA library"		
	/dev_stage="7 days neonate"		
	769. .1806		
CDS	/note="unnamed protein product; platelet-derived growth		
	factor, C polypeptide (MGD MGI:1859631, GB NM_019971,		
	evidence: BLASTN, 99%, match=2691)		
	putative"		
	/codon_start=1		
	/protein_id="BAC311358.1"		
	/db_xref="GI:26335315"		
	/translation="MLLGLLTSALAQGTGTRAEISLSSKLQSSDKBQGVDP		
	IKERVVTSIGSIHSKPFYPRNMVLAVDENVRIQLTDFRFLGDEPDD		
	ICFYDFVEEPESDGSLGRWCGSGVPGKTSKGNHRIKRVFSDYFSPGFCIH		
	SIIMPOVTETTSPLPSSLSLDLNNAVTAFSTLEELIRLYEPDWDLSLYKP		
	TWQLLKAFLYGKSKVNLKKEVKLYSCTPRNFPSVIRELKTDFIWPFGCLL		
	VRGCGNACCLHNECCVPRKVTCKTHEVLQLRPKTVGRGLSLTDVALEHHE		
	CDVCRCGNAGG"		
BASE COUNT	854 a 830 c 819 g 902 t		
ORIGIN			
Query Match	98.0%; Score 1444.8; DB 11; Length 3405;		
Best Local Similarity	99.4%; Pred. No. 0;		
Matches 1460; Conservative	0; Mismatches 8; Indels 1; Gaps 1;		
QY	2	ACCTGGAGACACAGAGAGCGCTCTAGGAAAATTTTGGATGGGATTTATGTGGAACCTA	61
Db	576	ACTGGAGACACAGAGAGCGCTCTAGGAAAATTTTGGATGGGATTTATGTGGAACCTA	635

QY 62 CCTGGATCTCTGTCGAGCGGCGGCGCTTCCACGCGAGCGAGCCTTTCCC 121  
Db 636 CCTGGATCTCTGTCGAGCGGCGGCGCTTCCACGCGAGCGAGCCTTTCCC 695  
QY 122 CGGGCTGGGCTGAGCCCTTGGAGTCTGCTTCCCAAGTCCCGCCGAGTGGAGCCCTCG 181  
Db 696 C-GGCTGGGCTGAGCCCTTGGAGTCTGCTTCCCAAGTCCCGCCGAGTGGAGCCCTCG 754  
QY 182 CCCAGTACGCAAAATGCTCTCTGCGCTCTCTCTGCTGACATCTGCGCTGGCGGCC 241  
Db 755 CCCAGTACGCAAAATGCTCTCTCTGCGCTCTCTCTGCTGACATCTGCGCTGGCGGCC 814  
QY 242 AAGAACGCGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTCAGCTCTCCAGCGACA 301  
Db 815 AAGAACGCGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTCAGCTCTCCAGCGACA 874  
QY 302 AGGAACAGAACCGGAGTCCGAAGATCCCGCGCATGAGAGAGTTGCACTATATCTGTAATG 361  
Db 875 AGGAACAGAACCGGAGTCCGAAGATCCCGCGCATGAGAGAGTTGCACTATATCTGTAATG 934  
QY 362 GGAGCATCCACAGCCGAGTTTCTCATACGTACCCAGAAATATGCTGCTGGA 421  
Db 935 GGAGCATCCACAGCCGAGTTTCTCATACGTACCCAGAAATATGCTGCTGGA 994  
QY 422 GATTAGTTGAGTAGATGAAATGTCGGATCCAGCTGACATTTGATGAGAGATTTGGGC 481  
Db 995 GATTAGTTGAGTAGATGAAATGTCGGATCCAGCTGACATTTGATGAGAGATTTGGGC 1054  
QY 482 TGAAGATCCAGAACGATATATGCAAGTATGATTTTGTAGAGTTGAGAGCCGAGTG 541  
Db 1055 TGAAGATCCAGAACGATATATGCAAGTATGATTTTGTAGAGTTGAGAGCCGAGTG 1114  
QY 542 ATGGAGTGTTTTAGACGCTGTGTGTTCTGGAGCTGCGAGGAAGACAGACTTCTA 601  
Db 1115 ATGGAGTGTTTTAGACGCTGTGTGTTCTGGAGCTGCGAGGAAGACAGACTTCTA 1174  
QY 602 AAGGAATCATATCAGATAGATTTTCTGATGATGATTTTCCATCTGAACCCGGAT 661  
Db 1175 AAGGAATCATATCAGATAGATTTTCTGATGATGATTTTCCATCTGAACCCGGAT 1234  
QY 662 TCTGCACTCACTCAGTATATATGCAAGTATGCAAGTATGCAAGTATGCAAGTATGCAAGT 721  
Db 1235 TCTGCACTCACTCAGTATATATGCAAGTATGCAAGTATGCAAGTATGCAAGTATGCAAGT 1294  
QY 722 TGCCCTCTCATCTTCTGATGAGTCTGCAACATGCTGACATGCTGACCTTCACTACCT 781  
Db 1295 TGCCCTCTCATCTTCTGATGAGTCTGCAACATGCTGACATGCTGACCTTCACTACCT 1354  
QY 782 TGAAGAGCTGATTCGCTACCTAGAGCCAGATGATGCGAGGTGAGTTCGACAGCTCT 841  
Db 1355 TGAAGAGCTGATTCGCTACCTAGAGCCAGATGATGCGAGGTGAGTTCGACAGCTCT 1414  
QY 842 ACAAGCCAAATGCGAGCTTTGGGCAAGCTTCTCTGATGGAAGAAAGCAAGTGG 901  
Db 1415 ACAAGCCAAATGCGAGCTTTGGGCAAGCTTCTCTGATGGAAGAAAGCAAGTGG 1474  
QY 902 TGAATCTGAATCTCTCAAGGAAGAGTAAACTCTACAGCTGACACCCCGGAATCTCT 961  
Db 1475 TGAATCTGAATCTCTCAAGGAAGAGTAAACTCTACAGCTGACACCCCGGAATCTCT 1534  
QY 962 CAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACATATTCGCGCAGTTGTCTCC 1021  
Db 1535 CAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACATATTCGCGCAGTTGTCTCC 1594  
QY 1022 TGGTCAAGCGCTGTGGAGGAATTTGCTGCTGCTCTCCATATTTGCAATGATGTCAGT 1081  
Db 1595 TGGTCAAGCGCTGTGGAGGAATTTGCTGCTGCTCTCCATATTTGCAATGATGTCAGT 1654  
QY 1082 GTGTCCCAAGTAAAGTTTACAAAAAGTACATGAGTCTCTCAGTTGAGACCAAAAACTG 1141  
Db 1555 GTGTCCCAAGTAAAGTTTACAAAAAGTACATGAGTCTCTCAGTTGAGACCAAAAACTG 1714  
QY 1142 GAGTCAAGGGATTCATAGTCACTCACTGATGCTGGAACACCAAGAGGAATGTG 1201

Db 1715 GAGTCAAGGGATTCATAGTCACTCACTGATGCTCTGGAACACCAAGAGGAATGTG 1774  
QY 1202 ACTGTGTGTGTAGAGAAAGCGAGGAGTAACTGAGCTTCTGAGCAGCACACCTGTAG 1261  
Db 1775 ACTGTGTGTGTAGAGAAAGCGAGGAGGTAATCTGAGCTTCTGAGCAGCACACCTGTAG 1834  
QY 1262 CACTGCACTTCTGTGTACCCGCCACAGCAACCTTCAATCCGCCACAGCTTTGGCCGAGGG 1321  
Db 1835 CACTGCACTTCTGTGTACCCGCCACAGCAACCTTCAATCCGCCACAGCTTTGGCCGAGGG 1894  
QY 1322 CTCTCAGCTGCTGATGCTGGCTATGTAAGATCTTACTGCTCTCAACCAAAATTTCTCAG 1381  
Db 1895 CTCTCAGCTGCTGATGCTGGCTATGTAAGATCTTACTGCTCTCAACCAAAATTTCTCAG 1954  
QY 1382 TTGTTTCTTCAATAGCTTCCCTCTCAGGACTTCAAGTGTCTTTAAAGACACAGAGGC 1441  
Db 1955 TTGTTTCTTCAATAGCTTCCCTCTCAGGACTTCAAGTGTCTTTAAAGACACAGAGGC 2014  
QY 1442 ACCAAGAGGAGTCAATCAAAAGCACTGC 1470  
Db 2015 ACCAAGAGGAGTCAATCAAAAGCACTGC 2043

## RESULT 4

LOCUS BC029099  
DEFINITION Mus musculus, Similar to platelet-derived growth factor, C

## ACCESSION

VERSION BC029099

## KEYWORDS

SOURCE HTc

## ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS Strausberg, R.

TITLE Direct Submission

## JOURNAL

Submitted (01-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: [cgaps-k@mail.nih.gov](mailto:cgaps-k@mail.nih.gov)

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)

Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,

Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAC Plate: 35 Row: p Column: 20

This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 10242384

This clone has the following problem: frame shifted.

## FEATURES

## source

1. 2893

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/clone="IMAGE:3660797"

/tissue\_type="Mammary tumor metastasized to lung."

MMTV-LTR/Wnt1 model. Expression driven by an MMTV-LTR



```

/mol_type="mRNA"
/db_xref="FVB/N-3"
/db_xref="taxon:10090"
/clone="IWAGE:6515520"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mam2"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT      224 a      233 c      240 g      205 t
ORIGIN
Query Match      59.3%; Score 873.6; DB 13; Length 902;
Best Local Similarity 99.3%; Pred. No. 3e-234;
Matches 896; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
QY 54 GGAACCTACCTCGATTCCTCTGCTGCGAGCGCGGCGGCTTCCACGCGAGCGAG 113
Db 1 GGAACCTACCTCGATTCCTCTGCTGCGAGCGCGGCGGCTTCCACGCGAGCGAG 60
QY 114 CTTTCCCGGGCTGGGCTGAGCTTGGAGTCGTGCTTCCCAAGTCCCGCGCGAGTG 173
Db 61 CTTTCCCGGCTGGGCTGAGCTTGGAGTCGTGCTTCCCAAGTCCCGCGCGAGTG 119
QY 174 AGCCCTCGCCCGAGTCAGCAAAATGCTCCTCGGCTCTCTGCTGCTGACATCTGCCT 233
Db 120 AGCCCTCGCCCGAGTCAGCAAAATGCTCCTCGGCTCTCTGCTGCTGACATCTGCCT 179
QY 234 GGCCGGCCAAAGAACCGGAGCTCGGGCTGAGTCAACTGAGCAGCAAGTTGCGAGCTC 293
Db 180 GGCCGGCCAAAGAACCGGAGCTCGGGCTGAGTCAACTGAGCAGCAAGTTGCGAGCTC 239
QY 294 CAGCGACAAGAACAGAGAGGAGTCAAGATCCCGGCTGAGAGAGTTGTCATATATC 353
Db 240 CAGCGACAAGAACAGAGAGGAGTCAAGATCCCGGCTGAGAGAGTTGTCATATATC 299
QY 354 TGTTAATGGGAGCATCCACAGCCCGAGTTTCTTCATACGTACCCAGAAATATGGTCT 413
Db 300 TGTTAATGGGAGCATCCACAGCCCGAGTTTCTTCATACGTACCCAGAAATATGGTCT 359
QY 414 GGTGTGAGATTAGTGCAGTAGATGAATAATGTGGGATCCAGTGTGATGATGAGAG 473
Db 360 GGTGTGAGATTAGTGCAGTAGATGAATAATGTGGGATCCAGTGTGATGATGAGAG 419
QY 474 ATTTGGGCTGGAAGATCCAGAGAGCATATATGCAAGTATGATTTTGTAGAGTTGAGGA 533
Db 420 ATTTGGGCTGGAAGATCCAGAGAGCATATATGCAAGTATGATTTTGTAGAGTTGAGGA 479
QY 534 GCCCAGTGATGGAAGTGTTTTGGACGCTGGTGTGTTCTGGGACTGTGCCAGGAAGCA 593
Db 480 GCCCAGTGATGGAAGCGTTTTTGGACGCTGGTGTGTTCTGGGACTGTGCCAGGAAGCA 539
QY 594 GACTTCTAAGGAATCATATCAGATAGAGTATGTTATCTCATGATGATTTTCCATCTGA 653
Db 540 GACTTCTAAGGAATCATATCAGATAGAGTATGTTATCTCATGATGATTTTCCATCTGA 599
QY 654 ACCCGGATTCGTCAATCAGTATGATGATGATGATGATGATGATGATGATGATGATG 713
Db 600 ACCCGGATTCGTCAATCAGTATGATGATGATGATGATGATGATGATGATGATGATG 659
QY 714 TTCGGTGTGCCCTTCATCTTTGTCAATGGAAGTCTGCTCAACAAATGCTGTGACTGCTT 773
Db 660 TTCGGTGTGCCCTTCATCTTTGTCAATGGAAGTCTGCTCAACAAATGCTGTGACTGCTT 719
QY 774 CAGTACCTTGAAGAGCTGATTCGGTACCTAGAGCAGATGATGAGGAGTGGAGTTGGA 833
Db 720 CAGTACCTTGAAGAGCTGATTCGGTACCTAGAGCAGATGATGAGGAGTGGAGTTGGA 779
QY 834 CAGCCTCTACAGGCAACATGGCAGCTTTTGGGCAAGGCTTTCTGTATGGAAAAAAG 893

```

```

Db 780 CAGCCTCTACAAG-CAACATGGCAGCTTTTGGGCAAGGCTTTCTGTATGGAAAAAAG 838
QY 894 CAAAGTGGTGAATCTGAATCTCTCTCAAGGAAGAGGTAAACCTCTACAGTGCACACCCCG 953
Db 839 CAAAGTGGTGAATCTGAATCTCTCTCAAGGAAGAGGTAAACCTCTACAGTGCACACCCCG 898
QY 954 GAAC 957
Db 899 GAAC 902

RESULT 6
AK081347
LOCUS
DEFINITION
Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched
library, clone:CL30008P20 product:platelet-derived growth factor,
C polypeptide, full insert sequence.
ACCESSION
AK081347
VERSION
AK081347.1 GI:26099857
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
MEDLINE
10349636
PUBMED
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
MEDLINE
11042159
PUBMED
3
Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsumi, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsui, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
MEDLINE
11076861
PUBMED
4
Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I.,
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
Kadoya, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,
Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G.,
Quackenbush, J., Schiraldi, L. M., Staubli, E., Suzuki, R., Tomita, M.,
Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,
Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,
Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H.,
Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L.,
Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
and Hayashizaki, Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)

```



USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
Tissue Procurement: CLONTECH  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www-shgc.stanford.edu>  
Contact: (Dickson, Mark) [md@paxil.stanford.edu](mailto:md@paxil.stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAL Plate: 4i Row: q Column: 9  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9994186  
This clone has the following problem: frame shifted.

Location/Qualifiers  
1. .2826  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4614150"  
/tissue\_type="Kidney"  
/clone\_lib="NIH\_MGC\_75"  
/lab\_host="DH105"  
/note="vector: pDNR-LIB"

BASE COUNT 870 a 519 c 591 g 846 t  
ORIGIN

Query Match 57.0%; Score 840; DB 11; Length 2826;  
Best Local Similarity 79.5%; Pred. No. 1.8e-224; Indels 65; Gaps 2;  
Matches 1048; Conservative 0; Mismatches 205;

QY 2 ACTGAGACACAGAGAGGCTCTAGAAAAATTTTGGATGGGATTTATGTGAAACTA 61  
DB 26 AACTGGAGACACAGAGAGGCTCTAGAAAAATTTTGGATGGGATTTATGTGAAACTA 85

QY 62 CCTCGGATCTCTGTCGACAGCGCGCCAGCGGCTTCACCGCAGCGAGCTTCC 121  
DB 86 CCTCGGATCTCTGTCGACAGCGCGCTTCACCGCAGCGAGCTTCC 145

QY 122 CGG---GCTGGGCTGAGCCTTGGAGTGTGCTTCCAGTGCCTCCGCGCGAGTGAGCC 177  
DB 146 TGGCGGTGGTGAAGAGACTCGGAGTGTGCTTCCAAAGTCCCGCGGTGAGTGACT 205

QY 178 CTGCCCCAGTCAGCAAAATGCTCTCTGCGCTCTCTCTGCTGCAATCTGCGCTGGCC 237  
DB 206 CTCACCCAGTCAGCCAAATGAGCCTTTCGGGCTTCTCTGCTGACATCTGCGCTGGCC 265

QY 238 GGCCTAAGAACGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCAAGCTCTCCAGC 297  
DB 266 GGCCTAAGAACGGGACTCGGGCTGAGTCCAACTGAGCAGCAAGTTGCAAGCTCTCCAGC 325

QY 298 GACAAGAACAGAAC----- 312  
DB 326 AACAAGAACAGAACGGTAGAACTATATCAAGCATCTGGACTGGCATAGAAAGAGGA 385

QY 313 -----GGAGTGAAGATCCCGGCTGAGAGAGTTGTCTACTATCTGG 356  
DB 386 GAAAGAACATTTAAAGAGGATCAAGATCTCTGAGCATGAGAGATTTATCTGTCTAC 445

QY 357 TAATGGGAGCATCCAGCCCGGAAGTTTCTCTAGTACCCCAAGAAATATGTGCTGGT 416  
DB 446 TAATGAAGATTTTCAAGCCCAAGTTTCTCTACTATTTATCCAGAAATACGCTCTGGT 505

QY 417 GTGGAGATTAGTTGCAAGTAAATGTGCGGATCCAGCTGACATTTGATGAGAGATT 476  
DB 506 ATGGAGATTAGTACGAGTAAATGTATGATACAACTTACGTTGATGAGAGATT 565

QY 477 TGGGCTGGAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAAAGTGGAGCC 536  
DB 566 TGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTTGTAGAAAGTGGAGAAC 625

QY 537 CAGTGTGGAAGTGTTTTAGGACGCTGTGGTCTGGGACTGTGCCAGGAAGCAGAC 596  
DB 626 CAGTGTGGAAGTGTTTTAGGACGCTGTGGTCTGGGACTGTGCCAGGAAGCAGAT 685

QY 597 TTCTAAGGAATCATATCAGGATAAGATTTGTATCTGATGAGTATTTTCCATCTGAACC 656  
DB 686 TTCTAAGGAATCAAATTTAGGATAAGATTTGTATCTGATGAGTATTTTCTTCTGAACC 745

QY 657 CGGATTTCTGCATCCATACAGTATTTATGATCCACAAAGTCCACAGAACCCAGTCTTC 716  
DB 746 AGGGTTCTGCATCCATACAGTATTTATGATCCACAAATTTACAGAAAGCTGTGAGTCTTC 805

QY 717 GGTGTTGCCCTTCTCATCTTTGTCATTTGACCTGCTCAAAATGCTGTGACTGCTTCAG 776  
DB 806 AGTGCTACCCCTTTCAGCTTTGCCACTGGACCTGCTTAATAATGCTATTAACCTGCTTAG 865

QY 777 TACCTTGGAGAGCTGATTCGGTACCTAGAGCCAGATCCGATGGCAGGTGGACTTGGACAG 836  
DB 866 TACCTTGGAGAGCTTATTCGATATCTTGAACCCAGAGAGATGGCAGTTGGACTTAGAGA 925

QY 837 CTCTACAAGCCAACTATGGCAGCTTTTGGCAAGGCTTTCTCTATGCGGAAAAAGCAAA 896  
DB 926 TCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTGTTTGGAGAAAAATCCAG 985

QY 897 AGTGTGTAATCGAATCTCTCAAGAGAGAGTAAACTCTACAGCTGACACACCCGAA 956  
DB 986 AGTGTGTAATCGAATCTCTCAAGAGAGAGTAAACTCTACAGCTGACACACCTCGTAA 1045

QY 957 CTCTCAGTGTCCATACCGGAGAGCTAAAGAGACAGATACCATTATTTTGGCCAGGTTG 1016  
DB 1046 CTCTCAGTGTCCATAGGAGAGAACTAAAGAGAACCGATACCATTCTTGGCCAGGTTG 1105

QY 1017 TCTCTGTCAGCGCTGTGGAGAAATTTGTGCTGTGTCTCTCAATTTGCAATGATG 1076  
DB 1106 TCTCTGTCAGCGCTGTGGAGAACTGTGCTGTGTCTCTCAATTTGCAATGATG 1165

QY 1077 TCAGTGTGCCAGCTGAAAGTTTCAAAAAGTACCATTAGGCTCTTCCAGTTGAGACAAA 1136  
DB 1166 TCAATGTGTCCCAAGCAAGTACTAAAAAATACCAGAGGTCTTCAATTTGAGACAAA 1225

QY 1137 AACTGAGTCAAGGGATTCATAAGTCACTCACTGATGTGGCTCTGGAACACCAAGGGA 1196  
DB 1226 GACCGGTGTGAGGGATTCACAAATCACTCACCGAGTGGCCCTGGAGACCATGAGA 1285

QY 1197 ATGTGATGTGTGTGAGAGAAACGACAGAGGTAACTCGAGCCTTCTGTAGAGCAC 1254  
DB 1286 GTGTGATGTGTGTGAGAGAGACAGAGAGTACCGCATCACCACGAGCAGCTC 1343

RESULT 8  
BU614825 823 bp mRNA linear EST 20-FEB-2003  
LOCUS UI-M-EV0-cbh-b-02-0-UI.r1 NIH BMAP EV0 Mus musculus cDNA clone  
DEFINITION UI-M-EV0-cbh-b-02-0-UI 5', mRNA sequence.  
ACCESSION BU614825  
VERSION BU614825.1 GI:23281040  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 823)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
Tissue Procurement: Dr. James Lin, University of Iowa  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa



cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Clone distribution information can be obtained  
 from Dr. M. Bento Soares, bento-soares@iowa.edu  
 This clone was contributed by the Brain Molecular Anatomy Project  
 (BMAP)

Seq primer: pYX-5.

#### FEATURES

##### source

Location/Qualifiers

1. 823

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6"

/db\_xref="taxon:10090"

/clone="UI-M-EVO-cbh-b-02-0-UI"

/tissue\_type="whole brain"

/dev\_stage="embryo 15.5 dpc"

/lab\_host="DH10B (T1 phage resistant)"

/clone\_lib="NIH BMAP EV0"

/note="Organ: brain; Vector: pYX-Asc; Site 1: EcoR I;

Site 2: Not I; The library was constructed according to  
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
 1996. Denatured mRNA was size fractionated on a 1% agarose  
 gel. First strand cDNA synthesis was primed with an  
 oligo-dT primer containing a Not I site. Double stranded  
 cDNA was size selected according to mRNA size fraction,  
 ligated with EcoR I adaptor, digested with Not I, and then  
 cloned directionally into pYX-Asc vector. The library tag  
 sequence located between the Not I site and the polyA tail  
 is GTGGCGTGAA. This library was created for the  
 University of Iowa Mouse Brain Molecular Anatomy Project  
 (BMAP): 'Gene Discovery in the Developing Mouse Nervous  
 System', supported by National Institutes of Mental Health  
 (NIMH), Hemin Chin, Ph.D., program coordinator."

BASE COUNT 219 a 201 c 196 g 204 t 3 others

##### ORIGIN

Query Match 54.9%; Score 809; DB 13; Length 823;

Best Local Similarity 99.5%; Pred. No. 4.3e-216;

Matches 820; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 585 AGGAAAGCAGACTCTTAAAGGAATCATATCAGGATAAGATTGTATCTGATGATTTT 644  
 DB 1 AGGAAAGCAGACTCTTAAAGGAATCATATCAGGATAAGATTGTATCTGATGATTTT 60  
 QY 645 TCGATCTGAACCGGATTCGATCCACTACAGTATTATCATGCCACAGTTCACAGAAC 704  
 DB 61 TCGATCTGAACCGGATTCGATCCACTACAGTATTATCATGCCACAGTTCACAGAAC 120  
 QY 705 CACGAGTCCCTCGGTGTGGCCCTTTCATCTTTGTCATTGGACCTGCTCAACAATGCTGT 764  
 DB 121 CACGAGTCCCTCGGTGTGGCCCTTTCATCTTTGTCATTGGACCTGCTCAACAATGCTGT 180  
 QY 765 GACTGCTTCAGTACCTTGGAGAGCTGATTGGTACCTAGAGCCAGATCGGAGGT 824  
 DB 181 GACTGCTTCAGTACCTTGGAGAGCTGATTGGTACCTAGAGCCAGATCGGAGGT 240  
 QY 825 GCACTGGHACAGCTCTACAGCCACATGGCAGCTTTGGGCAAGCTTCTGTATGG 884  
 DB 241 GCACTGGHACAGCTCTACAGCCACATGGCAGCTTTGGGCAAGCTTCTGTATGG 300  
 QY 885 GAAAAAAGCAAGTGGTGAATCTGAATCTCTCAAGGAAGAGTAAACTCTACAGCTG 944  
 DB 301 GAAAAAAGCAAGTGGTGAATCTGAATCTCTCAAGGAAGAGTAAACTCTACAGCTG 360  
 QY 945 CACACCCCGAACTTCTAGTGTCCATACGGGAAGAGCTAAAGAGACAGATACCATATT 1004  
 DB 361 CACACCCCGAACTTCTAGTGTCCATACGGGAAGAGCTAAAGAGACAGATACCATATT 420  
 QY 1005 CTGGCCAGGTGTCTCTGCTCAAGCGCTGTGGAGGAATTTGCTGTTGCTCCATTA 1064  
 DB 421 CTGGCCAGGTGTCTCTGCTCAAGCGCTGTGGAGGAATTTGCTGTTGCTCCATTA 480  
 QY 1065 TTGCAATGAATGTGAGTGTGCCACGTAAAGTTACAAAAAAGTACCATGAGGTCTTCA 1124

Db 481 TTCAATGAATGTGAGTGTCCAGGTAAAGTTACAAAAAGTACCATGAGGTCTTCA 540  
 QY 1125 GTTGAGACCAAAACTCGAGTCAAGGATTGCAATAGTCACTCACTGATGGCTCTGGA 1184  
 DB 541 GTTGAGACCAAAACTCGAGTCAAGGATTGCAATAGTCACTCACTGATGGCTCTGGA 600  
 QY 1185 ACACACGAGGAATGTGACTGTGTGTAGAGAAACGAGGAGGTAATGACGCTTC 1244  
 DB 601 ACACACGAGGAATGTGACTGTGTGTAGAGAAACGAGGAGGTAATGACGCTTC 660  
 QY 1245 GTAGCAGCACACGTGAGCAGCTGCTGCTGTGTACCCCAACAGACACCTTCAATCC 1304  
 DB 661 GTAGCAGCACACGTGAGCAGCTGCTGCTGTGTGTACCCCAACAGACACCTTCAATCC 720  
 QY 1305 CAGCGTTGGCCGAGGAGCTCTCAGCTGCTGATGCTGCTATGTAAGATCTTACTCGTC 1364  
 DB 721 CAGCGTTGGCCGAGGAGCTCTCAGCTGCTGATGCTGCTATGTAAGATCTTACTCGTC 780  
 QY 1365 TCCAAACAAATTCAGTGTGTTGCTTCAATAGCCTTCCCTGTC 1408  
 DB 781 TCC-AACANATTCAGTGTGTTGCTTCAATAGCCTTCCCTGTC 823

##### RESULT 9

##### BC051876

##### LOCUS

##### DEFINITION

##### ACCESSION

##### VERSION

##### KEYWORDS

##### SOURCE

##### ORGANISM

##### REFERENCE

##### AUTHORS

##### TITLE

##### JOURNAL

##### MEDLINE

##### PUBMED

##### REFERENCE

##### AUTHORS

##### TITLE

##### JOURNAL

##### REMARK

##### COMMENT

BC051876 2655 bp mRNA linear HTC 05-MAY-2003  
 Homo sapiens cDNA clone IMAGE:6527736, containing frame-shift errors.  
 BC051876 GI:30354290  
 HTC.  
 Homo sapiens (human)  
 Homo sapiens  
 Homo sapiens  
 Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 2655)  
 Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Schletch,T.E., Brownstein,M.J., Udwin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butlerfield,Y.S., Krzywinski,M.I., Skalska,U., Smalusz,D.E., Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A.  
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

##### REFERENCE

##### AUTHORS

##### TITLE

##### JOURNAL

##### REMARK

##### COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: [cgabbs@mail.nih.gov](mailto:cgabbs@mail.nih.gov)

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)



DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305  
 Web site: <http://www-shgc.stanford.edu>  
 Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)  
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>  
Series: IRAK Plate: 110 Row: 4 Column: 4  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 9994186  
This clone has the following problem: frame shifted.

## FEATURES

source

```
1. .2555
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="caxon:9606"
/clones="IMAGE:6527736"
/tissue_type="Uterus, le
/clone_lib="NH MG_71"
/lab_host="DH10B"
/note="vector: pcMV-SPO
479 c 551 a 80
```

a	479 c	551 g	803 b
---	-------	-------	-------

**ORIGIN**

Query Match	51.4%;	Score 757.6;	DB 11;	Length 2655;
Best Local Similarity	79.6%;	Pred. No. 2.6e-201;		
Matches 936;	Conservative	0;	Mismatches 179;	Indels 61;
				Gaps 1;

140	Qy	140	GGAGTGTGCTTCCCACAGTCCCGCGCGAGTGGAGCCCTCGCCCCAGTACGCCAAATGC	199	
			16	GGAGTGTGCTTCCCAAAGTSCCGCGGTGAGTGAGCTCTCACCCGAGTCAGCCAAATGA	75
	Db				
	Qy	200	TCCTCCTCGGCTCCTCTCTGTGACATCTGCGCTGGCGCGCCAAAGAACGGGGACTCGGG	259	
	Db	76	GCCTCTTCGGGCTTCTCTCTGTGACATCTGCGCTGGCGCGCCAGAGACAGGGGACTCAGG	135	
	Qy	260	CTGAGTCCAACTGAGCAGCAGAGTTGGAGCTCTCCAGCGACAAGGAACAGAAAC	312	
	Db	136	CGGAATCCAACTGAGTAGTAAATTCAGATTTCACGCAACAAGGAAACAGAACCGGTAGGA	195	
	Qy	313	-----GGAGTG	318	
	Db	196	ACTATATCCAAAGCATCTGGACTGGCATAGAAAAGAGGAGAAGAAACATTTAAAAGGAGTA	255	
	Qy	319	CAAGATCCCCGGCATGAGAGAGTTGTCACTATATCTGGTAATGGGAGCATCCACAGCCCG	378	
	Db	256	CAAGATCCTCAGCATGAGAGAATTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCA	315	
	Qy	379	AAGTTTTCGTATAGTACCCCAAGAAATATGTGTGTGTGTGGAGATTTAGTTGCGAGTAGAT	438	
	Db	316	AGGTTTTCCTCATATCTTATCCAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAG	375	
	Qy	439	GAAATGTGCGGATCCAGCTCACATTTTGATCAGAGATTGGGCTGGAAGATCCAGAACAC	498	
	Db	376	GAAATGTATGATACAACTTACGTTTGATGAGAATTGGGCTTGAGACCCAGAGAT	435	
	Qy	499	GATATATGCAAGTAGATTTTGTAGAAATTGAGAGTCCAGTGTAGGAAGTGTTTTAGGA	558	
	Db	436	GACATATGCAAGTAGATTTTGTAGAAATTGAGGAACCCAGTGTAGGAACCTATATTAGG	495	
	Qy	559	CGCTGGTGTGTTCTGGGACTGTGCGCAGGAAGCAGACTTCTTAAGGAAATCATATCAGG	618	
	Db	496	CGCTGGTGTGTTCTGGTACTGTACCGAGAAACAGATTTCTTAAGGAAATCAAATTAGG	555	
	Qy	619	ATAAGATTGTATCTGATGAGTATTTTCCATCTGAACCCGGATTCTCGCATCCACTACAGT	678	
	Db	556	ATAAGATTGTATCTGATGAATATTTTCTCTGNAACAGGGTCTCGCATCCACTACAC	615	
	Qy	679	ATTATCATGCCAAGTCAAGAAACACGAGTCTCTCGGTGTGTGCCCTTCATCTTTTG	738	
	Db	616	ATTGTATGCAACAATTCACAGAGCTGTGAGTCTCTCAGTGTCTACCCCTTCAGCTTG	675	

```
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mam2"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site:1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 257 a 212 c 225 g 206 t 1 others
ORIGIN
Query Match 48.0%; Score 707; DB 13; Length 901;
Best Local Similarity 99.7%; Pred. No. 2.3e-187; Indels 0; Gaps 0;
Matches 707; Conservative 0; Mismatches 2;
QY 762 TGTGACTTCGACAGCTTCAGTACCTTGGAGAGCTGATTTCGGTACCTAGAGCAGATCGATGGCA 821
Db 1 TGTGACTTCGACAGCTTCAGTACCTTGGAGAGCTGATTTCGGTACCTAGAGCAGATCGATGGCA 60
QY 822 GTTGAGCTTGACAGCTTCACAGCCCAACATGGCAGCTTTTGGGGAAGCTTTCCTGTGA 881
Db 61 GTTGAGCTTGACAGCTTCACAGCCCAACATGGCAGCTTTTGGGGAAGCTTTCCTGTGA 120
QY 882 TGGGAAAAAAGCAAGTGGTGAATCTCTCAAGCAAGAGGTAAACCTCTACAG 941
Db 121 TGGGAAAAAAGCAAGTGGTGAATCTCTCAAGCAAGAGGTAAACCTCTACAG 180
QY 942 CTGCACACCCCGGAATCTTCAGTGTCCATACGGGAAGAGCTAAAGAGCAGATACCAT 1001
Db 181 CTGCACACCCCGGAATCTTCAGTGTCCATACGGGAAGAGCTAAAGAGCAGATACCAT 240
QY 1002 ATTCTGCCAGGTGTCTCTGCTGTCAGCCCTGCGAGGAAATGTGCTGTGTCTCCA 1061
Db 241 ATTCTGCCAGGTGTCTCTGCTGTCAGCCCTGCGAGGAAATGTGCTGTGTCTCCA 300
QY 1062 TAATTGCAATGAATGTGAGTGTGTCACCGTAAAGTTTACAAAAAGTACCATGAGTCTCT 1121
Db 301 TAATTGCAATGAATGTGAGTGTGTCACCGTAAAGTTTACAAAAAGTACCATGAGTCTCT 360
QY 1122 TCAGTTGAGACCAAAACTCGAGTCAAGGAGTTCATAGTCACTCTGATGCGCTCT 1181
Db 361 TCAGTTGAGACCAAAACTCGAGTCAAGGAGTTCATAGTCACTCTGATGCGCTCT 420
QY 1182 GGAACACACAGAGAAATGCTGCTGTGTGTAGAGGAAAGCAGGAGGTAATCTGCAGCC 1241
Db 421 GGAACACACAGAGAAATGCTGCTGTGTGTAGAGGAAAGCAGGAGGTAATCTGCAGCC 480
QY 1242 TTGCTAGCAGCACACGTGAGCACTTGGCAATCTGTGTACCCCAACCAACCTTTCATCCC 1301
Db 481 TTGCTAGCAGCACACGTGAGCACTTGGCAATCTGTGTACCCCAACCAACCTTTCATCCC 540
QY 1302 CACGAGGTTGGCGCAGGCTCTCAGCTGCTGATGTGCTGATGTGCTGATGTGCTGATGTGCT 1361
Db 541 CACGAGGTTGGCGCAGGCTCTCAGCTGCTGATGTGCTGATGTGCTGATGTGCTGATGTGCT 600
QY 1362 GTCTCCAAACCAATCTCAGTGTGTTTCTCAATAGCTTCCCTCGCAGGACTTCAAGTG 1421
Db 601 GTCTCCAAACCAATCTCAGTGTGTTTCTCAATAGCTTCCCTCGCAGGACTTCAAGTG 660
QY 1422 TCTTTAAAGACAGAGGACCAANAAGAGTCAATCACAAGACCTGTC 1470
Db 661 TCTTTAAAGACAGAGGACCAAGAGGAGTCAATCACAAGACCTGTC 709
```

```
RESULT 11
BQ068266
LOCUS
DEFINITION AGENCOURT_6794408 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5770510
5', mRNA sequence.
ACCESSION BQ068266
VERSION BQ068266.1 GI:19897312
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
```

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 999)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished

Contact: Robert Strausberg, Ph.D.  
Email: cgaps-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLAM12833 row: k column: 23

High quality sequence stop: 676.

Location/Qualifiers

1. .999

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5770510"

/lab\_host="DH10B"

/clone\_lib="NIH\_MGC\_121"

/notes="Organ: brain; Vector: pCMV-SPORT6; Site:1: NotI; Site\_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH MGC Library."

BASE COUNT 290 a 213 c 235 g 261 t

ORIGIN

Query Match 41.8%; Score 616.4; DB 13; Length 999;  
Best Local Similarity 83.1%; Pred. No. 7.8e-162;  
Matches 738; Conservative 0; Mismatches 146; Indels 4; Gaps 3;

QY 228 TGCCCTGCGCGCAAGAAACGGGACTCGGGCTGAGTCCAACTGAGCAAGTTGCA 287

Db 1 TGCCCTGCGCGCAGAGACAGGGGACTCAGGGGGAATCCAACTGAGTAAATTTCA 60

QY 288 GCTCTCCAGCAGCAAGAAACAGACGAGTCCCGGATCCCGCATGAGAGTTGTCAC 347

Db 61 GTTTTCCAGCAACAGAAACAGACGAGTCCCGGATCCCGCATGAGAGTTATTTAC 120

QY 348 TATATCTGTAATGGGAGCATCCACAGCCGGAAGTTTCTCATACGTACCCAGAAATAT 407

Db 121 TGTGCTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCATACTATTCAGAAATAC 180

QY 408 GGTGCTGCTGTGAGATAGTTCAGTAGATGAAATGTGCGGATCCAGCTGACATTTGA 467

Db 181 GGTCTTGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGATACAACTTACGTTGA 240

QY 468 TGAGAGATTTGGCTGGAAGATCCAGAAAGCATATATGCAAGTATGATGTTTGTAGAGT 527

Db 241 TGAAGATTTGGGCTTGAAGACCCAGAAAGATGATGCAAGTATGATTTGTAGAGT 300

QY 528 TGAGGAGCCCAAGTATGGAAGTGTGTTAGGACGCTGGTGTGTTCTGGGACTGTGCCAGG 587

Db 301 TGAGGAGCCCAAGTATGGAAGTATATAGGCGCTGTGTGTGTTCTGTACTGTACCAAGG 360

QY 588 AAGCAGACTTCTAAAGGAAATCATATCAGATAAGATTTGTATCTGATGAGTATTTTCC 647

Db 361 AAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATTTTCC 420

QY 648 ATCTGAACCCGAGTTCCTGCATCCACTACATATATCATGCCACAGTCCAGAGAACAC 707

Db 421 TTCTGAACCCAGGTTCTGTCATCCACTACAAATTTGTCATCCCAATTTCCAGAGCTGT 480

```

QY 708 GAGTCCTCGGTGTCGCCCTTCATCTTTGTTCATTGGACCTGCTCAACAATGCTGTGAC 767
Db 481 GAGTCCTTCAGTGTCTACCCCTTCAGCTTTTGCCACTGGACCTGCTTAATAATGCTATAAC 540

QY 768 TGCCCTTCAGTACCTTGGAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGGA 827
Db 541 TGCCCTTAGTACCTTGGAGACCTTATCGATATCTTTGAACAGAGAGATGGCAGTTGGA 600

QY 828 CTTGGACAGCCTCTACAGCCACATGCGAGCTTTTGGGCAAGCTTTCTCTGTATGGAA 887
Db 601 CTTAGAAGATCTATATAGGCCAACTTTGGCAACTTTCTGGCAAGCCTTTTGTGGAAG 660

QY 888 ABAAGCAGAGTGGTGAATCTGAATCTCCTCAAGGAGAGGTAAACCTCTACAGCTGCAC 947
Db 661 ABAATCCAGAGTGGTGAATCTGAATCTCTAAACAGAGAGGTAAATATACAGCTGCAC 720

QY 948 ACCCCGGAACTTCTCAGTGTCC--ATACGGGAAGAGCTAAAGAGGACAGATACCA-TAAT 1004
Db 721 ACCTCGTAATCTCTCAGTGTCCATAAGGGGAAGACTAAAGAGAACCGATACCAATTTT 780

QY 1005 CTGGCAGAGTGTCTCTGTCAGCGCTGTGGAGGAATGTGCTGCTGTTGCTCCATAA 1064
Db 781 CTGGCCAGTGTCTCTGCTGTTAAACGCTGTGGTGGAACTGTGCTGCTGTTGCTCCCAA 840

QY 1065 TTGCAATGAATGT-CAGTGTGTCCACGTAAAGTTACAAAAAAGTACC 1111
Db 841 TTGCAATGAATGTCCATGGTGTCCCAAGCAAGTTCTTAAATAATAC 888

```

```

RESULT 12
BG243001 60235974F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4483938 5',
LOCUS mRNA sequence.
DEFINITION BG243001
VERSION BG243001.1 GI:12752725
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NTH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL0323 row: d column: 19
High quality sequence stop: 690.
FEATURES
Location/Qualifiers
1..910
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4483938"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
/clone_lib="NCI_CGAP Mam1"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 242 a 220 c 250 g 198 t

```

## ORIGIN

```

Query Match 40.5%; Score 597.6; DB 10; Length 910;
Best Local Similarity 95.4%; Pred. No. 1.4e-156;
Matches 701; Conservative 0; Mismatches 25; Indels 9; Gaps 8;

QY 736 TTGTCAATTGGACCTGCTCAACAATGCTGTGACCTTCACTTTCAGTACCTTTGGAGAGCTGATT 795
Db 22 TTGTCAATTGGACCTGCTCAACAATGCTGTGACCTTCACTTTCAGTACCTTTGGAGAGCTGATT 80

QY 796 CGGTACTTAGAGCCAGATCGATGCGAGGTGGACTTGGACAGCCTCTACAGCCACACATGG 855
Db 81 CGGTACTTAGAGCCAGATCGATGCGAGGTGGACTTGGACAGCCTCTACAGCCACACATGG 140

QY 856 CAGCTTTTGGGCAAGCTTTCTCTGTATGGAAAAAAGAAAGTGGTGAATCTTGAATCTC 915
Db 141 CAGC-TTTGGGCAAGCTTTCTCTGTATGGAAAAAAGAAAGTGGTGAATCTTGAATCTC 199

QY 916 CTCAAGGAAGAGGTAAACCTCTACAGCTGCACACCCCGGAACTTCTCAGTGTCCATACGG 975
Db 200 CTCAAGGAAGAGGTAAACCTCTACAGCTGCACACCCCGGAACTTCTCAGTGTCCATACGG 259

QY 976 GAAGACTTAAAGAGGACAGATACCATATTTCTGCGCAGGTTGTCTCTGCTCAAGCGCTGT 1035
Db 260 GAAGACTTAAAGAGGACAGATACCATATTTCTGCGCAGGTTGTCTCTGCTCAAGCGCTGT 319

QY 1036 GGAGGAAATGTGCTGTTCTCTCCATAATTTGCAATGAATGTGAGTGTGTCACACGTAAA 1095
Db 320 GGAGGAAA-TGTGCTGTTGTCTCTCCATAATTTGCAATGAATGTGAGTGTGTCACACGTAAA 378

QY 1096 GTTACAAAAAAGTACCATGAGGTCTTTCAGTTGAGACCAAAAACTGGAGTCAAGGGATTG 1155
Db 379 GTTACAAAAAAGTACCATGAGGTCTTTCAGTTGAGACCAAAAACT-GAGTCAAGGGATTG 437

QY 1156 CATAAGTCACTCACTGATGTGGCTCTGGAACACACAGCAAGTGTGACTGTGTGTGAGA 1215
Db 438 CATAAGTCACTCACTGATGTGGCTCTGGAACACACAGCAAGTGTGACTGTGTGTGAGA 497

QY 1216 GGAACCGCAGAGGTAACCTGACGCTTCTGTAGCAGCACACGTGAGCA-CTGGCATTTCTG 1274
Db 498 GGAACCGCAGAGGTAACCTGACGCTTCTGTAGCAGCACACGTGAGCACTGGCATTTCTG 557

QY 1275 TGTACCCCCCAACAGCAACCTTCACTCCACACAGCGTTGGCGGAGGCTCTCAGCTGCTG 1334
Db 558 TGTACCCCCCAACAGCAACCTTCACTCCACACAGCGTTGGCGG--AGGCTCTCAGCTGCTG 614

QY 1335 ATGCTGCTATGTAAAGATCTTACTGCTTCCACCAAAATTTCTCAGTTGTTGCTTCAA 1394
Db 615 ATGCTGCTATGTAAAGATCTTACTGCTTCCACCAAAATTTCTCAGTTGTTGCTTCAA 674

QY 1395 TAGCTTTCCCTGCGAGGACTTCAAGTGTCTTCTAAAAAGACAGAGGACCAANAGGAGTC 1454
Db 675 TAGCTTTCCCTGCGAGGATTTTCAAGTGTCTTCTAAAAAGACAGAGGACCAANAGGAGTC 734

QY 1455 AATCACAAGGACCTG 1469
Db 735 -ATCACAAGGACCTG 748

```

```

RESULT 13
BF137533
LOCUS 601780532F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4008799 5',
DEFINITION mRNA sequence.
ACCESSION BF137533
VERSION BF137533.1 GI:10976573
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 877)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.

```

TITLE  
JOURNAL  
COMMENT

National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: Gilbert Smith, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L1AM9243 row: o column: 08  
High quality sequence stop: 677.

## FEATURES

source  
1. .877  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="CZECH II"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4008799"  
/tissue\_type="tumor, metastatic to mammary"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP Lu30"  
/notes="Organ: lung; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: SalI; transgenic model MNT-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies.  
Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT 221 a 220 c 233 g 203 t

ORIGIN

Query Match 40.4%; Score 595.6; DB 10; Length 877;  
Best Local Similarity 91.3%; Pred. No. 5.2e-156;  
Matches 665; Conservative 0; Mismatches 59; Indels 4; Gaps 3;

QY 314 GAGTGAAGATCCCGCATGAGAGTTCCTACTATCTGCTGATGAGATCCACA 373  
DB 30 GAGTGAAGATCCCGCATGAGAGTTCCTACTATCTGCTGATGAGATCCACA 89  
QY 374 GCCGGAAGTTTCTCTACCTACCCAGAAATATGCTGCTGAGATGATGTCAG 433  
DB 90 GCCGGAAGTTTCTCTACCTACCCAGAAATATGCTGCTGAGATGATGTCAG 149  
QY 434 TAGATGAATAATGTCGGATCCAGCTGACATTTGATGAGAGATTTGGCTGGAATCCAG 493  
DB 150 TAGATGAATAATGTCGGATCCAGCTGACATTTGATGAGAGATTTGGCTGGAATCCAG 209  
QY 494 AGACGATATATCAAGTATGATTTGTAGAGTTGAGGAGCCAGTGTGAGAGTGT 553  
DB 210 AGACGATATATCAAGTATGATTTGTAGAGTTGAGGAGCCAGTGTGAGAGTGT 269  
QY 554 TAGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 613  
DB 270 TAGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 329  
QY 614 TCAGGATAGATTTGATCTGATGAGTATTTTCATCTGACCCGAGTTCTGATCCACT 673  
DB 330 TCAGGATAGATTTGATCTGATGAGTATTTTCATCTGACCCGAGTTCTGATCCACT 389  
QY 674 ACAGTATATCATGCCACAGTACAGAAACCCAGTCTCTGCTGCTGCTGCTGCTGCTGCT 733  
DB 390 ACAGTATATCATGCCACAGTACAGAAACCCAGTCTCTGCTGCTGCTGCTGCTGCTGCT 449  
QY 734 CTTTGTCTATTCGACCTCTCAACAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 792  
DB 450 CTTTGTCTATTCGACCTCTCAACAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 509  
QY 793 ATTGGTACTTAGAGCCAGATCGATGAGTGGATTTGAGCAGCTCTCAAGCCAAACA 852  
DB 510 ATTGGTACTTAGAGCCAGATCGATGAGTGGATTTGAGCAGCTCTCAAGCCAAACA 569  
QY 853 TGGCAGCTTTTGGCAGGCTTTCTCTGATGGGAAAGAAAGCAGGCTGTGATCTGAAT 912

Db 570 TGGCAGCTTTTGGCAGGCTTTCTCTGATGGGAAACCCAGGCTGATCTGAAT 629  
QY 913 CTCCTCAAGGAAG--AGGTAATACTCTACAGCTGCACACCCCGAACTTCTCAGTGCCA 970  
Db 630 CTCCTAAAGGGAGAGGTAACAACACTCTACAGCTGGCACACCCCGAATTCCTCAGGTTCCA 689  
QY 971 TAGCGGAAGAGCTAAAGAGACAGATACCATATTTCTGGCCAGGTTGTCTCTCTGCTCAAGC 1030  
Db 690 TAACGGGAACAACATAAG-GGACAGATACCATATTTCTGGCAGCTGCGGTCACACGC 748  
QY 1031 GCTGTGGA 1038  
Db 749 GGGGACGA 756

## RESULT 14

BI693338

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

COMMENT

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1AM11945 row: c column: 18

High quality sequence stop: 711.

FEATURES

source

1. .712

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="FVB/N-3"

/db\_xref="taxon:10090"

/clone="IMAGE:5371337"

/tissue\_type="tumor, biopsy sample"

/dev\_stage="5 months"

/lab\_host="DH10B"

/clone\_lib="NCI\_CGAP Mam2"

/notes="Organ: mammary; Vector: pCMV-SPORT6; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT 205 a 174 c 171 g 162 t

ORIGIN

Query Match 40.4%; Score 595; DB 12; Length 712;

Best Local Similarity 99.7%; Pred. No. 6.7e-156;

Matches 606; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 864 GGGCAGGCTTTCTGATGGGAAAAAGCAAGTGGTGAATCTGAATCTCTCAAGGA 923

Db 1 GGGCAGGCTTTCTGATGGGAAAAAGCAAGTGGTGAATCTGAATCTCTCAAGGA 60

QY 924 AGAGGTAAAAACTCTACAGCTGCACACCCCGAACTTCTCAGTGTCCATAGCGGAGAGCT 983

Db 61 AGAGGTAAAAACTCTACAGCTGCACACCCCGAACTTCTCAGTGTCCATAGCGGAGAGCT 120

QY 984 AAAGAGACAGATACCATATTTCTGGCCAGGTTGTCTCTCTGTCAGCGCTGTGGAGAAA 1043



Db 317 AAAGAACGGGGAAGCTCGGGCTGAGTCCAAACCTGAGCAGCAAGTTGCAGCTCTCCAGCGACA 376  
QY 302 AGGAACAGAACGGAGTGCAGATCCCGCGCATGAGAGAGTTGTCACTATATCTGGTAATG 361  
Db 377 AGGAACAGAACGGAGTGCAGATCCCGCGCATGAGAGAGTTGTCACTATATCTGGTAATG 436  
QY 362 GGAGCATCCACAGCCCGGAAGTTTCCTCATACGTACCCCAAGAAATATGGTCTGGTGTGGA 421  
Db 437 GGAGCATCCACAGCCCGGAAGTTTCCTCATACGTACCCCAAGAAATATGGTCTGGTGTGGA 496  
QY 422 GATTAGTTGCAGTAGATGAAATGTGCGGATCCAGCTGCATTTGATGAGAGATTGGGC 481  
Db 497 GATTAGTTGCAGTAGATGAAATGTGCGGATCCAGCTGCATTTGATGAGAGATTGGGC 556  
QY 482 TGGAAAGATCCAGAGACGATATATGCAAGTATGATTTTGTAGAAAGTTGAGAGCCCAAGTG 541  
Db 557 TGGAAAGATCCAGAGACGATATATGNCAGTATGATTTTGTAGAAAGTTGAGAGCCCAAGTG 616  
QY 542 ATGGAAGTGTTTTAGGACGCTGGTGTGGTCTGGGACTGTGCCAGGAAAGCAGACTTCTA 601  
Db 617 ATGGAAGTGTTTTAGGACGCTGGTGTGGTCTGGGACTGTGCCAGG-AAACAGACTTCTA 675  
QY 602 A 602  
Db 676 A 676

Search completed: November 26, 2003, 05:47:56  
Job time : 2158.47 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 20:55:13 ; Search time 35.9375 Seconds  
(without alignments)  
1523.775 Million cell updates/sec

Title: US-09-852-209a-7

Perfect score: 1848

Sequence: 1 MLLGLLLTSLAAGRTGT.....DVALEHHEBCDCVCRNAGG 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_19Jun03:\*\*

1:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:**
2:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:**
3:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:**
4:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:**
5:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:**
6:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:**
7:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:**
8:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:**
9:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:**
10:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:**
11:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:**
12:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:**
13:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:**
14:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:**
15:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:**
16:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:**
17:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:**
18:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:**
19:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:**
20:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:**
21:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:**
22:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:**
23:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:**
24:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1848	100.0	345	21	Mouse zveg3, SEQ
2	1848	100.0	345	21	Murine vascular en
3	1848	100.0	345	21	A murine platelet-
4	1848	100.0	345	22	Mouse zveg3 prote
5	1848	100.0	345	23	Mouse VEGF-like pr
6	1848	100.0	345	23	Mouse zveg3. Mus
7	1848	100.0	345	23	Mouse platelet-der
8	1848	100.0	345	24	Mouse growth facto
9	1667	90.2	345	20	Human VEGF-E prote

10	1667	90.2	345	20	AAV411766	Human PRO200 prote
11	1667	90.2	345	20	AAV30023	Human vascular end
12	1667	90.2	345	21	AAV48657	Human zveg3, SEQ
13	1667	90.2	345	21	AAV24250	Human platelet-der
14	1667	90.2	345	21	AAV44322	Human PRO200 (UNQ1
15	1667	90.2	345	21	AAV10633	Human RACE generat
16	1667	90.2	345	21	AAV10635	Human VEGF-X prote
17	1667	90.2	345	21	AAV10644	Human VEGF-X prote
18	1667	90.2	345	21	AAV10650	Human 990126vegk p
19	1667	90.2	345	21	AAV10651	Human VEGF-X prote
20	1667	90.2	345	21	AAV19578	Human PRO200 (vasc
21	1667	90.2	345	21	AAV33414	Human PRO200 prote
22	1667	90.2	345	21	AAV24412	Human PRO713 prote
23	1667	90.2	345	21	AAV01419	Human TANGO 128.
24	1667	90.2	345	21	AAV96858	Human growth facto
25	1667	90.2	345	21	AAV59285	Bone morphogenic p
26	1667	90.2	345	22	AAV65603	Human zveg3 polyp
27	1667	90.2	345	22	AAU08465	Polypeptide for hu
28	1667	90.2	345	22	AAU12314	Human PRO200 polyp
29	1667	90.2	345	22	AAV74028	Human VEGF/PDGF-11
30	1667	90.2	345	22	AAE02649	Human LP8, a PDGF-
31	1667	90.2	345	22	AAE00997	Human zveg3 prote
32	1667	90.2	345	22	AAV50980	Human PRO200 prote
33	1667	90.2	345	22	AAV49895	Human PRO200 prote
34	1667	90.2	345	22	AAV53074	Human angiogenesis
35	1667	90.2	345	23	ABV79984	Human vascular end
36	1667	90.2	345	23	ABV92889	Human VEGF-like pr
37	1667	90.2	345	23	ABV81331	Human VEGF/PDGF-11
38	1667	90.2	345	23	AAV47889	Human zveg3. Hom
39	1667	90.2	345	23	AAU76884	Human zveg3 prote
40	1667	90.2	345	24	ABV76393	Human growth facto
41	1667	90.2	345	24	ABU66712	Human PRO polypept
42	1667	90.2	345	24	ABU66988	Human secreted/tra
43	1667	90.2	345	24	ABU59793	Novel secreted and
44	1667	90.2	345	24	ABU61152	Human PRO200 polyp
45	1667	90.2	345	24	ABV72132	Human vascular end

#### ALIGNMENTS

#### RESULT 1

AAV48658  
ID AAV48658 standard; Protein; 345 AA.

XX AAV48658;

XX AC

XX 09-MAR-2001 (first entry)

XX Mouse zveg3, SEQ ID NO:35.

XX Mouse; zveg3; zveg4 fusion; growth factor homologue; VEGF/PDGF family;  
XX murine; CUB domain; PDGF-like activity; mitogenic; osteogenic;  
XX neovascularisation; tissue repair; proliferation; differentiation;  
XX liver damage; neurodegenerative; Alzheimer's disease; multiple sclerosis;  
XX periodontal disease; bone fracture; wound healing; vulnery; ischaemia;  
XX immunomodulation; hepatic.

XX Mus musculus.

XX WO200066736-A1.

XX 09-NOV-2000.

XX 03-MAY-2000; 2000WO-US40047.

XX 03-MAY-1999; 99US-0304216.

XX 10-NOV-1999; 99US-0164463.

XX 04-FEB-2000; 2000US-0180169.

XX (ZYMO ) ZYMOGENETICS INC.

XX Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;

XX WPI; 2000-687541/67.  
DR N-PSDB; AAC81583.  
XX  
PT Growth factor homologs and the nucleic acids that encode them, useful  
PT e.g. for treating liver damage, ischemia, multiple sclerosis and  
PT Alzheimer's disease -  
XX  
PS Disclosure; Page 130-131; 143pp; English.  
XX  
CC The invention relates to the human growth factor homologue zvegfg4  
CC (AAB48653), and nucleic acids encoding it (AAC81555). Zvegfg4 is a member  
CC of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial  
CC growth factor) family. Zvegfg4 has a growth factor domain (AAB48654)  
CC characterised by a PDGF cysteine knot structure, and a CUB domain  
CC (AAB48655) which has a beta barrel structure. Zvegfg4 has PDGF-like  
CC activity, having mitogenic activity on fibroblasts, vascular smooth  
CC muscle cells and pericytes, and has also been shown to stimulate bone  
CC growth. The invention also relates to fusion proteins comprising human  
CC zvegfg4 or fragments thereof, particularly human zvegfg4/human zvegfg3  
CC fusions; expression constructs and host cells comprising human zvegfg4  
CC nucleic acids; the recombinant expression of human zvegfg4; an antibody  
CC which binds to human zvegfg4 or a fragment thereof; a method of activating  
CC a cell-surface PDGF receptor using a zvegfg4-derived polypeptide; a  
CC method of modulating the proliferation, differentiation, migration or  
CC metabolism of bone cells, comprising exposing bone cells to  
CC zvegfg4-derived polypeptides; and a method of detecting a genetic  
CC abnormality in the zvegfg4 gene of a patient. Zvegfg4 proteins and derived  
CC fragments may be used to stimulate tissue development or repair, or  
CC cellular differentiation or proliferation. They are particularly used for  
CC the treatment or repair of liver damage, and may also be used to  
CC modulate neurite growth (e.g., in the treatment of Alzheimer's disease or  
CC multiple sclerosis). Due to their osteogenic activity, they may also be  
CC in the treatment of periodontal disease and fractures. They may also be  
CC used to enhance expansion and mobilisation of haematopoietic stem cells  
CC and endothelial precursor stem cells, which may be useful in the  
CC treatment of ischaemia, in wound healing, and in the modulation of the  
CC immune system. The present sequence represents mouse zvegfg3.  
XX  
SQ Sequence 345 AA;  
Query Match 100.0%; Score 1848; DB 21; Length 345;  
Best Local Similarity 100.0%; Pred. No. 4e-182;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLLGLLLLSALAGQGTGFAESNLSSKQLSSDKQNGVQDPRHVRVTTISNGSIHS 60  
DB 1 MLLGLLLLSALAGQGTGFAESNLSSKQLSSDKQNGVQDPRHVRVTTISNGSIHS 60  
QY 61 PKPHTYPRNNVLVRLVAVDENVRILQTFDERFGLDEPDDEDDICKYDFVEVEPDSGSLV 120  
DB 61 PKPHTYPRNNVLVRLVAVDENVRILQTFDERFGLDEPDDEDDICKYDFVEVEPDSGSLV 120  
QY 121 GRWCGSGTVPGKQTSKGNHRIIRVSDYEPSEFGCIHYSIIMPQVTTSPSVLPSS 180  
DB 121 GRWCGSGTVPGKQTSKGNHRIIRVSDYEPSEFGCIHYSIIMPQVTTSPSVLPSS 180  
QY 181 LSLDLLNNAVAFSTLBELIRYLPDRQVQDLSLYKPTWQLLKAFYLGKSKVNLNL 240  
DB 181 LSLDLLNNAVAFSTLBELIRYLPDRQVQDLSLYKPTWQLLKAFYLGKSKVNLNL 240  
QY 241 LKEEVKLYSCTPRNFVSIRBELRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPRK 300  
DB 241 LKEEVKLYSCTPRNFVSIRBELRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPRK 300  
QY 301 VTKKYHEVLQRPKTVKGLHSLTDVALEHHEBCDCVCRNAGG 345  
DB 301 VTKKYHEVLQRPKTVKGLHSLTDVALEHHEBCDCVCRNAGG 345  
RESULT 2  
RAY96861  
ID AAY96861 standard; Protein; 345 AA.

XX AAY96861;  
XX 26-SEP-2000 (first entry)  
DT Murine vascular endothelial growth factor homologue, ZVEGF3.  
DB  
XX Vascular endothelial growth factor; homologue; zvegfg3; CUB domain;  
XX Cysteine knot; platelet-derived growth factor; PDGF; neuropilin;  
KW chromosome 4q28.3; cytotstatic; anti-psoriatic; anti-inflammatory;  
KW anti-diabetic; ophthalmological; anti-rheumatic; anti-arthritis;  
KW vulnery.  
XX Mus musculus.  
OS WO200034474-A2.  
XX  
XX 15-JUN-2000.  
XX 07-DEC-1999; 99WO-US28968.  
XX 07-DEC-1998; 98US-0207120.  
XX 06-JUL-1999; 99US-0142576.  
XX 21-OCT-1999; 99US-0161653.  
XX 12-NOV-1999; 99US-0165255.  
XX (ZYMO ) ZYMOGENETICS INC.  
XX Gao Z, Hart CB, Piddington CS, Sheppard PO, Shoemaker KE;  
PI Gilbertson DG, West JW;  
XX WPI; 2000-4234420/36.  
XX N-PSDB; AAA51527.  
XX Novel zvegfg3 polypeptides and nucleotides encoding them useful for  
XX stimulating growth of smooth muscle cells and fibroblasts comprising an  
XX epitope bearing portion of a specific amino acid sequence  
XX  
XX Claim 1; Page 169-170; 173pp; English.  
XX  
XX This shows a murine ZVEGF3 a novel vascular endothelial growth factor  
XX homologue. Polypeptides comprising an epitope-bearing portion human or  
XX murine ZVEGF3 are claimed. The growth factors comprise a growth factor  
XX domain and a CUB domain (generic sequence motifs are shown in AAY96859  
XX and AAY96860). The growth factor domain is characterized by an  
XX arrangement of cysteine residues and beta-strands that is characteristic  
XX of the "cysteine knot" structure of the platelet-derived growth factor  
XX (PDGF) family. The CUB domain shows homology to CUB domains in  
XX neuropilins, human bone morphogenetic protein-1, porcine seminal plasma  
XX protein, bovine acidic seminal fluid protein and Xenopus laevis  
XX tolloid-like protein. Structural analysis and homology predict that  
XX ZVEGF3 polypeptides complex with a second polypeptide to form multimeric  
XX proteins. The human zvegfg3 gene has been mapped to chromosome 4q28.3.  
XX ZVEGF3 is useful for stimulating the growth of fibroblasts or smooth  
XX muscle cells, for activating cell surface PDGF-alpha receptor and for  
XX inhibiting PDGF-alpha receptor mediated cellular processes. ZVEGF3 is  
XX useful for regulating (post-development) organ growth, regeneration and  
XX maintenance, as well as tissue maintenance and repair processes. ZVEGF3  
XX antagonists are useful for treating cancer, rheumatoid arthritis,  
XX diabetic retinopathy, ischemic limb disease, peripheral vascular  
XX disease, myocardial ischemia, vascular intimal hyperplasia,  
XX atherosclerosis, wound healing, chronic liver disease and haemangioma  
XX formation. ZVEGF3 can also be used to modulate neurite growth and  
XX development of the nervous system, and for treating neurodegenerative  
XX diseases.  
XX  
SQ Sequence 345 AA;  
Query Match 100.0%; Score 1848; DB 21; Length 345;  
Best Local Similarity 100.0%; Pred. No. 4e-182;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLLGLLLLSALAGQGTGFAESNLSSKQLSSDKQNGVQDPRHVRVTTISNGSIHS 60



```

Db 1 MLLGLLLLTSAAGQRTGTRAESNLSSKLQSSDKQNGVQDPRHERVVTISNGSIHS 60
Qy 61 PKPHTYPRNMVLVRLVAVDENVRIOITDFERFGLDPEDDICKYDFVEEPESDGSVL 120
Db 61 PKPHTYPRNMVLVRLVAVDENVRIOITDFERFGLDPEDDICKYDFVEEPESDGSVL 120
Qy 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDEYFSPFSGFCIHYSIIMPQVTTTSPSVLPSS 180
Db 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDEYFSPFSGFCIHYSIIMPQVTTTSPSVLPSS 180
Qy 181 LSLDLLNNAVTAFSTLEELRYLEPDRQVLDLSLYKPTWQLLGAFLYKSKVNNL 240
Db 181 LSLDLLNNAVTAFSTLEELRYLEPDRQVLDLSLYKPTWQLLGAFLYKSKVNNL 240
Qy 241 LKEEVKLYSCTPRNFSVSIREEKRTDTIIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
Db 241 LKEEVKLYSCTPRNFSVSIREEKRTDTIIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
Qy 301 VTKYHEVLQRLPKTVGKGLHKSITDVALEHHEECDCVCRNAGG 345
Db 301 VTKYHEVLQRLPKTVGKGLHKSITDVALEHHEECDCVCRNAGG 345

RESULT 3
AA084559
ID AA084559 standard; Protein; 345 AA.
XX
AC AA084559;
XX
DT 25-JUL-2000 (first entry)
XX
DE A murine platelet-derived growth factor C (PDGF-C).
XX
KW Platelet-derived growth factor C; PDGF-C; cell proliferation;
KW growth factor; heparin; connective tissue; wound healing; VEGF-F;
KW fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth;
KW choriocarcinoma; Wilms tumour; megakaryoblastic leukaemia;
KW lung carcinoma; erythroleukemia; tissue remodelling.
XX
OS Mus sp.
XX
XX WO200018212-A2.
XX
XX 06-APR-2000.
XX
XX 30-SEP-1999; 99WO-US22668.
XX
XX 30-SEP-1998; 98US-0102461.
XX 12-NOV-1998; 98US-0108109.
XX 03-DEC-1998; 98US-0110749.
XX 18-DEC-1998; 98US-0113002.
XX 21-MAY-1999; 99US-0135426.
XX 15-JUL-1999; 99US-0144022.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX (UYHE-) UNIV HELSINKI LICENSING LTD.
XX
XX Eriksson U, Aase K, Lee X, Ponten A, Untela M, Alitalo K;
XX Oestman A, Heldin C, Betsholz C;
XX
XX WPI; 2000-292954/25.
XX N-PSDB; AAA12525.
XX
XX Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation,
XX differentiation, growth and motility of cells expressing the PDGF-C
XX receptor -
XX
XX Claim 27; Fig 6; 135pp; English.
XX
XX The present sequence represents murine platelet-derived growth factor C
XX (PDGF-C) (formally designated VEGF-F). PDGF-C polypeptides have the
XX ability to stimulate and enhance proliferation or differentiation,

```

```

CC and/or growth or motility of cells expressing a PDGF-C receptor.
CC PDGF-C polypeptides can be used in pharmaceuticals for promoting cell
CC proliferation, preferably in combination with one other growth factor
CC and heparin. Pharmaceuticals comprising PDGF-C polypeptides can also
CC be used for stimulating connective tissue or wound healing. The
CC PDGF-C polypeptide can be enzymatically processed to generate the active
CC truncated form of PDGF-C and used to regulate the receptor-binding
CC specificity of PDGF-C. PDGF-C can also be used to promote fibroblast
CC mitogenesis in a mammal and to induce PDGF alpha receptor activation.
CC PDGF-C antagonists can be used to inhibit tumour growth of a tumour
CC expressing PDGF-C in a mammal. Specific types of human tumours, e.g.
CC choriocarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma
CC and erythroleukemia, can be identified by testing for expression of
CC PDGF-C. PDGF-C antagonists can also be used to inhibit tissue
CC remodelling during invasion of tumour cells into a normal population of
CC cells. Antagonists can also be used to treat fibrotic conditions,
CC especially found in the lung, kidney or liver.
XX
SQ Sequence 345 AA;
Query Match 100.0%; Score 1848; DB 21; Length 345;
Best Local Similarity 100.0%; Pred. No. 4e-182;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLGLLLLTSAAGQRTGTRAESNLSSKLQSSDKQNGVQDPRHERVVTISNGSIHS 60
Db 1 MLLGLLLLTSAAGQRTGTRAESNLSSKLQSSDKQNGVQDPRHERVVTISNGSIHS 60
Qy 61 PKPHTYPRNMVLVRLVAVDENVRIOITDFERFGLDPEDDICKYDFVEEPESDGSVL 120
Db 61 PKPHTYPRNMVLVRLVAVDENVRIOITDFERFGLDPEDDICKYDFVEEPESDGSVL 120
Qy 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDEYFSPFSGFCIHYSIIMPQVTTTSPSVLPSS 180
Db 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDEYFSPFSGFCIHYSIIMPQVTTTSPSVLPSS 180
Qy 181 LSLDLLNNAVTAFSTLEELRYLEPDRQVLDLSLYKPTWQLLGAFLYKSKVNNL 240
Db 181 LSLDLLNNAVTAFSTLEELRYLEPDRQVLDLSLYKPTWQLLGAFLYKSKVNNL 240
Qy 241 LKEEVKLYSCTPRNFSVSIREEKRTDTIIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
Db 241 LKEEVKLYSCTPRNFSVSIREEKRTDTIIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300
Qy 301 VTKYHEVLQRLPKTVGKGLHKSITDVALEHHEECDCVCRNAGG 345
Db 301 VTKYHEVLQRLPKTVGKGLHKSITDVALEHHEECDCVCRNAGG 345

RESULT 4
AAE00998
ID AAE00998 standard; Protein; 345 AA.
XX
AC AAE00998;
XX
DT 04-JUL-2001 (first entry)
XX
DE Mouse Zveg3 protein.
XX
KW Mouse; Zveg3 antagonist; cell proliferation; stellate cell activation;
KW extracellular matrix production; fibrosis; VEGF-R; PDGF-C;
KW platelet-derived growth factor; PDGF; vascular endothelial growth factor;
KW VEGF; mitogenic effect; therapy; keloid; scleroderma; fibrotic disorder;
KW chronic active hepatitis; fulminant viral hepatitis; amyloidosis;
KW diabetic nephropathy; alpha-1-antitrypsin deficiency; silicosis;
KW asbestosis; renal arteriosclerosis; post necrotic cirrhosis;
KW diabetic glomerulosclerosis; focal glomerulosclerosis; hyperostosis;
KW pulmonary hypertension; idiopathic pulmonary fibrosis; osteopetrosis;
KW bronchiolitis obliterans-organising pneumonia; transplant vasculopathy;
KW fibroproliferative disorder.
XX
OS Mus musculus.
XX

```

PN WO200128586-A1.  
XX  
XX  
XX 26-APR-2001.  
XX  
XX 23-OCT-2000; 2000WO-US292270.  
XX  
XX 21-OCT-1999; 99US-0161653.  
PR 12-NOV-1999; 99US-0165255.  
PR 01-AUG-2000; 2000US-0222223.  
XX  
XX (ZYMO ) ZYMOGENETICS INC.  
XX  
XX Gilbertson DG;  
XX  
XX WPI; 2001-300278/31.  
DR N-PSDB; AAD04650.  
XX  
XX Use of zvegf3 antagonist for reducing fibroproliferative disorder of  
PT kidney, liver and bone, reducing extracellular matrix production,  
PT treating fibrosis or reducing stellate cell activation in mammal -  
XX  
XX Example 2; Fig 2; 70pp; English.  
XX  
XX The patent discloses materials and methods for reducing cell  
CC proliferation or extracellular matrix production, treating fibrosis and  
CC reducing stellate cell activation in a mammal. The method comprises  
CC administering a composition containing a Zvegf3 antagonist in combination  
CC with a delivery vehicle. The Zvegf3 is a protein that is structurally  
CC related to platelet-derived growth factor (PDGF) and the vascular  
CC endothelial growth factors (VEGF). The Zvegf3 protein is also designated  
CC as "VEGF-R" and "PDGF-C". The Zvegf3 antagonist is useful to block the  
CC mitogenic effects of zvegf3 and thereby to inhibit or prevent and treat  
CC keloids, scleroderma, fibrotic disorders of liver such as chronic active  
CC hepatitis, fulminant viral hepatitis, post necrotic cirrhosis and  
CC alpha-1-antitrypsin deficiency, fibrotic disorders of the kidney such as  
CC diabetic glomerulosclerosis, focal glomerulosclerosis, diabetic  
CC nephropathy, amyloidosis and renal arteriosclerosis, fibrotic disorders  
CC of the lung such as silicosis, asbestosis, idiopathic pulmonary fibrosis,  
CC bronchiolitis obliterans-organising pneumonia and pulmonary hypertension,  
CC fibrotic disorders of pancreas, fibroproliferative disorders of the  
CC vasculature such as transplant vasculopathy and fibroproliferative  
CC disorders of the bone such as osteopetrosis and hyperostosis.  
CC The present sequence is mouse Zvegf3 protein.  
XX  
SQ Sequence 345 AA;  
Query Match 100.0%; Score 1848; DB 22; Length 345;  
Best Local Similarity 100.0%; Pred. No. 4e-182;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MLLGLLLLTALAGQRTGTRAESNLSSKQLSSDKQNGVQDPRHERVVTISNGSIHS 60  
Db 1 MLLGLLLLTALAGQRTGTRAESNLSSKQLSSDKQNGVQDPRHERVVTISNGSIHS 60  
  
Qy 61 PKFHTYPRNNVLVWRLVAVDENVRILQTFPERGLEDPEDDICKYDFVEEESDGSVL 120  
Db 61 PKFHTYPRNNVLVWRLVAVDENVRILQTFPERGLEDPEDDICKYDFVEEESDGSVL 120  
  
Qy 121 GRWCGSGTVPGKQTSKGNHIRFVSDYFVPESEPGFCFHYSLIMPQVTTTSPSLPPSS 180  
Db 121 GRWCGSGTVPGKQTSKGNHIRFVSDYFVPESEPGFCFHYSLIMPQVTTTSPSLPPSS 180  
  
Qy 181 LSLDLLNNAVTAFTLEELIRYLEPRDQVLDLSLYKFTWQLGKAFYLGKSKVNNLN 240  
Db 181 LSLDLLNNAVTAFTLEELIRYLEPRDQVLDLSLYKFTWQLGKAFYLGKSKVNNLN 240  
  
Qy 241 LKEEVKLYSCTPRNPVSIRELKTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300  
Db 241 LKEEVKLYSCTPRNPVSIRELKTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300  
  
Qy 301 VTKKHYEVLQRPKTVGKGLHSLTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKKHYEVLQRPKTVGKGLHSLTDVALEHHEECDCVCRGNAGG 345

RESULT 5  
ABG92894  
ID ABG92894 standard; Protein; 345 AA.  
XX  
XX AC ABG92894;  
XX  
XX DT 19-NOV-2002 (first entry)  
XX  
XX DE Mouse VEGF-like protein zvegf 3.  
XX  
XX VEGF; vascular endothelial growth factor; zvegf 3; mouse;  
KW chromosome 3; cell proliferation; differentiation; metabolism;  
KW migration; revascularisation; solid tumour; diabetic retinopathy;  
KW psoriasis; rheumatoid arthritis; cancer; autoimmune disease;  
KW inflammation; myocardial ischaemia; scleroderma; fibrosis;  
KW glomerulosclerosis; atherosclerosis; skin wound; ulcer; burn;  
KW skin grafting; female reproductive tract disorder; chronic liver disease;  
KW circulatory disorder; heart failure; neurodegenerative disease;  
KW multiple sclerosis; Parkinson's disease; Alzheimer's disease; stroke;  
KW neurite outgrowth.  
XX  
XX Mus musculus.  
XX  
XX US6432673-B1.  
XX  
XX PD 13-AUG-2002.  
XX  
XX PF 07-DEC-1999; 99US-0457086.  
XX  
XX PR 07-DEC-1998; 98US-111173P.  
PR 06-JUL-1999; 99US-142576P.  
PR 21-OCT-1999; 99US-161653P.  
PR 12-NOV-1999; 99US-165255P.  
XX  
XX (ZYMO ) ZYMOGENETICS INC.  
XX  
XX Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KB;  
PI Gilbertson DG, West JW;  
XX  
XX WPI; 2002-689759/74.  
XX  
XX N-PSDB; ABS68648.  
XX  
XX Novel polypeptide, designated zvegf3 useful for treating skin wounds,  
PT ulcers, burns, skin grafting, female reproductive tract disorders,  
PT Parkinson's disease, and Alzheimer's disease -  
XX  
XX Example 4; Fig 2; 69pp; English.

XX The invention relates to an isolated polypeptide, designated zvegf3  
CC (a vascular endothelial growth factor-like protein) of 111-136 amino acid  
CC residues in length and comprises the sequence appearing as ABG92889  
CC from amino acid residues 235-345. Also included are an isolated  
CC protein comprising a first polypeptide disulphide bonded to a second  
CC polypeptide, where each of the first and second polypeptides is from  
CC zvegf 3, and where the protein modulates cell proliferation,  
CC differentiation, metabolism or migration, the zvegf 3 encoding  
CC polynucleotides and zvegf 3 expression vectors and host cells  
CC zvegf 3 is useful as additives in tissue adhesives for promoting the  
CC revascularisation of the healing tissue, for designing molecules that  
CC antagonise semaphorin-stimulated activities, including neurite growth,  
CC cardiovascular development, cartilage and limb development, and T and  
CC B-cell function, and for imaging tumours or other sites of abnormal cell  
CC proliferation and in gene therapy applications. The proteins are useful  
CC therapeutically to stimulate tissue development or repair, or cellular  
CC differentiation or proliferation, for stimulating the growth of  
CC fibroblast or smooth muscle cells, as molecular weight standards, as  
CC reagents in assays for determining circulatory level of the protein or as  
CC standards in the analysis of cell phenotype, for identifying inhibitors  
CC of their activity which are useful for reducing the growth of solid  
CC tumours, for treating diabetic retinopathy, psoriasis, rheumatoid  
CC arthritis, various forms of cancers, autoimmune disease, inflammation,

CC myocardial ischaemia, scleroderma, and reducing fibrosis, including scar  
CC formation, keloids, liver fibrosis, lung fibrosis (e.g. silicosis,  
CC asbestosis), kidney fibrosis (including diabetic nephropathy),  
CC glomerulosclerosis, atherosclerosis, skin wounds, ulcers, burns, skin  
CC grafting, and female reproductive tract disorders, chronic liver disease  
CC (hepatitis), cirrhosis, Reye's syndrome, Wilson's disease, circulatory  
CC disorders e.g. heart failure, hepatic or portal vein thrombosis, cardiac  
CC sclerosis, neurodegenerative diseases such as multiple sclerosis,  
CC Parkinson's disease, Alzheimer's disease, and for regenerating neurite  
CC outgrowths following strokes. The gene for mouse zveg3 is located on  
CC chromosome 3. The present sequence represents zveg3.  
XX  
SQ Sequence 345 AA;

Query Match 100.0%; Score 1848; DB 23; Length 345;  
Best Local Similarity 100.0%; Pred. No. 4e-182;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MLLGLLLLTALAGQRTGTRAESNLSSKQLSSDKQNGVQDPRHVVITSGNGSIHS 60  
Db 1 MLLGLLLLTALAGQRTGTRAESNLSSKQLSSDKQNGVQDPRHVVITSGNGSIHS 60  
Qy 61 PKPHTYPRNMVLWRLVAVDENVRIOITDPERFGLDPEDDICKYDFVEEVEPSDGSVL 120  
Db 61 PKPHTYPRNMVLWRLVAVDENVRIOITDPERFGLDPEDDICKYDFVEEVEPSDGSVL 120  
Qy 121 GRWCGSTVPGKQTSKGNHIRFVSDYFPEFPGFCIHYSIIMPQVTTTSPSLPSS 180  
Db 121 GRWCGSTVPGKQTSKGNHIRFVSDYFPEFPGFCIHYSIIMPQVTTTSPSLPSS 180  
Qy 181 LSDDLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLKAFLYGKSKVNLNL 240  
Db 181 LSDDLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLKAFLYGKSKVNLNL 240  
Qy 241 LKEEVKLYSCTPRNFSVSIREEELKRTDTIIFWPGCLLVKRCGNCACCLHNCNECQCVPK 300  
Db 241 LKEEVKLYSCTPRNFSVSIREEELKRTDTIIFWPGCLLVKRCGNCACCLHNCNECQCVPK 300  
Qy 301 VTKKYHEVLQRPKTVGKGLHKSITDVALEHHEECDCVCRNAGG 345  
Db 301 VTKKYHEVLQRPKTVGKGLHKSITDVALEHHEECDCVCRNAGG 345

RESULT 6  
AAB47890  
ID AAB47890 standard; Protein; 345 AA.  
XX  
AC AAB47890;  
XX  
DT 16-MAY-2002 (first entry)  
XX  
XX Mouse zveg3.  
XX Human; mouse; zveg3; zveg4; platelet derived growth factor;  
KW PDGF; homolog; growth; bone; ligament; cartilage; proliferation;  
KW osteoblast; chondrocyte; bony defect; fracture; bone graft;  
KW implant; periodontal pocket; osteoclast; bone marrow stem cell;  
KW osteoporosis.  
XX  
OS Mus musculus.  
XX  
PN US2002004225-A1.  
XX  
PD 10-JAN-2002.  
XX  
XX 29-MAR-2001; 2001US-0823033.  
XX  
PR 07-DEC-1998; 98US-111173P.  
PR 06-JUL-1999; 99US-142576P.  
PR 21-OCT-1999; 99US-161653P.  
PR 12-NOV-1999; 99US-165255P.  
PR 31-MAR-2000; 2000US-193723P.  
PR 07-DEC-1999; 99US-0457066.

XX (HART/) HART C E.  
PA (GILB/) GILBERTSON D G.  
XX  
XX Hart CE, Gilbertson DG;  
XX  
XX WPI; 2002-171026/22.  
DR N-PSDB; AAI72444.  
XX  
PT Promoting growth of bone, ligament or cartilage in a mammal, involves  
PT administering to the mammal a protein which comprises growth factor  
PT domain of zveg3 protein, a homolog of platelet-derived growth factor  
XX  
XX Claim 1; Page 19-20; 31pp; English.

XX The sequences given in AAB4789-90 represent human and mouse zveg3,  
CC respectively. zveg3 is a platelet derived growth factor (PDGF) homolog  
CC and it was used in the method of the invention for promoting growth of  
CC bone, ligament or cartilage and stimulating proliferation of osteoblasts  
CC or chondrocytes in a mammal. The proteins used were preferably a dimeric  
CC protein of residues 235-345 of human zveg3 or all of the mouse zveg3  
CC protein, with a delivery vehicle. The method of the invention is useful  
CC for promoting growth of bone, ligament or cartilage in a mammal, where  
CC the composition is administered at a site of a bony defect, preferably  
CC a fracture, bone graft site, implant site, or periodontal pocket, and  
CC for stimulating proliferation of osteoblasts or chondrocytes in a  
CC mammal. It is further useful for promoting proliferation of osteoblasts,  
CC osteoclasts, chondrocytes or bone marrow stem cells, where the bone  
CC marrow stem cells are harvested from a patient prior to culture. The  
CC method is therefore useful for treating osteoporosis.  
XX

SQ Sequence 345 AA;

Query Match 100.0%; Score 1848; DB 23; Length 345;  
Best Local Similarity 100.0%; Pred. No. 4e-182;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MLLGLLLLTALAGQRTGTRAESNLSSKQLSSDKQNGVQDPRHVVITSGNGSIHS 60  
Db 1 MLLGLLLLTALAGQRTGTRAESNLSSKQLSSDKQNGVQDPRHVVITSGNGSIHS 60  
Qy 61 PKPHTYPRNMVLWRLVAVDENVRIOITDPERFGLDPEDDICKYDFVEEVEPSDGSVL 120  
Db 61 PKPHTYPRNMVLWRLVAVDENVRIOITDPERFGLDPEDDICKYDFVEEVEPSDGSVL 120  
Qy 121 GRWCGSTVPGKQTSKGNHIRFVSDYFPEFPGFCIHYSIIMPQVTTTSPSLPSS 180  
Db 121 GRWCGSTVPGKQTSKGNHIRFVSDYFPEFPGFCIHYSIIMPQVTTTSPSLPSS 180  
Qy 181 LSDDLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLKAFLYGKSKVNLNL 240  
Db 181 LSDDLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLKAFLYGKSKVNLNL 240  
Qy 241 LKEEVKLYSCTPRNFSVSIREEELKRTDTIIFWPGCLLVKRCGNCACCLHNCNECQCVPK 300  
Db 241 LKEEVKLYSCTPRNFSVSIREEELKRTDTIIFWPGCLLVKRCGNCACCLHNCNECQCVPK 300  
Qy 301 VTKKYHEVLQRPKTVGKGLHKSITDVALEHHEECDCVCRNAGG 345  
Db 301 VTKKYHEVLQRPKTVGKGLHKSITDVALEHHEECDCVCRNAGG 345

RESULT 7  
AAE13213  
ID AAE13213 standard; Protein; 345 AA.  
XX  
AC AAE13213;  
XX  
DT 12-FEB-2002 (first entry)  
XX  
DE Mouse platelet-derived growth factor (PDGF-C) protein.  
XX

KW Mouse; transgenic animal; platelet derived growth factor C; PDGF-C;  
XX cardiac hypertrophy; fibrosis.

OS Mus sp.

PN WO200172132-A1.

XX 04-OCT-2001.

XX 28-MAR-2001; 2001WO-US09855.

XX 28-MAR-2000; 2000US-192507P.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Eriksson U, Li X, Ponten A, Aase K, Li H;

XX WPI; 2002-010700/01.

XX A transgenic animal over-expressing platelet derived growth factor C is  
PT useful to study and find therapy for disease associated with PDGF-C  
PT over-expression, including cardiac hypertrophy and fibrosis -

XX Example 4; Page 42-43; 48pp; English.

XX The patent discloses a method for producing a transgenic, non-human  
CC animal over-expressing a platelet derived growth factor C (PDGF-C),  
CC or its functional fragment or analogue. The method involves introducing  
CC a transgenic PDGF-C DNA into a cell of a non-human animal, introducing  
CC the cell into a non-human animal and allowing the cell to develop into  
CC a transgenic, non-human animal. The transgenic animal is useful as a  
CC model to study disease states characterised by over-expression of PDGF-C  
CC and to find therapy for those diseases, particularly hypertrophy and  
CC fibrosis in various organs including the heart. The present sequence  
CC is PDGF-C protein from mouse.

XX Sequence 345 AA;

Query Match 100.0%; Score 1848; DB 23; Length 345;  
Best Local Similarity 100.0%; Pred. No. 4e-182;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MLLGLLLLSALAGQRTGTRAESNLSSKQLSDKEQNGVQDPRHVRVTISGNGSIHS 60  
Db 1 MLLGLLLLSALAGQRTGTRAESNLSSKQLSDKEQNGVQDPRHVRVTISGNGSIHS 60  
  
QY 61 PKPPTYPRNNVLWRLVAVDENVRIQLTDERFGLDPEDDICKYDFVVERPSDGSVL 120  
Db 61 PKPPTYPRNNVLWRLVAVDENVRIQLTDERFGLDPEDDICKYDFVVERPSDGSVL 120  
  
QY 121 GRWCGSGTVFGKQTSKGNHIRFVSDYFSEPFSGFCIHYSIIMPQVTTTSPSLPSS 180  
Db 121 GRWCGSGTVFGKQTSKGNHIRFVSDYFSEPFSGFCIHYSIIMPQVTTTSPSLPSS 180  
  
QY 181 LSLDLLNNAVTAFTLEELRYLEPDWQVLDLSLYKPTWQLGKAFYLGKSKVNLNL 240  
Db 181 LSLDLLNNAVTAFTLEELRYLEPDWQVLDLSLYKPTWQLGKAFYLGKSKVNLNL 240  
  
QY 241 LKEEVLKYSTPFRNFVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPK 300  
Db 241 LKEEVLKYSTPFRNFVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPK 300  
  
QY 301 VTKKYEVLQRPKTVGKGLHLSLTDVALEHHEBCDCVCRNAGG 345  
Db 301 VTKKYEVLQRPKTVGKGLHLSLTDVALEHHEBCDCVCRNAGG 345

RESULT 8  
ID ABG76398  
XX standard; Protein; 345 AA.  
AC  
XX ABG76398;

DT 22-MAY-2003 (first entry)  
XX Mouse growth factor homologue, zveg3.  
XX  
XX Mouse; growth factor homologue; zveg3; fibroblast; smooth muscle cell;  
KW cell-surface platelet-derived growth factor alpha receptor; PDGF;  
KW full-thickness skin wound; female reproductive tract; duodenal ulcer;  
KW prolonged bleeding; periodontal disease; tissue adhesive; liver damage;  
KW revascularisation; healing tissue; liver disease; CPC; CHN; cirrhosis;  
KW chronic active hepatitis; hepatic chronic passive congestion; stroke;  
KW central haemorrhagic necrosis; hepatic vein thrombosis; ischaemia;  
KW portal vein thrombosis; cardiac sclerosis; new vessel formation;  
KW endothelial precursor stem cell; neovascularisation; wound healing;  
KW organ transplant; tissue grafting; peripheral neuropathy; spinal cord;  
KW sensory neurite outgrowth; brain damage; head injury; paralysis;  
KW spinal injury; neurodegenerative disease; diabetic retinopathy;  
KW psoriasis; arthritis; scleroderma; keloid; liver fibrosis; psoriasis;  
KW lung fibrosis; kidney fibrosis; glomerulosclerosis; cancer;  
KW proliferative vascular disorder; ocular neovascularisation;  
KW inflammatory disorder; rheumatoid arthritis; vasculogenesis;  
KW angiogenesis; nervous system disorder; cytostatic; hepatotropic;  
KW vulnary; tranquilliser; cerebroprotective; neuroprotective; nootropic;  
KW ophthalmological; dermatological; coagulant; cardiant.  
XX  
OS Mus musculus.  
XX  
XX US2002177193-A1.  
XX  
XX 28-NOV-2002.  
XX  
XX 02-MAY-2002; 2002US-0139593.  
XX  
XX 07-DEC-1998; 98US-111173P.  
XX 06-JUL-1999; 99US-142576P.  
XX 21-OCT-1999; 99US-161653P.  
XX 12-NOV-1999; 99US-185235P.  
XX 07-DEC-1999; 99US-04527066.  
XX  
XX (ZYMO ) ZYMOGENETICS INC.  
XX  
XX Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;  
XX Gilbertson DG, West JW;  
XX  
XX WPI; 2003-328485/31.  
XX N-PSDB; ABX93182.  
XX  
XX New isolated zveg3 polypeptide, useful for treating cancer.  
XX Alzheimer's disease, Parkinson's disease, chronic active hepatitis,  
XX hepatic vein thrombosis, comprises growth factor domain and CUB domain  
XX  
XX Claim 1; Fig 6; 73pp; English.  
XX  
XX The present invention relates to the isolation of a growth factor  
XX homologue referred to as zveg3, and the polynucleotide sequence  
XX encoding it. The zveg3 polypeptide is useful for stimulating the  
XX growth of fibroblasts or smooth muscle cells, or for activating a  
XX cell-surface platelet-derived growth factor (PDGF) alpha receptor.  
XX The zveg3 polypeptide is useful as a PDGF alpha receptor agonist and  
XX thus is useful for treating full-thickness skin wounds, female  
XX reproductive tract and prolonged bleeding, periodontal disease,  
XX damaged liver tissue, and duodenal ulcers. The polypeptide is also  
XX useful as an additive in tissue adhesives for promoting  
XX revascularisation of healing tissue. The zveg3 polypeptide is also  
XX useful for treating liver damage including damage due to liver  
XX disease, chronic active hepatitis, hepatic chronic passive congestion  
XX (CPC), central haemorrhagic necrosis (CHN), hepatic vein thrombosis,  
XX portal vein thrombosis, cardiac sclerosis, and many types of cirrhosis.  
XX The polypeptide is useful for enhancing expansion and mobilisation of  
XX endothelial precursor stem cells, creating and stabilising new vessel  
XX formation in areas requiring neovascularisation, including areas of  
XX ischaemia, organ transplants, wound healing, and tissue grafting. It  
XX may be used for treating peripheral neuropathies by increasing spinal

cord and sensory neurite outgrowth, and as part of therapeutic treatment for the regeneration of neurite outgrowths following strokes, brain damage caused by head injuries, and paralysis caused by spinal injuries. Application may also be made in treating neurodegenerative diseases (e.g. multiple sclerosis, Alzheimer's disease, Parkinson's disease), diabetic retinopathy, psoriasis, arthritis, scleroderma, and reducing fibrosis, keloids, liver fibrosis, lung fibrosis, kidney fibrosis, and glomerulosclerosis. An antibody that binds vgef3 is useful for blocking the mitogenic, chemotactic, or angiogenic effects of vgef3, and for treating proliferative vascular disorders, ocular neovascularisation, inflammatory disorders, rheumatoid arthritis, psoriasis, cancer, impaired or excessive vasculogenesis or angiogenesis, and diseases of the nervous system. The present sequence represents mouse vgef3.

SQ Sequence 345 AA;  
Query Match 100.0%; Score 1848; DB 24; Length 345;  
Best Local Similarity 100.0%; Pred. No. 4e-182;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLLGLLLTSALAGORTGTRAESNLSSKQLSSDKQNGVQDPRHVVTTISGNSIHS 60  
Db 1 MLLGLLLTSALAGORTGTRAESNLSSKQLSSDKQNGVQDPRHVVTTISGNSIHS 60  
QY 61 PKPHTYPRNMVLVWRLVAVDENVRQLTDFERFGLDEPDDICKYDFVEVEPSPDGSVL 120  
Db 61 PKPHTYPRNMVLVWRLVAVDENVRQLTDFERFGLDEPDDICKYDFVEVEPSPDGSVL 120  
QY 121 GRWCGSGTVPGKOTSGKNHRIHFVSDEYFSPGFCIHYSIIMPQTTSVLPSPSS 180  
Db 121 GRWCGSGTVPGKOTSGKNHRIHFVSDEYFSPGFCIHYSIIMPQTTSVLPSPSS 180  
QY 181 LSLDLLNNAVTAFTSLLEELIRYLEPRQWVDLSLYKPTWQLLGKAFLYGKSKVNLNL 240  
Db 181 LSLDLLNNAVTAFTSLLEELIRYLEPRQWVDLSLYKPTWQLLGKAFLYGKSKVNLNL 240  
QY 241 LKEEVKLYSCTPRNFSVIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPRK 300  
Db 241 LKEEVKLYSCTPRNFSVIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPRK 300  
QY 301 VTKKYHEVLQLRPKTGKGLHKSITDVALHHBECDVCVRGNAGG 345  
Db 301 VTKKYHEVLQLRPKTGKGLHKSITDVALHHBECDVCVRGNAGG 345

RESULT 9  
ID AAY33679 standard; Protein; 345 AA.

XX AAY33679;  
XX 11-JAN-2000 (first entry)  
XX Human VEGF-E protein.  
XX VEGF-E; human; vascular endothelial cell growth factor; wound repair;  
KW treatment; cardiovascular disorder; endothelial disorder; therapy;  
KW tissue generation; regeneration; cardiac hypertrophy; cancer; detection;  
KW angiogenic disorder; age-related macular degeneration; vascular disease;  
KW neovascularization; tumor; gene mapping.  
XX Homo sapiens.  
XX WO9947677-A2.  
XX 23-SEP-1999.  
XX 10-MAR-1999; 99WO-US05190.  
XX 17-MAR-1998; 98US-0040220.  
XX 02-NOV-1998; 98US-0184216.

PA (GETH ) GENENTECH INC.  
XX Ferrara N, Kuo SS;  
XX WPI; 1999-580306/49.  
DR N-PSDB; AAZ23691.

XX New growth factor polypeptide useful for treating cardiovascular or endothelial disorders, e.g. cardiac hypertrophy -  
XX Claim 1; Fig 2; 122pp; English.

XX This invention describes the isolation of a novel human vascular endothelial cell growth factor-E (VEGF-E) polypeptide which has tranquilizer, vulnery and cardiant activity. VEGF-E can be administered therapeutically, especially by expressing encoding polynucleotides, to treat cardiovascular or endothelial disorders in mammals, especially humans. It is useful in wound repair and tissue generation and regeneration, and may especially be used to treat cardiac hypertrophy. It can be combined with a carrier in pharmaceutical compositions, which can be administered to treat disorders as above. VEGF-E can be used to screen for antagonists and agonists, and the antagonists administered to treat angiogenic disorders in mammals (especially humans) e.g. cancer or age-related macular degeneration. It can be used to generate antibodies, useful therapeutically as antagonists, as above. The antibodies are also useful to detect VEGF-E polypeptide, especially to diagnose (e.g. cardiovascular, endothelial or angiogenic disorders in mammals (e.g. vascular disease, or neovascularization associated with tumor formation), by contacting the antibody with a tissue sample and detecting formation of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding VEGF-E can be used to diagnose cardiovascular and endothelial disorders in mammals, by detecting abnormally high or low VEGF-E gene expression in tissue samples. They can also be used to diagnose a disease or susceptibility to a disease related to a mutated form of VEGF-E (e.g. a cardiovascular, endothelial or angiogenic disorder such as a tumor), by detecting a mutation in the VEGF-E encoding sequence isolated from a sample. They may also be used to produce probes useful to detect related sequences or for gene mapping. This sequence represents the human VEGF-E protein described in the method of the invention.

SQ Sequence 345 AA;

Query Match 90.2%; Score 1667; DB 20; Length 345;  
Best Local Similarity 87.0%; Pred. No. 2.1e-163;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTSALAGORTGTRAESNLSSKQLSSDKQNGVQDPRHVVTTISGNSIHS 60  
Db 1 MSLFGLLLTSALAGORQQAESNLSSKFQFSNKQNGVQDPOHERIITVTSNGSIHS 60  
QY 61 PKPHTYPRNMVLVWRLVAVDENVRQLTDFERFGLDEPDDICKYDFVEVEPSPDGSVL 120  
Db 61 PRFPHTYPRNTVLVWRLVAVDENVRQLTDFERFGLDEPDDICKYDFVEVEPSPDGSVL 120  
QY 121 GRWCGSGTVPGKOTSGKNHRIHFVSDEYFSPGFCIHYSIIMPQTTSVLPSPSS 180  
Db 121 GRWCGSGTVPGKOTSGKNHRIHFVSDEYFSPGFCIHYSIIMPQTTSVLPSPSS 180  
QY 181 LSLDLLNNAVTAFTSLLEELIRYLEPRQWVDLSLYKPTWQLLGKAFLYGKSKVNLNL 240  
Db 181 LPDDLNNNAVTAFTSLLEELIRYLEPRQWVDLSLYKPTWQLLGKAFVFGKSRVDNLNL 240  
QY 241 LKEEVKLYSCTPRNFSVIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPRK 300  
Db 241 LKEEVKLYSCTPRNFSVIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPRK 300  
QY 301 VTKKYHEVLQLRPKTGKGLHKSITDVALHHBECDVCVRGNAGG 345  
Db 301 VTKKYHEVLQLRPKTGKGLHKSITDVALHHBECDVCVRGNAGG 345

RESULT 10  
AAY41766



Db 61 PRFPHTYPRNTVLVWRLVAEENVMQLTDFDERFGLDEPDDICKYDFVEEPPSDGTIL 120  
QY 121 GRWCGSGTVPGKOTSGKNHIRIRFVSDVEYFPPGFCIHYSIIMPOVTTTSPSVLPSS 180  
Db 121 GRWCGSGTVPGKOTSGKNHIRIRFVSDVEYFPPGFCIHYSIIMPOVTTTSPSVLPSS 180  
QY 181 LSLDLNNAVTAFSTLEELIRYLEPDRWQVDDLSLYKPTWQLLGKAFYGGKSKVNNLNL 240  
Db 181 LFLDLNNAITAFSTLEELIRYLEPDRWQVDDLSLYKPTWQLLGKAFYGGKSKVNNLNL 240  
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNCACCLHNCNECQCVPRK 300  
Db 241 LTEEVRLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNCACCLHNCNECQCVPSK 300  
QY 301 VTKKYHEVLQLRPKTGVKGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKKYHEVLQLRPKTGVKGLHKSLLTDVALEHHEECDCVCRGSTGG 345

RESULT 11  
AAY30023  
ID AAY30023 standard; Protein; 345 AA.  
XX  
AC AAY30023;  
XX  
DT 11-OCT-1999 (first entry)  
XX  
DE Human vascular endothelial growth factor related protein.  
XX  
KW Vascular endothelial growth factor related protein; VEGF-R protein;  
KW tissue growth inhibition; tumour growth; cancer; tissue growth;  
KW angiogenesis; coronary artery blockage.  
XX  
OS Homo sapiens.  
XX  
FN WO9937671-A1.  
XX  
PD 29-JUL-1999.  
XX  
PF 26-JAN-1999; 99WO-US01574.  
XX  
PR 31-AUG-1998; 98US-0098548.  
PR 27-JAN-1998; 98US-0072635.  
PR 05-JUN-1998; 98US-0088089.  
PR 24-JUN-1998; 98US-0090544.  
XX  
PA (ELIL) LILLY & CO ELI.  
XX  
PI Dou S, Na S, Song HY;  
XX  
DR WPI; 1999-458680/38.  
DR N-PSDB; AAX86352.

XX  
XX A vascular endothelial growth factor related protein and related  
PT polynucleotide, useful for identifying antagonists and binding  
PT compounds  
XX  
PS Claim 1; Page 56-58; 62pp; English.

XX  
XX The present sequence represents a vascular endothelial growth factor  
CC related (VEGF-R) protein. VEGF-R can be used in assays to identify  
CC compounds that bind to it or that antagonize its activity. VEGF-R  
CC antagonists (e.g. anti-VEGF-R antibodies) are useful for inhibiting  
CC tissue growth. This is useful for inhibiting tumour growth and for  
CC treating cancer. VEGF-R itself can be used to stimulate tissue  
CC growth, angiogenesis and to treat coronary artery blockage. The  
CC VEGF-R coding sequence can be used for the recombinant production of  
XX the VEGF-R protein.

SQ Sequence 345 AA;  
Query Match 90.2%; Score 1667; DB 20; Length 345;  
Best Local Similarity 87.0%; Pred. No. 2.1e-163;

Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;  
QY 1 MULLGILLITLSALAGORTGTRAESNLSSKLQLSSDKEQNGVQDPRHVVTTISNGSIHS 60  
Db 1 MSLFGLLITLSALAGORQCTQAESNLSSKQFSSNKEQNGVQDPOHERIITVSTNGSIHS 60  
QY 61 PRFPHTYPRNTVLVWRLVAEENVMQLTDFDERFGLDEPDDICKYDFVEEPPSDGTIL 120  
Db 61 PRFPHTYPRNTVLVWRLVAEENVMQLTDFDERFGLDEPDDICKYDFVEEPPSDGTIL 120  
QY 121 GRWCGSGTVPGKOTSGKNHIRIRFVSDVEYFPPGFCIHYSIIMPOVTTTSPSVLPSS 180  
Db 121 GRWCGSGTVPGKOTSGKNHIRIRFVSDVEYFPPGFCIHYSIIMPOVTTTSPSVLPSS 180  
QY 181 LSLDLNNAVTAFSTLEELIRYLEPDRWQVDDLSLYKPTWQLLGKAFYGGKSKVNNLNL 240  
Db 181 LFLDLNNAITAFSTLEELIRYLEPDRWQVDDLSLYKPTWQLLGKAFYGGKSKVNNLNL 240  
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNCACCLHNCNECQCVPRK 300  
Db 241 LTEEVRLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNCACCLHNCNECQCVPSK 300  
QY 301 VTKKYHEVLQLRPKTGVKGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKKYHEVLQLRPKTGVKGLHKSLLTDVALEHHEECDCVCRGSTGG 345

RESULT 12  
AAB48657  
ID AAB48657 standard; Protein; 345 AA.  
XX  
AC AAB48657;  
XX  
DT 09-MAR-2001 (first entry)  
XX  
DE Human zveg3, SEQ ID NO:33.  
XX  
KW Human; zveg3; zveg4 fusion; growth factor homologue; VEGF/PDGF family;  
KW CUB domain; PDGF-like activity; mitogenic; osteogenic;  
KW neovascularisation; tissue repair; proliferation; differentiation;  
KW liver damage; neurodegenerative; Alzheimer's disease; multiple sclerosis;  
KW periodontal disease; bone fracture; wound healing; vulnery; ischaemia;  
KW immunomodulation; hepatic.  
XX  
OS Homo sapiens.  
XX  
PN WO200066736-A1.  
XX  
PD 09-NOV-2000.  
XX  
PF 03-MAY-2000; 2000WO-US40047.  
XX  
PR 03-MAY-1999; 99US-0304216.  
PR 10-NOV-1999; 99US-0164463.  
PR 04-FEB-2000; 2000US-0180169.  
XX  
XX (ZYMO) ZYMOGENETICS INC.  
XX  
PI Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;  
XX  
DR WPI; 2000-687541/67.  
DR N-PSDB; AAC81582.  
XX  
PT Growth factor homologs and the nucleic acids that encode them, useful  
PT e.g. for treating liver damage, ischemia, multiple sclerosis and  
PT Alzheimer's disease -  
XX  
PS Claim 48; Page 125-126; 143pp; English.

XX  
XX The invention relates to the human growth factor homologue zveg4  
CC (AAB48653), and nucleic acids encoding it (AAC81555). Zveg4 is a member  
CC of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial  
CC growth factor) family. Zveg4 has a growth factor domain (AAB48654)

characterised by a PDGF cystine knot structure, and a CUB domain (AAB48655) which has a beta barrel structure. Zveg4 has PDGF-like activity, having mitogenic activity on fibroblasts, vascular smooth muscle cells and pericytes, and has also been shown to stimulate bone growth. The invention also relates to fusion proteins comprising human zveg4 or fragments thereof, particularly human zveg4/human zveg3 fusions; expression constructs and host cells comprising human zveg4 nucleic acids; the recombinant expression of human zveg4; an antibody which binds to human zveg4 or a fragment thereof; a method of activating a cell-surface PDGF receptor using a zveg4-derived polypeptide; a method of modulating the proliferation, differentiation, migration or metabolism of bone cells, comprising exposing bone cells to zveg4-derived polypeptides; and a method of detecting a genetic abnormality in the zveg4 gene of a patient. Zveg4 proteins and derived fragments may be used to stimulate tissue development or repair, or cellular differentiation or proliferation. They are particularly used for the treatment or repair of liver damage, and may also be used to modulate neurite growth (e.g., in the treatment of Alzheimer's disease or multiple sclerosis). Due to their osteogenic activity, they may also be used in the treatment of periodontal disease and fractures. They may also be used to enhance expansion and mobilisation of haematopoietic stem cells and endothelial precursor stem cells, which may be useful in the treatment of ischaemia, in wound healing, and in the modulation of the immune system. The present sequence represents human zveg3.

Query Match 90.2%; Score 1667; DB 21; Length 345;  
Best Local Similarity 87.0%; Pred. No. 2.1e-163;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;  
QY 1 MLLGLLLTSLALAGTCTRAESNLSSKQLSSDKEQNGVDPHRRVVTISGNGSIHS 60  
Db 1 MSLFGLLLTSLALAGTCTRAESNLSSKQLSSDKEQNGVDPHRRVVTISGNGSIHS 60  
QY 61 PKFPHYPRNMLVWRLVAVDENVRITLTFDERFGLDEDDICKYDFVEVEEPPSDGTVL 120  
Db 61 PKFPHYPRNMLVWRLVAVDENVRITLTFDERFGLDEDDICKYDFVEVEEPPSDGTVL 120  
QY 121 GRWCGSGTVPKQTSKGNHIRIRFVSDEYFPFSGFCIHYSIIMPQVTTSPSVLPSS 180  
Db 121 GRWCGSGTVPKQTSKGNHIRIRFVSDEYFPFSGFCIHYSIIMPQVTTSPSVLPSS 180  
QY 181 LSLLDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWLLGKAFYKSKSVNLLNL 240  
Db 181 LPDLNNAITAFSTLEELIRYLEPDRWQVLDLSLYKPTWLLGKAFYKSKSVNLLNL 240  
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPCLLVVKRCGNCACCLHNCNCCQVPRK 300  
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPCLLVVKRCGNCACCLHNCNCCQVPRK 300  
QY 301 VTKKYHEVLQRPKTVGKGLHKSLLTDVALEHHECDVCVCKGNAGG 345  
Db 301 VTKKYHEVLQRPKTVGKGLHKSLLTDVALEHHECDVCVCKGNAGG 345

RESULT 13  
AAB24250  
ID AAB24250 standard; Protein; 345 AA.  
XX AAB24250;  
XX  
XX 08-FEB-2001 (first entry)  
XX Human platelet-derived growth factor related protein LP8.  
XX Human; platelet derived growth factor related protein; LP8; VEGFh;  
KW vascular endothelial growth factor h; tissue regeneration; vulnery;  
KW atherosclerosis; PDGF-related protein; antiarteriosclerotic.  
XX Homo sapiens.  
XX  
XX WO200059940-A2.  
PN

12-OCT-2000.  
24-MAR-2000; 2000WO-US06427.  
06-APR-1999; 99US-0127913.  
(ELIL ) LILLY & CO ELI.  
Hammond LJ, Na S;  
WPI; 2000-664991/64.  
N-PSDB; AAC64426.  
Enhancing tissue growth and promoting wound healing by administering platelet-derived growth factor related protein, LP8 or its analog and treating atherosclerosis by administering LP8 antagonist  
Claim 4; Page 63-64; 64pp; English.  
The present invention describes a method for enhancing tissue growth, promoting wound healing or stimulating smooth muscle growth by administering a platelet-derived growth factor (PDGF) related protein, designated LP8 or its analogue. Also described is a method of slowing the progress of atherosclerosis or treating atherosclerosis comprising the administration of an LP8 antagonist. The method is useful for enhancing tissue growth, promoting wound healing and stimulating smooth muscle growth. Antagonists of LP8 are useful for treating atherosclerosis. The present sequence represents human LP8, which is also called VEGFh.

Query Match 90.2%; Score 1667; DB 21; Length 345;  
Best Local Similarity 87.0%; Pred. No. 2.1e-163;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;  
QY 1 MLLGLLLTSLALAGTCTRAESNLSSKQLSSDKEQNGVDPHRRVVTISGNGSIHS 60  
Db 1 MSLFGLLLTSLALAGTCTRAESNLSSKQLSSDKEQNGVDPHRRVVTISGNGSIHS 60  
QY 61 PKFPHYPRNMLVWRLVAVDENVRITLTFDERFGLDEDDICKYDFVEVEEPPSDGTVL 120  
Db 61 PKFPHYPRNMLVWRLVAVDENVRITLTFDERFGLDEDDICKYDFVEVEEPPSDGTVL 120  
QY 121 GRWCGSGTVPKQTSKGNHIRIRFVSDEYFPFSGFCIHYSIIMPQVTTSPSVLPSS 180  
Db 121 GRWCGSGTVPKQTSKGNHIRIRFVSDEYFPFSGFCIHYSIIMPQVTTSPSVLPSS 180  
QY 181 LSLLDLNNAVTAFSTLEELIRYLEPDRWQVLDLSLYKPTWLLGKAFYKSKSVNLLNL 240  
Db 181 LPDLNNAITAFSTLEELIRYLEPDRWQVLDLSLYKPTWLLGKAFYKSKSVNLLNL 240  
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPCLLVVKRCGNCACCLHNCNCCQVPRK 300  
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPCLLVVKRCGNCACCLHNCNCCQVPRK 300  
QY 301 VTKKYHEVLQRPKTVGKGLHKSLLTDVALEHHECDVCVCKGNAGG 345  
Db 301 VTKKYHEVLQRPKTVGKGLHKSLLTDVALEHHECDVCVCKGNAGG 345

RESULT 14  
AAB44322  
ID AAB44322 standard; Protein; 345 AA.  
XX AAB44322;  
XX 08-FEB-2001 (first entry)  
XX Human PRO200 (UNQ174) protein sequence SEQ ID NO:488.  
XX Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;  
KW





CC vascularization. This sequence represents the RACE generated human VEGF-X  
CC protein described in the method of the invention.

.....

Sequence	345 AA;
AA	
SQ	

Q	Sequence	345 AA;
	Query Match	90.2%; Score 1667; DB 21; Length 345;
	Best Local Similarity	87.0%; Pred. No. 2.1e-163;
	Matches	300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;
Qy	1	MLLIGLLLLTSALAGQRTGTPAESNLASKQLSSDKEQNGVQDPRHRRVVTISNGSIHS 60
Db	1	MSLFGLLLLTSALAGQRTGTPAESNLASKQFSNKEQNGVQDQPHRIIIVTSNGSIHS 60
Qy	61	PKPFHTYPRNNVLVRLVAVDENVKRIQLTFDERFGLDEDPDDICKYDFVEVEEFSQSVL 120
Db	61	PRPFHTYPRNTVLVRLVAVEEVNWIKLTFDERFGLDEDPDDICKYDFVEVEEFSQGITL 120
Qy	121	GRWCGSGTVPGKQSKGNHRIIRVFSDEYPPSPGFCIHYSIIMPQVTTETSPSVLPSS 180
Db	121	GRWCGSGTVPGKQISKGNQIRIRVFSDEYFPSEPGFCIHVNIWMPQTEAVSPSVLPSPA 180
Qy	181	LSLDLIANNATVAFSTIELRYLEPPDQWVDLDSLYKETQOLLCKAFLYGKKSKVNNL 240
Db	181	LPLDLIANNATVAFSTLSDIRYLEPERWQLDLELYRPTWQLLGKAFVFGRRSRVDLNL 240
Qy	241	LKEEVKLYSCTPRNFVSIRBELKRTDTIWPFGCLLVKRCGCGNACCIHNCNEQCQVPK 300
Db	241	LTEEVRLYSCTPRNFVSIRBELKRTDTIWPFGCLLVKRCGCGNACCLHNCNEQCQVPK 300
Qy	301	VTKKYHEVLQLRPKTVGKVLGHKSLTDVALEHHEECDCVCRNAGG 345
Db	301	VTKKYHEVLQLRPKTVGRLGHKSLTDVALEHHEECDCVCRGSTG 345

Search completed: November 25, 2003, 21:02:15  
Job time : 36.9375 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 21:00:19 ; Search time 13.006 Seconds  
(without alignments)  
1122.351 Million cell updates/sec

Title: US-09-852-209A-7  
Perfect score: 1848  
Sequence: 1 MLLGLLLLTALAGQRTGT.....DVALEHHEEDCVCRGNAGG 345

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/1aa/5A COMB.pep.\*  
2: /cgn2\_6/ptodata/1/1aa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1848	100.0	345	4	US-09-457-066-43
2	1848	100.0	345	4	US-09-564-595D-35
3	1848	100.0	345	4	US-09-706-968-43
4	1667	90.2	345	4	US-09-040-220D-2
5	1667	90.2	345	4	US-09-457-066-2
6	1667	90.2	345	4	US-09-265-686-2
7	1667	90.2	345	4	US-09-540-224-5
8	1667	90.2	345	4	US-09-564-595D-33
9	1667	90.2	345	4	US-09-706-968-2
10	1204.5	65.2	303	4	US-09-564-595D-57
11	1200	64.9	302	4	US-09-564-595D-54
12	1035.5	56.0	317	4	US-09-564-595D-56
13	1019	55.1	316	4	US-09-564-595D-55
14	752	40.7	370	4	US-09-457-066-37
15	752	40.7	370	4	US-09-540-224-2
16	752	40.7	370	4	US-09-564-595D-2
17	752	40.7	370	4	US-09-706-968-37
18	746.5	40.4	370	4	US-09-540-224-4
19	746.5	40.4	370	4	US-09-564-595D-53
20	185	10.0	1015	4	US-09-285-385C-2
21	183	9.9	1012	4	US-09-285-385C-4
22	181	9.8	788	1	US-08-572-225-1
23	181	9.8	986	4	US-09-285-385C-19
24	177.5	9.6	730	3	US-08-872-757-2
25	177.5	9.6	730	4	US-09-850-048A-2
26	175	9.5	101	3	US-09-374-135-6
27	172	9.3	922	4	US-09-116-473-4
					Sequence 43, Appl
					Sequence 35, Appl
					Sequence 43, Appl
					Sequence 2, Appl
					Sequence 2, Appl
					Sequence 5, Appl
					Sequence 2, Appl
					Sequence 3, Appl
					Sequence 2, Appl
					Sequence 57, Appl
					Sequence 54, Appl
					Sequence 56, Appl
					Sequence 55, Appl
					Sequence 37, Appl
					Sequence 2, Appl
					Sequence 37, Appl
					Sequence 4, Appl
					Sequence 53, Appl
					Sequence 2, Appl
					Sequence 1, Appl
					Sequence 19, Appl
					Sequence 2, Appl
					Sequence 2, Appl
					Sequence 6, Appl

28	169	9.1	923	3	US-08-936-135-6	Sequence 6, Appl
29	168	9.1	986	3	US-08-872-757-4	Sequence 4, Appl
30	168	9.1	986	3	US-09-850-048A-4	Sequence 4, Appl
31	165	8.9	1013	2	US-08-866-650-3	Sequence 3, Appl
32	165	8.9	1013	2	US-09-021-287-3	Sequence 3, Appl
33	165	8.9	1013	3	US-09-240-473-3	Sequence 3, Appl
34	162	8.8	591	3	US-08-991-408-4	Sequence 4, Appl
35	162	8.8	591	4	US-09-432-473-4	Sequence 4, Appl
36	162	8.8	1013	2	US-08-866-650-5	Sequence 5, Appl
37	162	8.8	1013	2	US-09-021-287-5	Sequence 5, Appl
38	162	8.8	1013	3	US-08-991-408-2	Sequence 2, Appl
39	162	8.8	1013	3	US-09-240-473-5	Sequence 5, Appl
40	162	8.8	1013	4	US-09-432-473-2	Sequence 2, Appl
41	162	8.8	1013	4	US-09-285-385C-20	Sequence 20, Appl
42	158	8.5	449	2	US-08-839-008-2	Sequence 2, Appl
43	158	8.5	449	2	US-08-839-008-9	Sequence 9, Appl
44	158	8.5	3623	4	US-09-341-461-2	Sequence 2, Appl
45	156.5	8.5	111	4	US-09-341-461-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1  
US-09-457-066-43  
; Sequence 43, Application US/09457066  
; Patent No. 6432673  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60  
; CURRENT APPLICATION NUMBER: US/09/457,066  
; CURRENT FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 43  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-457-066-43

Query Match	100.0%	Score 1848;	DB 4;	Length 345;
Best Local Similarity	100.0%;	Pred. No. 7.2e-195;	Mismatches 0;	Indels 0;
Matches 345;	Conservative 0;			Gaps 0;
QY	1	MLLGLLLLTALAGQRTGTTRAESNLSKQLQSSDKQNGVQDPHRRVVTISGNGSIHS	60	
Db	1	MLLGLLLLTALAGQRTGTTRAESNLSKQLQSSDKQNGVQDPHRRVVTISGNGSIHS	60	
QY	61	PKFPHTYPRNMLVWRLVAVDENVRIQLTFDERFGLDEPDDICKYDFVEVEPSPGSLV	120	
Db	61	PKFPHTYPRNMLVWRLVAVDENVRIQLTFDERFGLDEPDDICKYDFVEVEPSPGSLV	120	
QY	121	GRWCGSGTVPGKOTSGNHIRIRFVSDYFPPSPGFCIHYSIIMPQVTTTSPSVLPSS	180	
Db	121	GRWCGSGTVPGKOTSGNHIRIRFVSDYFPPSPGFCIHYSIIMPQVTTTSPSVLPSS	180	
QY	181	LSLDLNNVATFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGAFLYKSKSVNNLN	240	
Db	181	LSLDLNNVATFSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGAFLYKSKSVNNLN	240	
QY	241	LKEEVKLYSCTPRNFSVSIREEIKRTDTTFWPQCLLVKRCGNCACCLHNCNCQCVPRK	300	
Db	241	LKEEVKLYSCTPRNFSVSIREEIKRTDTTFWPQCLLVKRCGNCACCLHNCNCQCVPRK	300	
QY	301	VTKKHEVTQLRPKTVKGLHSLTDVALEHHEEDCVCRGNAGG	345	

Db 301 VTKYHEVLQRLPKTGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345

## RESULT 2

US-09-564-595D-35  
; Sequence 35, Application US/09564595D  
; Patent No. 6495668  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4  
; FILE REFERENCE: 99-19  
; CURRENT APPLICATION NUMBER: US/09/564,595D  
; CURRENT FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: US 09/304,216  
; PRIOR FILING DATE: 1999-05-03  
; PRIOR APPLICATION NUMBER: US 60/164,463  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: US 60/180,169  
; PRIOR FILING DATE: 2000-02-04  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 35  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-564-595D-35

Query Match 100.0%; Score 1848; DB 4; Length 345;  
Best Local Similarity 100.0%; Pred. No. 7.2e-195;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLLTALAGORTGTRAESNLSSKLQSSDKQNGVDPHRRVVTISGNGSIHS 60  
Db 1 MLLGLLLLTALAGORTGTRAESNLSSKLQSSDKQNGVDPHRRVVTISGNGSIHS 60  
QY 61 PKPHTYPRNMLVWRLVAVDENVRITQFTDFRFGLEDDEDDICKYDFVEVEPSDGSVL 120  
Db 61 PKPHTYPRNMLVWRLVAVDENVRITQFTDFRFGLEDDEDDICKYDFVEVEPSDGSVL 120  
QY 121 GRWCGSTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180  
Db 121 GRWCGSTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180  
QY 181 LSLLDNLNNAVTAFSTLEELIRYLEPDRWQVDLSLYKPTWQLLGKAFLYGKSKVNLNL 240  
Db 181 LSLLDNLNNAVTAFSTLEELIRYLEPDRWQVDLSLYKPTWQLLGKAFLYGKSKVNLNL 240  
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNACCLHNCNECQCVPK 300  
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNACCLHNCNECQCVPK 300  
QY 301 VTKYHEVLQRLPKTGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKYHEVLQRLPKTGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345

## RESULT 3

US-09-706-968-43  
; Sequence 43, Application US/09706968  
; Patent No. 6528050  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60C1  
; CURRENT APPLICATION NUMBER: US/09/706,968

; CURRENT FILING DATE: 2000-11-06  
; PRIOR APPLICATION NUMBER: US/09/541,752  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 43  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-706-968-43

Query Match 100.0%; Score 1848; DB 4; Length 345;  
Best Local Similarity 100.0%; Pred. No. 7.2e-195;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLLTALAGORTGTRAESNLSSKLQSSDKQNGVDPHRRVVTISGNGSIHS 60  
Db 1 MLLGLLLLTALAGORTGTRAESNLSSKLQSSDKQNGVDPHRRVVTISGNGSIHS 60  
QY 61 PKPHTYPRNMLVWRLVAVDENVRITQFTDFRFGLEDDEDDICKYDFVEVEPSDGSVL 120  
Db 61 PKPHTYPRNMLVWRLVAVDENVRITQFTDFRFGLEDDEDDICKYDFVEVEPSDGSVL 120  
QY 121 GRWCGSTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180  
Db 121 GRWCGSTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180  
QY 181 LSLLDNLNNAVTAFSTLEELIRYLEPDRWQVDLSLYKPTWQLLGKAFLYGKSKVNLNL 240  
Db 181 LSLLDNLNNAVTAFSTLEELIRYLEPDRWQVDLSLYKPTWQLLGKAFLYGKSKVNLNL 240  
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNACCLHNCNECQCVPK 300  
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNACCLHNCNECQCVPK 300  
QY 301 VTKYHEVLQRLPKTGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKYHEVLQRLPKTGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345

## RESULT 4

US-09-040-220D-2  
; Sequence 2, Application US/09040220D  
; Patent No. 6391311  
; GENERAL INFORMATION:  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Kuo, Sophia S.  
; TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR  
; TITLE OF INVENTION: ENDOTHELIAL CELL GROWTH FACTOR AND BONE MORPHOGENETIC  
; TITLE OF INVENTION: PROTEIN 1 AND NUCLEIC ACIDS ENCODING SAME, THEIR USES,  
; FILE REFERENCE: P1122  
; CURRENT APPLICATION NUMBER: US/09/040,220D  
; CURRENT FILING DATE: 1998-03-17  
; NUMBER OF SEQ ID NOS: 8  
; SEQ ID NO 2  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Human  
US-09-040-220D-2

Query Match 90.2%; Score 1667; DB 4; Length 345;  
Best Local Similarity 87.0%; Pred. No. 6.2e-175;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLLTALAGORTGTRAESNLSSKLQSSDKQNGVDPHRRVVTISGNGSIHS 60  
Db 1 MLLGLLLLTALAGORTGTRAESNLSSKLQSSDKQNGVDPHRRVVTISGNGSIHS 60  
QY 61 PKPHTYPRNMLVWRLVAVDENVRITQFTDFRFGLEDDEDDICKYDFVEVEPSDGSVL 120  
Db 61 PKPHTYPRNMLVWRLVAVDENVRITQFTDFRFGLEDDEDDICKYDFVEVEPSDGSVL 120

121	GRWCGSGTVPQKQSKGNHIIIRIFVDSDFPSEPQFCIHYSIIMQVTTTSPSVLP	180
Qy		
121	GRWCGSGTVPQKQISKGNQIIRIFVDSDFPSEPQFCIHYNIVMPQFTEAVSPSVLP	180
Db		
181	LSLDLLNNNAVTAFTLEELIRVLEPDRQVOLDLSLYKPTQWLLGKAFLYGKSKVNNL	240
Qy		
181	LPDLNNNAITAFSTLEOLIIRVLEPERQVOLDIEDYRPTWLLGKAFAVGRKSRVVDNL	240
Db		
241	LKEEVKLYSCTPRNFSVIRBELKETDTIIFWPGCLLVKRCGGNCACCLHNCNECCVPRK	300
Qy		
241	LTEEVRLYSCTPRNFSVIRBELKETDTIIFWPGCLLVKRCGGNCACCLHNCNECCVPSK	300
Db		
301	VTKKYHEVLQRPKTGVKGLHKLSLTDVALEHHEECDCVCRGNAGG	345
Qy		
301	VTKKYHEVLQRPKTGVKGLHKLSLTDVALEHHEECDCVCRGSTGG	345
Db		

## RESULT 5

```

US-09-457-066-2
; Sequence 2, Application US/09457066
; Patent No. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-457-066-2

```

	Query Match	90.2%; Score 1667; DB 4; Length 345;
	Best Local Similarity	87.0%; Pred. No. 6.2e-175;
	Matches	300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;
QY	1	MLLLGLLLLTSALAGQTGTAEASNLASKQLSSDKSQGVDPDRHVVVITSGNGSIHS 60
		:                     :
Dd	1	MSLFGLLLLLSALAQOQGTAESNLKSKPFSSNKQGVQPDRHRRIIVSTNGSIHS 60
		:                     :
QY	61	KPKFHTYPRNMVLVWRLVAVDENVRIQLTFDERFEGLEDPEDDICKYDFVEVEEPSDGSVL 120
		:                     :
Dd	61	PPRPHTYPRNTLVWRLVAVEENVIQLTFDERFEGLEDPEDDICKYDFVEVEEPSDGTIL 120
		:                     :
QY	121	GRWCSGTVPGKKQS KGNHRIIRFSDEYFPSEBGFCHISIMPOVTETSPS VLPSPSS 180
		:                     :
Dd	121	GRWCSGTVPGKIQISKGNQIRIRFSDEYFFSEFGFIHYINVMPQTEAVPSV LPPSA 180
		:                     :
QY	181	LSDLNNNAVTAFTSLBELRYLEPDMDQVLDLSLYKPTOLLCKAFLYGKKSVVNLT 240
		:                     :
Dd	181	LPLDLLNNAITAFSTLEDIRILEPERWOLDEDLYRPTMOLLGKA FVGKRSRVDNL 240
		:                     :
QY	241	LKEBVKLYSCTPRNFVS IREELKRTDTI FWPGGCLLVKRCGGNCACCLHNCEQCQVPVK 300
		:                     :
Dd	241	LTEEVRLYSCTPRNFVS IREELKRTDTI FWPGGCLLVKRCGGNCACCLHNCEQCQVP SK 300
		:                     :
QY	301	VTKKYHEVLQLRPKTGVKGHLHKSLTDVALEHHHECDVCVRGNAGG 345
		:                     :
Dd	301	VTKKYHEVLQLRPKTGVRGFLHKS LTDVALEHHHECDVCVRGSTGG 345
		:                     :

## RESULT 6

US-09-265-686-2  
; Sequence 2, Application US/09265686

```

; Patent NO. 6455283
; GENERAL INFORMATION:
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Kuo, Sophia S.
; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND EMPI
; FILE REFERENCE: P1122P2
; CURRENT APPLICATION NUMBER: US/09/265,686
; CURRENT FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: US 09/040,220
; PRIOR FILING DATE: 1998-03-17
; PRIOR APPLICATION NUMBER: US 09/184,216
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Human
; US-09-265-686-2

```

Query Match	90.28;	Score 1667;	DB 4;	Length 345
Best Local Similarity	87.0%;	Pred. No. 6.2e-175;		
Matches 300;	Conservative 27;	Mismatches 18;	Indels	
Qy	1	MLLIGILLLSALAGQRTGTPAESNLSSKLQLSDDKEONGVQDPRHERVWV		
Db	1	MSLFGLLLLSALAGQRTGTPAESNLSSKFKFSSNKKEONGVQDPQHERII		
Qy	61	PKPHTYPRNNVLVRLVAVDENVRIQLTFDERGLEDPEDDICKYDFVEVE		
Db	61	PRPHTYPRNTVLVRLVAVDENVVIQLTFDERGLEDPEDDICKYDFVEVE		
Qy	121	GRWCGSTVPKQTSKGNHINIRFVSDVEYFPSEPGFCIHYSIIMPQVTT		
Db	121	GRWCGSTVPKQTSKGNQIRIRFVSDVEYFPSEPGFCIHYNIVMPQFTEA		
Qy	181	LSLDLIANNATFSTLEELRYLEPDRWQVDLSLYKPTWOLLGKAFYLYG		
Db	181	LPDLLNNAITAFSTLEDRLRYLEPERWQVQLEDLRYPTWOLLGKAFYVFG		
Qy	241	LKEBVKLYSCTPRNFVSIRBELKRTDTI FWPGLLVKRCGNCACCLLHN		
Db	241	LTEBVRLYSCTPRNFVSIRBELKRTDTI FWPGLLVKRCGNCACCLLHN		
Qy	301	VTKKYHEVLQLRPKTGVYKGLHKSITDVALEHHEECDCVCRGNAGG	345	
Db	301	VTKKYHEVLQLRPKTGVYKGLHKSITDVALEHHEECDCVCRSGTGG	345	

```

RESULT 7
US-09-540-224-5
; Sequence 5, Application US/09540224
; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-540-224-5

```

Query Match 90.2%; Score 1667; DB 4;  
Best Local Similarity 87.0%; Pred. No. 6.2e-175;  
Matches 300; Conservative 27; Mismatches 18; Indels

QY 1 MLLGLLLTTSALAGORTGTRAESNLSSKQLQSSDKQNGVQDPHRRVVTISNGSIHS 60  
Db 1 MSLFGLLLTTSALAGORQGTQAESNLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60  
QY 61 PKPPTYPRNMVLMVRLVAVDENVRQLTDFERFGLDEDDICKYDFVEVEBPSDGSVL 120  
Db 61 PRPPTYPRNTVLMVRLVAVDENVRQLTDFERFGLDEDDICKYDFVEVEBPSDGTIL 120  
QY 121 GRWCGSTVPKOTSGKNHIRIRFVSDYFPPSPGFCIHYSIIMPOVTTTSPSVLPSS 180  
Db 121 GRWCGSTVPKQISKGNQIRIRFVSDYFPPSPGFCIHYNIVMPQTEAVSVLPSSA 180  
QY 181 LSLDLNNAVTAFSTLEELIRYLEPDRQVLDLSLYKPTWQLLGKAFLYGKSKVNNLNL 240  
Db 181 LPDLNNAITAFSTLEELIRYLEPDRQVLDLSLYKPTWQLLGKAFVGRKSRVVDLNL 240  
QY 241 LKEEVLYSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPSK 300  
Db 241 LKEEVLYSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPSK 300  
QY 301 VTKKHEVLQRLPKTGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKKHEVLQRLPKTGVRGLHKSLLTDVALEHHEECDCVCRGSTGG 345

## RESULT 8

US-09-564-595D-33  
; Sequence 33, Application US/09564595D  
; Patent No. 6495668  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4  
; FILE REFERENCE: 99-19  
; CURRENT APPLICATION NUMBER: US/09/564,595D  
; PRIOR FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: US 09/304,216  
; PRIOR FILING DATE: 1999-05-03  
; PRIOR APPLICATION NUMBER: US 60/164,463  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: US 60/180,169  
; PRIOR FILING DATE: 2000-02-04  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 33  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-564-595D-33

Query Match 90.2%; Score 1667; DB 4; Length 345;  
Best Local Similarity 87.0%; Pred. No. 6.2e-175;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTTSALAGORTGTRAESNLSSKQLQSSDKQNGVQDPHRRVVTISNGSIHS 60  
Db 1 MSLFGLLLTTSALAGORQGTQAESNLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60  
QY 61 PKPPTYPRNMVLMVRLVAVDENVRQLTDFERFGLDEDDICKYDFVEVEBPSDGSVL 120  
Db 61 PRPPTYPRNTVLMVRLVAVDENVRQLTDFERFGLDEDDICKYDFVEVEBPSDGTIL 120  
QY 121 GRWCGSTVPKOTSGKNHIRIRFVSDYFPPSPGFCIHYSIIMPOVTTTSPSVLPSS 180  
Db 121 GRWCGSTVPKQISKGNQIRIRFVSDYFPPSPGFCIHYNIVMPQTEAVSVLPSSA 180  
QY 181 LSLDLNNAVTAFSTLEELIRYLEPDRQVLDLSLYKPTWQLLGKAFLYGKSKVNNLNL 240  
Db 181 LPDLNNAITAFSTLEELIRYLEPDRQVLDLSLYKPTWQLLGKAFVGRKSRVVDLNL 240  
QY 241 LKEEVLYSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPSK 300  
Db 241 LKEEVLYSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPSK 300

Db 241 LKEEVLYSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPSK 300  
QY 301 VTKKHEVLQRLPKTGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKKHEVLQRLPKTGVRGLHKSLLTDVALEHHEECDCVCRGSTGG 345

## RESULT 9

US-09-706-968-2  
; Sequence 2, Application US/09706968  
; Patent No. 6528050  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60C1  
; CURRENT APPLICATION NUMBER: US/09/706,968  
; PRIOR FILING DATE: 2000-11-06  
; PRIOR APPLICATION NUMBER: US/09/541,752  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-706-968-2

Query Match 90.2%; Score 1667; DB 4; Length 345;  
Best Local Similarity 87.0%; Pred. No. 6.2e-175;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTTSALAGORTGTRAESNLSSKQLQSSDKQNGVQDPHRRVVTISNGSIHS 60  
Db 1 MSLFGLLLTTSALAGORQGTQAESNLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60  
QY 61 PKPPTYPRNMVLMVRLVAVDENVRQLTDFERFGLDEDDICKYDFVEVEBPSDGSVL 120  
Db 61 PRPPTYPRNTVLMVRLVAVDENVRQLTDFERFGLDEDDICKYDFVEVEBPSDGTIL 120  
QY 121 GRWCGSTVPKOTSGKNHIRIRFVSDYFPPSPGFCIHYSIIMPOVTTTSPSVLPSS 180  
Db 121 GRWCGSTVPKQISKGNQIRIRFVSDYFPPSPGFCIHYNIVMPQTEAVSVLPSSA 180  
QY 181 LSLDLNNAVTAFSTLEELIRYLEPDRQVLDLSLYKPTWQLLGKAFLYGKSKVNNLNL 240  
Db 181 LPDLNNAITAFSTLEELIRYLEPDRQVLDLSLYKPTWQLLGKAFVGRKSRVVDLNL 240  
QY 241 LKEEVLYSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPSK 300  
Db 241 LKEEVLYSCTPRNFVSIRBELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPSK 300  
QY 301 VTKKHEVLQRLPKTGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKKHEVLQRLPKTGVRGLHKSLLTDVALEHHEECDCVCRGSTGG 345

## RESULT 10

US-09-564-595D-57  
; Sequence 57, Application US/09564595D  
; Patent No. 6495668  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4  
; FILE REFERENCE: 99-19



180 SWQEDLENMYLDTPRYGRSY-HDRKSKVVDLNNLLTEEVRLYSCTPRNFSVIREELKRT 238  
QY 267 DTIFWPGCLLVKRCGNCACCLHNCOCVPRKTKYKHYEVLQRPKTVGKGLHSLTD 326  
Db 239 DTIFWPGCLLVKRCGNCACCLHNCOCVPSKTKYKHYEVLQRPKTVGKGLHSLTD 298  
QY 327 VALEHHEECDCVCRNAGG 345  
Db 299 VALEHHEECDCVCRSTGG 317  
RESULT 13  
US-09-564-595D-55  
; Sequence 55, Application US/09564595D  
; Patent No. 6495668  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4  
; FILE REFERENCE: 99-19  
; CURRENT APPLICATION NUMBER: US/09/564,595D  
; PRIOR FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: US 09/304,216  
; PRIOR FILING DATE: 1999-05-03  
; PRIOR APPLICATION NUMBER: US 60/164,463  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: US 60/180,169  
; PRIOR FILING DATE: 2000-02-04  
; SOFTWARE: FastSeq for Windows Version 4.0  
; NUMBER OF SEQ ID NOS: 57  
; SEQ ID NO 55  
; LENGTH: 316  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: fusion polypeptide  
US-09-564-595D-55  
Query Match 55.1%; Score 1019; DB 4; Length 316;  
Best Local Similarity 60.4%; Pred. No. 1.3e-103;  
Matches 189; Conservative 41; Mismatches 61; Indels 22; Gaps 5;  
QY 46 HERVVTISNGSIHSPKFPHTYPRNVLVAVDENVRIQLTFDEFGLEDPEDDICK 105  
Db 1 HERIITVSTNGSIHSPKFPHTYPRNVLVAVDENVRIQLTFDEFGLEDPEDDICK 60  
QY 106 YDFVEVEEESDGSVLGRWCGSGTVPGKQSKGNHIRIRFVSDYFPSEPGFCIHYIIMP 165  
Db 61 YDFVEVEEESDGSVLGRWCGSGTVPGKQSKGNHIRIRFVSDYFPSEPGFCIHYIIMP 120  
QY 166 QVTET-----TSPSVLPSPSSLSLIDLNNAVTAFTLEELIRYLEPDRWQ 209  
Db 121 QFTAEATNWSVTSSISGVSYNSPSVTDPTLIADALDKKIAEFDIVEDLLKYFNESWQ 179  
QY 210 VLDLSLYKPTWQLLGAFLYKSKSVNLLKEVKLYSCTPRNFSVIREELKRTDTI 269  
Db 180 EDLENMYLDTPRYGRSY-HDRKSK-VLDLRLNDDAKRYCTPRNYSVNIIEELKLANV 237  
QY 270 FWPGLLVKRCGNCACCLHNCOCVPRKTKYKHYEVLQRP---KTGKGLHSLTD 326  
Db 238 FFPRLCLVQRCGNCAGTNNWRSCTNSGKTKYKHYEVLQFPFGHIKRRGRKTAVALVD 297  
QY 327 VALEHHEECDCVC 339  
Db 298 IQLDHHERCDCIC 310  
RESULT 14  
US-09-457-066-37  
; Sequence 37, Application US/09457066  
; Patent No. 6432673  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60  
; CURRENT APPLICATION NUMBER: US/09/457,066  
; CURRENT FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 37  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-457-066-37  
Query Match 40.7%; Score 752; DB 4; Length 370;  
Best Local Similarity 45.3%; Pred. No. 4.3e-74;  
Matches 148; Conservative 59; Mismatches 92; Indels 28; Gaps 9;

APPLICANT: Gao, Zeren  
APPLICANT: Hart, Charles E.  
APPLICANT: Piddington, Christopher S.  
APPLICANT: Sheppard, Paul O.  
APPLICANT: Shoemaker, Kimberly E.  
APPLICANT: Gilbertson, Debra G.  
APPLICANT: West, James W.  
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
FILE REFERENCE: 98-60  
CURRENT APPLICATION NUMBER: US/09/457,066  
CURRENT FILING DATE: 1999-12-07  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 37  
LENGTH: 370  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-457-066-37  
Query Match 40.7%; Score 752; DB 4; Length 370;  
Best Local Similarity 45.3%; Pred. No. 4.3e-74;  
Matches 148; Conservative 59; Mismatches 92; Indels 28; Gaps 9;  
QY 37 EONGVQD-PRHERVTISNGSIHSPKFPHTYPRNVLVAVDENVRIQLTFDEFG 95  
Db 42 ESNHLTDLYRDETITQVKGNGYVQSPRFPNSYPRNLLTWRLHS-QENTRIQLVFNQFG 100  
QY 96 LEDPEDDICKYDFVEVEEESDGSVL--GRWCGSGTVPGKQSKGNHIRIRFVSDYFPSE 153  
Db 101 LEEANDICRYDFVEVEDISESTIIRGWCQKGVPPRIKSRTNQIKITFKSDDYFAK 160  
QY 154 PGFCIHYSI--MPQVTETT-----SPSVLPSPSSLSLIDLNNAVTAFTST 195  
Db 161 PGFKIYSLLEDQFAAASSETNWSVTSSISGVSYNSPSVTDPTLIADALDKKIAEFT 219  
QY 196 LEEILRYLEPDRWQVLDLSLYKPTWQLLGAFLYKSKSVNLLKEVKLYSCTPRNF 255  
Db 220 VEDLLKYFNESWQEDLENNYLDTPRYGRSY-HDRKSK-VLDLRLNDDAKRYCTPRNY 277  
QY 256 SVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCOCVPRKTKYKHYEVLQRP-- 313  
Db 278 SVNIREELKLANVFPFRLCLVQRCGNCAGTNNWRSCTNSGKTKYKHYEVLQFPFGH 337  
QY 314 -KTGKGLHSLTDVALEHHEECDCVC 339  
Db 338 IKRRGRKTAVALVDIQLDHHERCDCIC 364  
RESULT 15  
US-09-540-224-2  
; Sequence 2, Application US/09540224  
; Patent No. 6468543  
; GENERAL INFORMATION:  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: Hart, Charles E.  
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,  
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4  
; FILE REFERENCE: 00-28  
; CURRENT APPLICATION NUMBER: US/09/540,224  
; CURRENT FILING DATE: 2000-03-31  
; EARLIER APPLICATION NUMBER: US 60/180,169  
; EARLIER FILING DATE: 2000-02-04  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-540-224-2  
Query Match 40.7%; Score 752; DB 4; Length 370;  
Best Local Similarity 45.3%; Pred. No. 4.3e-74;  
Matches 148; Conservative 59; Mismatches 92; Indels 28; Gaps 9;





GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 21:04:39 ; Search time 24.3006 Seconds  
(without alignments)  
2618.575 Million cell updates/sec

Title: US-09-852-209A-7  
Perfect score: 1848  
Sequence: 1 MLLGLLLTSALAGORTGT.....DVALEHHERCVCVRNAGG 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 673684 seqs, 18443283 residues

Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/prodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/prodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/prodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/prodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/prodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/prodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/prodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 10: /cgn2\_6/prodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/prodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/prodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/prodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/prodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/prodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/prodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/prodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1848	100.0	345	9	US-09-823-033-4
2	1848	100.0	345	9	US-09-818-943-2
3	1848	100.0	345	10	US-09-852-209A-7
4	1848	100.0	345	14	US-10-139-583-43
5	1848	100.0	345	15	US-10-131-600-7
6	1848	100.0	345	15	US-10-264-361-4
7	1667	90.2	345	9	US-09-823-033-2
8	1667	90.2	345	9	US-09-923-995-4
9	1667	90.2	345	10	US-09-795-006A-149
10	1667	90.2	345	10	US-09-978-295A-488
11	1667	90.2	345	10	US-09-978-697-488
12	1667	90.2	345	10	US-09-978-192A-488
13	1667	90.2	345	11	US-09-999-832A-488
14	1667	90.2	345	11	US-09-978-189-488
15	1667	90.2	345	11	US-09-796-753-6

16	1667	90.2	345	11	US-09-978-608A-488	Sequence 488, App
17	1667	90.2	345	11	US-09-978-585A-488	Sequence 488, App
18	1667	90.2	345	11	US-09-978-191A-488	Sequence 488, App
19	1667	90.2	345	11	US-09-978-403A-488	Sequence 488, App
20	1667	90.2	345	11	US-09-978-564A-488	Sequence 488, App
21	1667	90.2	345	11	US-09-999-833A-488	Sequence 488, App
22	1667	90.2	345	11	US-09-981-915A-488	Sequence 488, App
23	1667	90.2	345	11	US-09-978-824-488	Sequence 488, App
24	1667	90.2	345	11	US-09-918-585A-488	Sequence 488, App
25	1667	90.2	345	11	US-09-978-423A-488	Sequence 488, App
26	1667	90.2	345	11	US-09-978-193A-488	Sequence 488, App
27	1667	90.2	345	11	US-09-999-830A-488	Sequence 488, App
28	1667	90.2	345	11	US-09-978-757A-488	Sequence 488, App
29	1667	90.2	345	11	US-09-978-187B-488	Sequence 488, App
30	1667	90.2	345	11	US-09-978-643A-488	Sequence 488, App
31	1667	90.2	345	12	US-09-978-375A-488	Sequence 488, App
32	1667	90.2	345	12	US-09-978-188A-488	Sequence 488, App
33	1667	90.2	345	12	US-09-978-298A-488	Sequence 488, App
34	1667	90.2	345	12	US-10-137-870-286	Sequence 286, App
35	1667	90.2	345	12	US-10-140-018-286	Sequence 286, App
36	1667	90.2	345	12	US-10-140-021-286	Sequence 286, App
37	1667	90.2	345	12	US-10-140-274-286	Sequence 286, App
38	1667	90.2	345	12	US-10-140-471-286	Sequence 286, App
39	1667	90.2	345	12	US-10-140-807-286	Sequence 286, App
40	1667	90.2	345	12	US-10-140-922-286	Sequence 286, App
41	1667	90.2	345	12	US-10-140-924-286	Sequence 286, App
42	1667	90.2	345	12	US-10-140-926-286	Sequence 286, App
43	1667	90.2	345	12	US-10-141-698-286	Sequence 286, App
44	1667	90.2	345	12	US-10-141-702-286	Sequence 286, App
45	1667	90.2	345	12	US-10-141-704-286	Sequence 286, App

ALIGNMENTS

RESULT 1  
US-09-823-033-4  
; Sequence 4, Application US/09823033  
; Patent No. US2002004225A1  
; GENERAL INFORMATION:  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Gilbertson, Debra G.  
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,  
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE  
; FILE REFERENCE: 00-12  
; CURRENT APPLICATION NUMBER: US/09/823,033  
; CURRENT FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-823-033-4

Query Match 100.0%; Score 1848; DB 9; Length 345;  
Best Local Similarity 100.0%; Pred. No. 5,8e-174;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLLGLLLTSALAGORTGTRAESNLSSKQLSSDKEQNGVQDPRIHVVTTISNGSIIHS	60
Db	1	MLLGLLLTSALAGORTGTRAESNLSSKQLSSDKEQNGVQDPRIHVVTTISNGSIIHS	60
Qy	61	PKFPHYPRNMVLRVAVDENVRIOITFDERFGLDEPDDICKYDFVEVEEPSDGSVL	120
Db	61	PKFPHYPRNMVLRVAVDENVRIOITFDERFGLDEPDDICKYDFVEVEEPSDGSVL	120
Qy	121	GRWCSGTVPKQTSKGNHIRIRFVSDEYFPEPGFCIHYSIMPQVTTTSPSVLPSS	180
Db	121	GRWCSGTVPKQTSKGNHIRIRFVSDEYFPEPGFCIHYSIMPQVTTTSPSVLPSS	180
Qy	181	LSLDLNNAVTAFSTLEIRYLEPRQVQDLSLYKPTWQLLGKAFLYGKSKVYNLML	240

Db 181 LSLDLLNNAVTAFTSTLEELIRYLEPDRWQVDDLSLYKPTWQLLGKAFLYGKSKVNNLN 240  
QY 241 LKEEVKLYSCTPRNFSVIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPK 300  
Db 241 LKEEVKLYSCTPRNFSVIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPK 300  
QY 301 VTKKHEVLQRPKTVGKGLHKSITDVALEHHEBCDCVCRNAGG 345  
Db 301 VTKKHEVLQRPKTVGKGLHKSITDVALEHHEBCDCVCRNAGG 345

## RESULT 2

US-09-818-943-2  
; Sequence 2, Application US/09818943  
; Patent No. US20020049987A1  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: LI, Xuri  
; APPLICANT: PONTEN, Annica  
; APPLICANT: AASE, Karin  
; APPLICANT: LI, Hong  
; TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMALS EXPRESSING PLATELET-DERIVED GROWTH FACTOR C, DNA CODING  
; FILE REFERENCE: 1064/48487  
; CURRENT APPLICATION NUMBER: US/09/818,943  
; CURRENT FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: US 60/192,507  
; PRIOR FILING DATE: 2000-03-28  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 2  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Murinae gen. sp.  
US-09-818-943-2

Query Match 100.0%; Score 1848; DB 9; Length 345;  
Best Local Similarity 100.0%; Pred. No. 5.8e-174;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLLGLLLTTSALAGORTGTRAESNLSSKLQSSDKQNGVQDPRHVRVVTISGNGSIHS 60  
Db 1 MLLGLLLTTSALAGORTGTRAESNLSSKLQSSDKQNGVQDPRHVRVVTISGNGSIHS 60  
QY 61 PKPPTYPRNMVLVRLVAVDENVRITQTFDERFGLDEPDDICKYDFVEVEEPPSDGSLV 120  
Db 61 PKPPTYPRNMVLVRLVAVDENVRITQTFDERFGLDEPDDICKYDFVEVEEPPSDGSLV 120  
QY 121 GRWCGSGTVPGKOTSGNHIRIRFVSDYEPSPGFCIHYSIIMPQVTTTSPSVLPSS 180  
Db 121 GRWCGSGTVPGKOTSGNHIRIRFVSDYEPSPGFCIHYSIIMPQVTTTSPSVLPSS 180  
QY 181 LSLDLLNNAVTAFTSTLEELIRYLEPDRWQVDDLSLYKPTWQLLGKAFLYGKSKVNNLN 240  
Db 181 LSLDLLNNAVTAFTSTLEELIRYLEPDRWQVDDLSLYKPTWQLLGKAFLYGKSKVNNLN 240  
QY 241 LKEEVKLYSCTPRNFSVIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPK 300  
Db 241 LKEEVKLYSCTPRNFSVIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPK 300  
QY 301 VTKKHEVLQRPKTVGKGLHKSITDVALEHHEBCDCVCRNAGG 345  
Db 301 VTKKHEVLQRPKTVGKGLHKSITDVALEHHEBCDCVCRNAGG 345

## RESULT 3

US-09-852-209A-7  
; Sequence 7, Application US/09852209A  
; Patent No. US20020164687A1  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: AASE, Karin  
; APPLICANT: LEE, Xuri

; APPLICANT: PONTEN, Annica  
; APPLICANT: UTELA, Marko  
; APPLICANT: ALITALO, Kari  
; APPLICANT: OSTMAN, Arne  
; APPLICANT: HELDIN, Carl-Henrik  
; APPLICANT: BETSHOLTZ, Christer  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING  
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740  
; CURRENT APPLICATION NUMBER: US/09/852,209A  
; CURRENT FILING DATE: 2001-05-10  
; PRIOR APPLICATION NUMBER: 09/410,349  
; PRIOR FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: 60/110,749  
; PRIOR FILING DATE: 1998-12-03  
; PRIOR APPLICATION NUMBER: 60/113,002  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 60/135,426  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: 60/144,022  
; PRIOR FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Murinae gen. sp.  
US-09-852-209A-7

Query Match 100.0%; Score 1848; DB 10; Length 345;  
Best Local Similarity 100.0%; Pred. No. 5.8e-174;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLLGLLLTTSALAGORTGTRAESNLSSKLQSSDKQNGVQDPRHVRVVTISGNGSIHS 60  
Db 1 MLLGLLLTTSALAGORTGTRAESNLSSKLQSSDKQNGVQDPRHVRVVTISGNGSIHS 60  
QY 61 PKPPTYPRNMVLVRLVAVDENVRITQTFDERFGLDEPDDICKYDFVEVEEPPSDGSLV 120  
Db 61 PKPPTYPRNMVLVRLVAVDENVRITQTFDERFGLDEPDDICKYDFVEVEEPPSDGSLV 120  
QY 121 GRWCGSGTVPGKOTSGNHIRIRFVSDYEPSPGFCIHYSIIMPQVTTTSPSVLPSS 180  
Db 121 GRWCGSGTVPGKOTSGNHIRIRFVSDYEPSPGFCIHYSIIMPQVTTTSPSVLPSS 180  
QY 181 LSLDLLNNAVTAFTSTLEELIRYLEPDRWQVDDLSLYKPTWQLLGKAFLYGKSKVNNLN 240  
Db 181 LSLDLLNNAVTAFTSTLEELIRYLEPDRWQVDDLSLYKPTWQLLGKAFLYGKSKVNNLN 240  
QY 241 LKEEVKLYSCTPRNFSVIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPK 300  
Db 241 LKEEVKLYSCTPRNFSVIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPK 300  
QY 301 VTKKHEVLQRPKTVGKGLHKSITDVALEHHEBCDCVCRNAGG 345  
Db 301 VTKKHEVLQRPKTVGKGLHKSITDVALEHHEBCDCVCRNAGG 345

## RESULT 4

US-10-139-583-43  
; Sequence 43, Application US/10139583  
; Publication No. US20020177193A1  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60  
; CURRENT APPLICATION NUMBER: US/10/139,583

```
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 09/457,066
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-139-583-43

Query Match      100.0%; Score 1848; DB 14; Length 345;
Best Local Similarity 100.0%; Pred. No. 5.8e-174;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTTSALAGORTGTRAESNLSKQLSSDKQGVDPHRRVVTISGNGSIHS 60
   |||||
Db 1 MLLGLLLTTSALAGORTGTRAESNLSKQLSSDKQGVDPHRRVVTISGNGSIHS 60
   |||||

QY 61 PKFPHTYPRNMVLVWRLVAVDENVRILQTFDERFGLDEDDICKYDFVEVEPSPGVS 120
   |||||
Db 61 PKFPHTYPRNMVLVWRLVAVDENVRILQTFDERFGLDEDDICKYDFVEVEPSPGVS 120
   |||||

QY 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDYFPPSPGFCIHYSIIIMPQVTTTSPVLPSS 180
   |||||
Db 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDYFPPSPGFCIHYSIIIMPQVTTTSPVLPSS 180
   |||||

QY 181 LSLDLLNNAVTAFSTLEELIRYLEPDRQVLDLSLYKPTWQLLGKAFLYGKSKVNVN 240
   |||||
Db 181 LSLDLLNNAVTAFSTLEELIRYLEPDRQVLDLSLYKPTWQLLGKAFLYGKSKVNVN 240
   |||||

QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVP 300
   |||||
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVP 300
   |||||

QY 301 VTKKYHEVLQRPKTVGKGLHSLTDVALEHHEECDCVCRGNAGG 345
   |||||
Db 301 VTKKYHEVLQRPKTVGKGLHSLTDVALEHHEECDCVCRGNAGG 345
   |||||

RESULT 5
US-10-131-600-7
; Sequence 7, Application US/10131600
; Publication No. US20030082670A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: BETHSOLTZ, Christer
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
; CURRENT APPLICATION NUMBER: US/10/131,600
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/108,109
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/144,022
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 7
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-10-131-600-7

Query Match      100.0%; Score 1848; DB 15; Length 345;
Best Local Similarity 100.0%; Pred. No. 5.8e-174;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTTSALAGORTGTRAESNLSKQLSSDKQGVDPHRRVVTISGNGSIHS 60
   |||||
Db 1 MLLGLLLTTSALAGORTGTRAESNLSKQLSSDKQGVDPHRRVVTISGNGSIHS 60
   |||||

QY 61 PKFPHTYPRNMVLVWRLVAVDENVRILQTFDERFGLDEDDICKYDFVEVEPSPGVS 120
   |||||
Db 61 PKFPHTYPRNMVLVWRLVAVDENVRILQTFDERFGLDEDDICKYDFVEVEPSPGVS 120
   |||||

QY 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDYFPPSPGFCIHYSIIIMPQVTTTSPVLPSS 180
   |||||
Db 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDYFPPSPGFCIHYSIIIMPQVTTTSPVLPSS 180
   |||||

QY 181 LSLDLLNNAVTAFSTLEELIRYLEPDRQVLDLSLYKPTWQLLGKAFLYGKSKVNVN 240
   |||||
Db 181 LSLDLLNNAVTAFSTLEELIRYLEPDRQVLDLSLYKPTWQLLGKAFLYGKSKVNVN 240
   |||||

QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVP 300
   |||||
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVP 300
   |||||

QY 301 VTKKYHEVLQRPKTVGKGLHSLTDVALEHHEECDCVCRGNAGG 345
   |||||
Db 301 VTKKYHEVLQRPKTVGKGLHSLTDVALEHHEECDCVCRGNAGG 345
   |||||

RESULT 6
US-10-264-361-4
; Sequence 4, Application US/10264361
; Publication No. US20030087870A1
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHOD OF TREATING FIBROSIS
; FILE REFERENCE: 00-53
; CURRENT APPLICATION NUMBER: US/10/264,361
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US/09/695,121
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-264-361-4

Query Match      100.0%; Score 1848; DB 15; Length 345;
Best Local Similarity 100.0%; Pred. No. 5.8e-174;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTTSALAGORTGTRAESNLSKQLSSDKQGVDPHRRVVTISGNGSIHS 60
   |||||
Db 1 MLLGLLLTTSALAGORTGTRAESNLSKQLSSDKQGVDPHRRVVTISGNGSIHS 60
   |||||

QY 61 PKFPHTYPRNMVLVWRLVAVDENVRILQTFDERFGLDEDDICKYDFVEVEPSPGVS 120
   |||||
Db 61 PKFPHTYPRNMVLVWRLVAVDENVRILQTFDERFGLDEDDICKYDFVEVEPSPGVS 120
   |||||

QY 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDYFPPSPGFCIHYSIIIMPQVTTTSPVLPSS 180
   |||||
Db 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDYFPPSPGFCIHYSIIIMPQVTTTSPVLPSS 180
   |||||

QY 181 LSLDLLNNAVTAFSTLEELIRYLEPDRQVLDLSLYKPTWQLLGKAFLYGKSKVNVN 240
   |||||
Db 181 LSLDLLNNAVTAFSTLEELIRYLEPDRQVLDLSLYKPTWQLLGKAFLYGKSKVNVN 240
   |||||
```

Db 181 LSLDLNNAVTAFSTLEELIRYLEPRDQVVDLSLYKPTWQLLGKAFLYGKSKVNNLNL 240  
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQCVPRK 300  
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQCVPRK 300  
QY 301 VTKKYHEVLQLRPKTGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKKYHEVLQLRPKTGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345

RESULT 7  
US-09-823-033-2  
; Sequence 2, Application US/09823033  
; Patent No. US2002004225A1  
; GENERAL INFORMATION:  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Gilbertson, Debra G. PROMOTING GROWTH OF BONE,  
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE  
; FILE REFERENCE: 00-12  
; CURRENT APPLICATION NUMBER: US/09/823,033  
; CURRENT FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-823-033-2

Query Match 90.2%; Score 1667; DB 9; Length 345;  
Best Local Similarity 87.0%; Pred. No. 4.5e-156;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;  
QY 1 MLLGLLLLTALAGORTGTRAESNLSSKQLQSSDKQNGVQDPRHVRVVTISGNSIHS 60  
Db 1 MSFGLLLLTALAGORQGTQAESNLSSKQFQSSNKEQNGVQDQHERIITVSTNGSIHS 60  
QY 61 PKPPTYPRNMLVWRLVAVDENVRILQTFDERFGLDEPDDICKYDFVEVEPSPDGSVL 120  
Db 61 PRFPPTYPRNTVLWRLVAVDENVRILQTFDERFGLDEPDDICKYDFVEVEPSPDGTIL 120  
QY 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDEYFPPSPGFCIHYSIIMPQVTTTSVLPSS 180  
Db 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPPSPGFCIHYNIVMPQTEAVSPVLPSSA 180  
QY 181 LSLDLNNAVTAFSTLEELIRYLEPRDQVVDLSLYKPTWQLLGKAFLYGKSKVNNLNL 240  
Db 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLDELRYPTWQLLGKAFVFGKSRVVDNL 240  
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQCVPRK 300  
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQCVPRK 300  
QY 301 VTKKYHEVLQLRPKTGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKKYHEVLQLRPKTGVRGLHKSLLTDVALEHHEECDCVCRGSTGG 345

RESULT 8  
US-09-923-995-4  
; Sequence 4, Application US/09923995  
; Patent No. US20020081700A1  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: SNAKE VENOM POLYPEPTIDE ZSNK1  
; FILE REFERENCE: 00-47  
; CURRENT APPLICATION NUMBER: US/09/923,995  
; CURRENT FILING DATE: 2001-08-07  
; PRIOR APPLICATION NUMBER: US 60/223,164  
; PRIOR FILING DATE: 2000-08-07  
; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-923-995-4

Query Match 90.2%; Score 1667; DB 9; Length 345;  
Best Local Similarity 87.0%; Pred. No. 4.5e-156;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;  
QY 1 MLLGLLLLTALAGORTGTRAESNLSSKQLQSSDKQNGVQDPRHVRVVTISGNSIHS 60  
Db 1 MSFGLLLLTALAGORQGTQAESNLSSKQFQSSNKEQNGVQDQHERIITVSTNGSIHS 60  
QY 61 PKPPTYPRNMLVWRLVAVDENVRILQTFDERFGLDEPDDICKYDFVEVEPSPDGSVL 120  
Db 61 PRFPPTYPRNTVLWRLVAVDENVRILQTFDERFGLDEPDDICKYDFVEVEPSPDGTIL 120  
QY 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDEYFPPSPGFCIHYSIIMPQVTTTSVLPSS 180  
Db 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPPSPGFCIHYNIVMPQTEAVSPVLPSSA 180  
QY 181 LSLDLNNAVTAFSTLEELIRYLEPRDQVVDLSLYKPTWQLLGKAFLYGKSKVNNLNL 240  
Db 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLDELRYPTWQLLGKAFVFGKSRVVDNL 240  
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQCVPRK 300  
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQCVPRK 300  
QY 301 VTKKYHEVLQLRPKTGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKKYHEVLQLRPKTGVRGLHKSLLTDVALEHHEECDCVCRGSTGG 345

## RESULT 9

US-09-795-006A-149  
; Sequence 149, Application US/09795006A  
; Patent No. US20020151680A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo et al  
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR  
; TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAs AND PROTEINS  
; FILE REFERENCE: 28967/35977B  
; CURRENT APPLICATION NUMBER: US/09/795,006A  
; CURRENT FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: US 60/205,331  
; PRIOR FILING DATE: 2000-05-18  
; PRIOR APPLICATION NUMBER: US 60/185,205  
; PRIOR FILING DATE: 2000-02-25  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 149  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-795-006A-149

Query Match 90.2%; Score 1667; DB 10; Length 345;  
Best Local Similarity 87.0%; Pred. No. 4.5e-156;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;  
QY 1 MLLGLLLLTALAGORTGTRAESNLSSKQLQSSDKQNGVQDPRHVRVVTISGNSIHS 60  
Db 1 MSFGLLLLTALAGORQGTQAESNLSSKQFQSSNKEQNGVQDQHERIITVSTNGSIHS 60  
QY 61 PKPPTYPRNMLVWRLVAVDENVRILQTFDERFGLDEPDDICKYDFVEVEPSPDGSVL 120  
Db 61 PRFPPTYPRNTVLWRLVAVDENVRILQTFDERFGLDEPDDICKYDFVEVEPSPDGTIL 120  
QY 121 GRWCGSGTVPGKQTSKGNHRIIRFVSDEYFPPSPGFCIHYSIIMPQVTTTSVLPSS 180

Db 121 GRWCGSGTVPGKIQISKGNQIRIRFVSDYFPEGFCIHYNIVMPQFTBAVSFVLPPSA 180  
QY 181 LSLIDLLNNAVTAFSTLEELIRYLEPDRMQVDLSLYKPTWQLGKAFLYGKKSQVNLNL 240  
Db 181 LSLIDLLNNAVTAFSTLEELIRYLEPDRMQVDLSLYKPTWQLGKAFLYGKKSQVNLNL 240  
QY 241 LKEEVKLYSCTPRNFVSREELKRTDTTFWPGCLLVKRCGGNACCLHNCNCECQVPRK 300  
Db 241 LKEEVKLYSCTPRNFVSREELKRTDTTFWPGCLLVKRCGGNACCLHNCNCECQVPRK 300  
QY 301 VTKKXHEVLQLRPKTVGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKKXHEVLQLRPKTVGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345

RESULT 10  
US-09-978-295A-488  
; Sequence 488, Application US/09978295A  
; Patent No. US20020156006A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630PIC11  
; CURRENT APPLICATION NUMBER: US/09/978,295A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918595  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/077450  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 60/077632  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077641  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077649  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077791  
; PRIOR FILING DATE: 1998-03-12  
; PRIOR APPLICATION NUMBER: 60/078004

; PRIOR FILING DATE: 1998-03-13  
; PRIOR APPLICATION NUMBER: 60/078886  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078936  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/078939  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079664  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079663  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079786  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079920  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 60/079923  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 60/080105  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080107  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080165  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080194  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080327  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080328  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080333  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080334  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/081070  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081049  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081071  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081195  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081203  
; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 60/081229  
; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 60/081955  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081817  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081819  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081952  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081838  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/082568  
; PRIOR FILING DATE: 1998-04-21  
; PRIOR APPLICATION NUMBER: 60/082569  
; PRIOR FILING DATE: 1998-04-21  
; PRIOR APPLICATION NUMBER: 60/082704  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082804  
; PRIOR FILING DATE: 1998-04-22

;; PRIOR APPLICATION NUMBER: 60/082700  
;; PRIOR FILING DATE: 1998-04-22  
;; PRIOR APPLICATION NUMBER: 60/082797  
;; PRIOR FILING DATE: 1998-04-22  
;; PRIOR APPLICATION NUMBER: 60/082796  
;; PRIOR FILING DATE: 1998-04-23  
;; PRIOR APPLICATION NUMBER: 60/083336  
;; PRIOR FILING DATE: 1998-04-27  
;; PRIOR APPLICATION NUMBER: 60/083322  
;; PRIOR FILING DATE: 1998-04-28  
;; PRIOR APPLICATION NUMBER: 60/083392  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083495  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083496  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083499  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083545  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083554  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083558  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083559  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083500  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083742  
;; PRIOR FILING DATE: 1998-04-30  
;; PRIOR APPLICATION NUMBER: 60/084366  
;; PRIOR FILING DATE: 1998-05-05  
;; PRIOR APPLICATION NUMBER: 60/084414  
;; PRIOR FILING DATE: 1998-05-06  
;; PRIOR APPLICATION NUMBER: 60/084441  
;; PRIOR FILING DATE: 1998-05-06  
;; PRIOR APPLICATION NUMBER: 60/084637  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/084639  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/084640  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/084598  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/084600  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/084627  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/084643  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/085339  
;; PRIOR FILING DATE: 1998-05-13  
;; PRIOR APPLICATION NUMBER: 60/085338  
;; PRIOR FILING DATE: 1998-05-13  
;; PRIOR APPLICATION NUMBER: 60/085323  
;; PRIOR FILING DATE: 1998-05-13  
;; PRIOR APPLICATION NUMBER: 60/085582  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085700  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085689  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085579  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085580  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085573  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085704  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 90.2%; Score 1667; DB 10; Length 345;

Best Local Similarity 87.0%; Pred. No. 4.5e-156;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;  
  
QY 1 MLLGLLLTSLAGORTGTTRAEENSSKQLSSDKEQGVQDPRHVVVTISNGSIHS 60  
DB 1 MSLFGLLLTSLAGORQGTQAESNLSSKQFQFSNKEQGVQDQHERIITVTNGSIHS 60  
  
QY 61 PKFPHTYPRNMVLVRLVAVDENVRILQTFDERFGLDEPDDICKYDFVEVEPSSGVL 120  
DB 61 PRPHTYPRNTVLVRLVAVDENVRILQTFDERFGLDEPDDICKYDFVEVEPSSGVL 120  
  
QY 121 GRWCGSGTVPKQTSKGNHIRIRFVSDEYPPSPGFCIHYSIIMPQVTTTSPSLPSS 180  
DB 121 GRWCGSGTVPKQTSKGNHIRIRFVSDEYPPSPGFCIHYSIIMPQVTTTSPSLPSS 180  
  
QY 181 LSLDLNNAVTAFTLEELIRYLEPDRMQVLDLSLYKPTWQLLGKAPLYCKSKVNLNL 240  
DB 181 LPLDLNNAITAFSTLELIRYLEPDRMQVLDLSLYKPTWQLLGKAPLYCKSKVNLNL 240  
  
QY 241 LKEEVLYSCTPRNFSVSIREELKRTDTIFWPGLLVKRCGNCACCLHNCNECCQVPRK 300  
DB 241 LKEEVLYSCTPRNFSVSIREELKRTDTIFWPGLLVKRCGNCACCLHNCNECCQVPRK 300  
  
QY 301 VTKKYHEVLQRPKTGVKGLHKSLLTDVALEHHEECDCVCRNAGG 345  
DB 301 VTKKYHEVLQRPKTGVKGLHKSLLTDVALEHHEECDCVCRNAGG 345

RESULT 11

US-09-978-697-488  
; Sequence 488, Application US/09978697  
; Patent No. US20020169284A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C27  
; CURRENT APPLICATION NUMBER: US/09/978,697  
; CURRENT FILING DATE: 2001-10-16  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13





;; PRIOR APPLICATION NUMBER: 60/085689  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085579  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085580  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085573  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085704  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 90.2%; Score 1667; DB 10; Length 345;  
Best Local Similarity 87.0%; Pred. No. 4.5e-156;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;  
  
QY 1 MLLGLLLTSLAQGTGTRAESNLSSKLQLSSDKQNGVQDPHRRVVTISNGSGSIHS 60  
DB 1 MSLFLGLLLTSLAQGTGTRAESNLSSKQFSSKQNGVQDPQHERIITVSTNGSIHS 60  
  
QY 61 PKFPHYPRNMYLVRLVAVDENVRIQLTFDRFGLDEPDDICKYDFVEVEEPSDGSVL 120  
DB 61 PRFPHYPRNMYLVRLVAVDENVRIQLTFDRFGLDEPDDICKYDFVEVEEPSDGSVL 120  
  
QY 121 GRWCSGTVPGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180  
DB 121 GRWCSGTVPGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180  
  
QY 181 LSLDLNNVAFSTLEELIRVLEDRQVDLDSLYKPTWQLLKGAFLYGKSKVNNL 240  
DB 181 LPLDLNNVAFSTLEELIRVLEDRQVDLDSLYKPTWQLLKGAFLYGKSKVNNL 240  
  
QY 241 LKEEYKLSCTPRNFSVIREELKRTDTTFWPGCLLVKRCGGNCACCLHNCNECCVPSK 300  
DB 241 LKEEYKLSCTPRNFSVIREELKRTDTTFWPGCLLVKRCGGNCACCLHNCNECCVPSK 300  
  
QY 301 VTKYHEVLQRPKTVGKGLHLSLTDVALEHHEEDCVCVRGNAGG 345  
DB 301 VTKYHEVLQRPKTVGKGLHLSLTDVALEHHEEDCVCVRGNAGG 345

RESULT 12  
US-09-978-192A-488  
; Sequence 488, Application US/09978192A  
; Patent No. US2002017753A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE OF INVENTION: Acids Encoding the Same  
;; FILE REFERENCE: P2630PLC9  
;; CURRENT APPLICATION NUMBER: US/09/978,192A  
;; CURRENT FILING DATE: 2001-10-15  
;; PRIOR APPLICATION NUMBER: 09/918585  
;; PRIOR FILING DATE: 2001-07-30  
;; PRIOR APPLICATION NUMBER: 60/062250  
;; PRIOR FILING DATE: 1997-10-17  
;; PRIOR APPLICATION NUMBER: 60/064249  
;; PRIOR FILING DATE: 1997-11-03  
;; PRIOR APPLICATION NUMBER: 60/065311  
;; PRIOR FILING DATE: 1997-11-13  
;; PRIOR APPLICATION NUMBER: 60/066364  
;; PRIOR FILING DATE: 1997-11-21  
;; PRIOR APPLICATION NUMBER: 60/077450  
;; PRIOR FILING DATE: 1998-03-10  
;; PRIOR APPLICATION NUMBER: 60/077632  
;; PRIOR FILING DATE: 1998-03-11  
;; PRIOR APPLICATION NUMBER: 60/077641  
;; PRIOR FILING DATE: 1998-03-11  
;; PRIOR APPLICATION NUMBER: 60/077649  
;; PRIOR FILING DATE: 1998-03-11  
;; PRIOR APPLICATION NUMBER: 60/077791  
;; PRIOR FILING DATE: 1998-03-12  
;; PRIOR APPLICATION NUMBER: 60/078004  
;; PRIOR FILING DATE: 1998-03-13  
;; PRIOR APPLICATION NUMBER: 60/078886  
;; PRIOR FILING DATE: 1998-03-20  
;; PRIOR APPLICATION NUMBER: 60/078936  
;; PRIOR FILING DATE: 1998-03-20  
;; PRIOR APPLICATION NUMBER: 60/078910  
;; PRIOR FILING DATE: 1998-03-20  
;; PRIOR APPLICATION NUMBER: 60/078939  
;; PRIOR FILING DATE: 1998-03-20  
;; PRIOR APPLICATION NUMBER: 60/079294  
;; PRIOR FILING DATE: 1998-03-25  
;; PRIOR APPLICATION NUMBER: 60/079656  
;; PRIOR FILING DATE: 1998-03-26  
;; PRIOR APPLICATION NUMBER: 60/079664  
;; PRIOR FILING DATE: 1998-03-27  
;; PRIOR APPLICATION NUMBER: 60/079689  
;; PRIOR FILING DATE: 1998-03-27  
;; PRIOR APPLICATION NUMBER: 60/079663  
;; PRIOR FILING DATE: 1998-03-27  
;; PRIOR APPLICATION NUMBER: 60/079728  
;; PRIOR FILING DATE: 1998-03-27  
;; PRIOR APPLICATION NUMBER: 60/079786  
;; PRIOR FILING DATE: 1998-03-27  
;; PRIOR APPLICATION NUMBER: 60/079920  
;; PRIOR FILING DATE: 1998-03-30  
;; PRIOR APPLICATION NUMBER: 60/079923  
;; PRIOR FILING DATE: 1998-03-30  
;; PRIOR APPLICATION NUMBER: 60/080105  
;; PRIOR FILING DATE: 1998-03-31  
;; PRIOR APPLICATION NUMBER: 60/080107  
;; PRIOR FILING DATE: 1998-03-31  
;; PRIOR APPLICATION NUMBER: 60/080165  
;; PRIOR FILING DATE: 1998-03-31  
;; PRIOR APPLICATION NUMBER: 60/080194  
;; PRIOR FILING DATE: 1998-03-31  
;; PRIOR APPLICATION NUMBER: 60/080327  
;; PRIOR FILING DATE: 1998-04-01  
;; PRIOR APPLICATION NUMBER: 60/080328  
;; PRIOR FILING DATE: 1998-04-01  
;; PRIOR APPLICATION NUMBER: 60/080333  
;; PRIOR FILING DATE: 1998-04-01  
;; PRIOR APPLICATION NUMBER: 60/080334  
;; PRIOR FILING DATE: 1998-04-01  
;; PRIOR APPLICATION NUMBER: 60/081070  
;; PRIOR FILING DATE: 1998-04-08  
;; PRIOR APPLICATION NUMBER: 60/081049  
;; PRIOR FILING DATE: 1998-04-08

;; PRIOR APPLICATION NUMBER: 60/081071  
;; PRIOR FILING DATE: 1998-04-08  
;; PRIOR APPLICATION NUMBER: 60/081195  
;; PRIOR FILING DATE: 1998-04-08  
;; PRIOR APPLICATION NUMBER: 60/081203  
;; PRIOR FILING DATE: 1998-04-09  
;; PRIOR APPLICATION NUMBER: 60/081229  
;; PRIOR FILING DATE: 1998-04-09  
;; PRIOR APPLICATION NUMBER: 60/081955  
;; PRIOR FILING DATE: 1998-04-15  
;; PRIOR APPLICATION NUMBER: 60/081817  
;; PRIOR FILING DATE: 1998-04-15  
;; PRIOR APPLICATION NUMBER: 60/081819  
;; PRIOR FILING DATE: 1998-04-15  
;; PRIOR APPLICATION NUMBER: 60/081952  
;; PRIOR FILING DATE: 1998-04-15  
;; PRIOR APPLICATION NUMBER: 60/081838  
;; PRIOR FILING DATE: 1998-04-15  
;; PRIOR APPLICATION NUMBER: 60/082568  
;; PRIOR FILING DATE: 1998-04-21  
;; PRIOR APPLICATION NUMBER: 60/082569  
;; PRIOR FILING DATE: 1998-04-21  
;; PRIOR APPLICATION NUMBER: 60/082704  
;; PRIOR FILING DATE: 1998-04-22  
;; PRIOR APPLICATION NUMBER: 60/082804  
;; PRIOR FILING DATE: 1998-04-22  
;; PRIOR APPLICATION NUMBER: 60/082700  
;; PRIOR FILING DATE: 1998-04-22  
;; PRIOR APPLICATION NUMBER: 60/082797  
;; PRIOR FILING DATE: 1998-04-22  
;; PRIOR APPLICATION NUMBER: 60/082796  
;; PRIOR FILING DATE: 1998-04-23  
;; PRIOR APPLICATION NUMBER: 60/083336  
;; PRIOR FILING DATE: 1998-04-27  
;; PRIOR APPLICATION NUMBER: 60/083322  
;; PRIOR FILING DATE: 1998-04-28  
;; PRIOR APPLICATION NUMBER: 60/083392  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083495  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083496  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083499  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083545  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083554  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083558  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083559  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083500  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083742  
;; PRIOR FILING DATE: 1998-04-30  
;; PRIOR APPLICATION NUMBER: 60/084366  
;; PRIOR FILING DATE: 1998-05-05  
;; PRIOR APPLICATION NUMBER: 60/084414  
;; PRIOR FILING DATE: 1998-05-06  
;; PRIOR APPLICATION NUMBER: 60/084441  
;; PRIOR FILING DATE: 1998-05-06  
;; PRIOR APPLICATION NUMBER: 60/084637  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/084639  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/084640  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/084598  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/084600  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/084627

;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/084643  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/085339  
;; PRIOR FILING DATE: 1998-05-13  
;; PRIOR APPLICATION NUMBER: 60/085338  
;; PRIOR FILING DATE: 1998-05-13  
;; PRIOR APPLICATION NUMBER: 60/085323  
;; PRIOR FILING DATE: 1998-05-13  
;; PRIOR APPLICATION NUMBER: 60/085582  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085700  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085689  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085579  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085580  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085573  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085704  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697  
  
Query Match 90.2%; Score 1667; DB 10; Length 345;  
Best Local Similarity 87.0%; Pred. No. 4.5e-156;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;  
  
QY 1 MLLGLLLTTSALAGORTGTRAESNLSSKQLSSDKQNGVDPHRRVVTISGNGSIHS 60  
DB 1 MSLFGLLLTTSALAGORQTQAESNLSSKFSSKQNGVDPQHERIITVSTNGSIHS 60  
  
QY 61 PKFPHYPRNMLVWRLVAVDENVRIOITFDERFGLDEPDICKYDFVEVEEPSDGSVL 120  
DB 61 PRFPHYPRNTVLVWRLVAVENVMIOITFDERFGLDEPDICKYDFVEVEEPSDGTIL 120  
  
QY 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDDEYFPPEPFGFCHYHSIMPQVTTTSPSVLPSS 180  
DB 121 GRWCGSGTVPGKQISKGNQIRIRFVSDDEYFPPEPFGFCHYHNVMPQFTEAVSPSVLPSSA 180  
  
QY 181 LSLDLNNAVTAFTLEELIRYLEPRMOVDLSLYKPTWOLLGKAFYLGKSKVYNLNL 240  
DB 181 LPDLNNAITAPSTLEDLIRYLEPERWQDLEDLIRPTWOLLGKAFYFGKSRVVDLNL 240  
  
QY 241 LKEEVLKYSCTPRNFSVSIREBELKRTDTTFWPGCLLVKRCGGNCACCLHNCNECQCVPK 300  
DB 241 LTEEVLKYSCTPRNFSVSIREBELKRTDTTFWPGCLLVKRCGGNCACCLHNCNECQCVPK 300  
  
QY 301 VTKKYHEVLQLRPKTVGKGLHLSLTDVALEHHEECDCVCRGNAGG 345  
DB 301 VTKKYHEVLQLRPKTVGKGLHLSLTDVALEHHEECDCVCRGSTGG 345  
  
RESULT 13  
US-09-999-832A-488  
; Sequence 488, Application US/09999832A  
; Publication No. US20020192706A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerbert, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PLC63  
CURRENT APPLICATION NUMBER: US/09/999,832A  
CURRENT FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004  
PRIOR FILING DATE: 1998-03-13  
PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078936  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078939  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079664  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079663  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079786  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079920  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/079923  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/080105  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080107  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080194  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080327  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080328  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080333  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080334  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/081070  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081049  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081071  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081195  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081203  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081229  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081955  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081817  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081819  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081952  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081838  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/082568  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082569  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082704  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082700  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082796  
PRIOR FILING DATE: 1998-04-23  
PRIOR APPLICATION NUMBER: 60/083336  
PRIOR FILING DATE: 1998-04-27  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/083392  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083495  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083496  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083499  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083545  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083554  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083558  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083559  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083500  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742  
PRIOR FILING DATE: 1998-04-30  
PRIOR APPLICATION NUMBER: 60/084366  
PRIOR FILING DATE: 1998-05-05  
PRIOR APPLICATION NUMBER: 60/084414  
PRIOR FILING DATE: 1998-05-06

APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630PIC7  
CURRENT APPLICATION NUMBER: US/09/978,189  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004  
PRIOR FILING DATE: 1998-03-13  
PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078936  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078939  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079664  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079663  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27

Query Match 90.2%; Score 1667; DB 10; Length 345;  
Best Local Similarity 87.0%; Pred. No. 4.5e-156;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;  
QY 1 MLLGLLLLTALAGQRTGTARSNLSKQLQSSDKQNGVQDPHRRVVIISNGSHTS 60  
DB 1 MSLFGLLLLTALAGQRTGTARSNLSKQFQSSNKEQNGVQDPQHERIITVSTNGSHTS 60  
QY 61 PKFPHYPRNMYLVRLVAVDENVRILTDFRFGLEDPEDDICKYDFVEVEEPSDGSVL 120  
DB 61 PRFPHYPRNTVLVRLVAVDENVRILTDFRFGLEDPEDDICKYDFVEVEEPSDGSVL 120  
QY 121 GRWCSGTVPGKQTSKGNHIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180  
DB 121 GRWCSGTVPGKQISKGNQIRIRFVSDYFPPSEPGFCIHYNIVMPQFTEAVSPSVLPESA 180  
QY 181 LSLDLNNVAFSTLELIRVLEPDRQVDLSLYKPTWLLGKAFLYGKSKVNNL 240  
DB 181 LPLDLNNAITAFSTLEDLIRVLEPERWOLDLELRPTWLLGKAFVPGKRSVVDLNL 240  
QY 241 LKEEVKLYSCTPRNFSVSIREEKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPSK 300  
DB 241 LTEEVRVLSCTPRNFSVSIREEKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPSK 300  
QY 301 VTKKYHEVLQRPKTVGKGLHLSLTDVALEHHEBCDVCRCGNAGG 345  
DB 301 VTKKYHEVLQRPKTVGRLHLSLTDVALEHHEBCDVCRCGSTGG 345

RESULT 14  
US-09-978-189-488  
Sequence 488, Application US/09978189  
Publication No. US20030004102A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi

1 PRIOR APPLICATION NUMBER: 60/079786  
1 PRIOR FILING DATE: 1998-03-27  
1 PRIOR APPLICATION NUMBER: 60/079920  
1 PRIOR FILING DATE: 1998-03-30  
1 PRIOR APPLICATION NUMBER: 60/079923  
1 PRIOR FILING DATE: 1998-03-30  
1 PRIOR APPLICATION NUMBER: 60/080105  
1 PRIOR FILING DATE: 1998-03-31  
1 PRIOR APPLICATION NUMBER: 60/080107  
1 PRIOR FILING DATE: 1998-03-31  
1 PRIOR APPLICATION NUMBER: 60/080165  
1 PRIOR FILING DATE: 1998-03-31  
1 PRIOR APPLICATION NUMBER: 60/080194  
1 PRIOR FILING DATE: 1998-03-31  
1 PRIOR APPLICATION NUMBER: 60/080327  
1 PRIOR FILING DATE: 1998-04-01  
1 PRIOR APPLICATION NUMBER: 60/080328  
1 PRIOR FILING DATE: 1998-04-01  
1 PRIOR APPLICATION NUMBER: 60/080333  
1 PRIOR FILING DATE: 1998-04-01  
1 PRIOR APPLICATION NUMBER: 60/080334  
1 PRIOR FILING DATE: 1998-04-01  
1 PRIOR APPLICATION NUMBER: 60/081070  
1 PRIOR FILING DATE: 1998-04-08  
1 PRIOR APPLICATION NUMBER: 60/081049  
1 PRIOR FILING DATE: 1998-04-08  
1 PRIOR APPLICATION NUMBER: 60/081071  
1 PRIOR FILING DATE: 1998-04-08  
1 PRIOR APPLICATION NUMBER: 60/081195  
1 PRIOR FILING DATE: 1998-04-08  
1 PRIOR APPLICATION NUMBER: 60/081203  
1 PRIOR FILING DATE: 1998-04-09  
1 PRIOR APPLICATION NUMBER: 60/081229  
1 PRIOR FILING DATE: 1998-04-09  
1 PRIOR APPLICATION NUMBER: 60/081955  
1 PRIOR FILING DATE: 1998-04-15  
1 PRIOR APPLICATION NUMBER: 60/081817  
1 PRIOR FILING DATE: 1998-04-15  
1 PRIOR APPLICATION NUMBER: 60/081819  
1 PRIOR FILING DATE: 1998-04-15  
1 PRIOR APPLICATION NUMBER: 60/081952  
1 PRIOR FILING DATE: 1998-04-15  
1 PRIOR APPLICATION NUMBER: 60/081838  
1 PRIOR FILING DATE: 1998-04-15  
1 PRIOR APPLICATION NUMBER: 60/082568  
1 PRIOR FILING DATE: 1998-04-21  
1 PRIOR APPLICATION NUMBER: 60/082569  
1 PRIOR FILING DATE: 1998-04-21  
1 PRIOR APPLICATION NUMBER: 60/082704  
1 PRIOR FILING DATE: 1998-04-22  
1 PRIOR APPLICATION NUMBER: 60/082804  
1 PRIOR FILING DATE: 1998-04-22  
1 PRIOR APPLICATION NUMBER: 60/082700  
1 PRIOR FILING DATE: 1998-04-22  
1 PRIOR APPLICATION NUMBER: 60/082797  
1 PRIOR FILING DATE: 1998-04-22  
1 PRIOR APPLICATION NUMBER: 60/082796  
1 PRIOR FILING DATE: 1998-04-23  
1 PRIOR APPLICATION NUMBER: 60/083336  
1 PRIOR FILING DATE: 1998-04-27  
1 PRIOR APPLICATION NUMBER: 60/083322  
1 PRIOR FILING DATE: 1998-04-28  
1 PRIOR APPLICATION NUMBER: 60/083392  
1 PRIOR FILING DATE: 1998-04-29  
1 PRIOR APPLICATION NUMBER: 60/083495  
1 PRIOR FILING DATE: 1998-04-29  
1 PRIOR APPLICATION NUMBER: 60/083496  
1 PRIOR FILING DATE: 1998-04-29  
1 PRIOR APPLICATION NUMBER: 60/083499  
1 PRIOR FILING DATE: 1998-04-29  
1 PRIOR APPLICATION NUMBER: 60/083545  
1 PRIOR FILING DATE: 1998-04-29  
1 PRIOR APPLICATION NUMBER: 60/083554

1 PRIOR FILING DATE: 1998-04-29  
1 PRIOR APPLICATION NUMBER: 60/083558  
1 PRIOR FILING DATE: 1998-04-29  
1 PRIOR APPLICATION NUMBER: 60/083559  
1 PRIOR FILING DATE: 1998-04-29  
1 PRIOR APPLICATION NUMBER: 60/083500  
1 PRIOR FILING DATE: 1998-04-29  
1 PRIOR APPLICATION NUMBER: 60/083742  
1 PRIOR FILING DATE: 1998-04-30  
1 PRIOR APPLICATION NUMBER: 60/084366  
1 PRIOR FILING DATE: 1998-05-05  
1 PRIOR APPLICATION NUMBER: 60/084414  
1 PRIOR FILING DATE: 1998-05-06  
1 PRIOR APPLICATION NUMBER: 60/084441  
1 PRIOR FILING DATE: 1998-05-06  
1 PRIOR APPLICATION NUMBER: 60/084637  
1 PRIOR FILING DATE: 1998-05-07  
1 PRIOR APPLICATION NUMBER: 60/084639  
1 PRIOR FILING DATE: 1998-05-07  
1 PRIOR APPLICATION NUMBER: 60/084640  
1 PRIOR FILING DATE: 1998-05-07  
1 PRIOR APPLICATION NUMBER: 60/084598  
1 PRIOR FILING DATE: 1998-05-07  
1 PRIOR APPLICATION NUMBER: 60/084600  
1 PRIOR FILING DATE: 1998-5-07  
1 PRIOR APPLICATION NUMBER: 60/084627  
1 PRIOR FILING DATE: 1998-05-07  
1 PRIOR APPLICATION NUMBER: 60/084643  
1 PRIOR FILING DATE: 1998-05-07  
1 PRIOR APPLICATION NUMBER: 60/085339  
1 PRIOR FILING DATE: 1998-05-13  
1 PRIOR APPLICATION NUMBER: 60/085338  
1 PRIOR FILING DATE: 1998-05-13  
1 PRIOR APPLICATION NUMBER: 60/085323  
1 PRIOR FILING DATE: 1998-05-13  
1 PRIOR APPLICATION NUMBER: 60/085582  
1 PRIOR FILING DATE: 1998-05-15  
1 PRIOR APPLICATION NUMBER: 60/085700  
1 PRIOR FILING DATE: 1998-05-15  
1 PRIOR APPLICATION NUMBER: 60/085689  
1 PRIOR FILING DATE: 1998-05-15  
1 PRIOR APPLICATION NUMBER: 60/085579  
1 PRIOR FILING DATE: 1998-05-15  
1 PRIOR APPLICATION NUMBER: 60/085580  
1 PRIOR FILING DATE: 1998-05-15  
1 PRIOR APPLICATION NUMBER: 60/085573  
1 PRIOR FILING DATE: 1998-05-15  
1 PRIOR APPLICATION NUMBER: 60/085704  
1 PRIOR FILING DATE: 1998-05-15  
1 PRIOR APPLICATION NUMBER: 60/085697

Query Match 90.2%; Score 1667; DB 11; Length 345;  
Best Local Similarity 87.0%; Pred. No. 4.5e-156;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLITLSALAGORTGTRAESNLSSKQLSSDKQNGVQDPHRRVVTTCNGSIIHS 60  
Db 1 MSLFGLLLITLSALAGORQCTQAESNLSSKQFSSNKQNGVQDPQHERITVTSTNGSIIHS 60  
QY 61 PKFPHYPRNMYLVWRLVAVDENVRITQLTDFERFGLDEPDDICKYDFVEVEPSDGSVL 120  
Db 61 PRFPHYPRNTVLVWRLVAVENVMITQLTDFERFGLDEPDDICKYDFVEVEPSDGTIL 120  
QY 121 GRWCGSGTVPKGQTSKGNHIRIRFVSDVEYFPSEPQFCIHYSIMPQVTTTSPSVLPSS 180  
Db 121 GRWCGSGTVPKGQTSKGNHIRIRFVSDVEYFPSEPQFCIHYNIVMQFTTAVSPSVLPSSA 180  
QY 181 LSLDLLNNAVTAFSTLEELIRYLEPRDRMQVDLDSLYKPTWQLLKGAFLYGKXSKVNLNL 240  
Db 181 LPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLKGAFVFGKSRVVDLNL 240  
QY 241 LKEEVKLYSCYPRNFSVSIRELKETDTITFWPGCLLVKRCGNCACCLHNCNCCQVPRK 300



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 21:02:19 ; Search time 169.42 Seconds  
(without alignments)  
1852.926 Million cell updates/sec

Title: US-09-852-209A-7  
Perfect score: 1848  
Sequence: 1 MLLGLLLLTALAGQRTGT.....DVALEHHBECDVCGRNAGG 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents\_AA\_Main:\*

1: /cgn2\_6/ptodata/1/paa/US06 COMB.pcp:\*

2: /cgn2\_6/ptodata/1/paa/US07 COMB.pcp:\*

3: /cgn2\_6/ptodata/1/paa/US08 COMB.pcp:\*

4: /cgn2\_6/ptodata/1/paa/US09 COMB.pcp:\*

5: /cgn2\_6/ptodata/1/paa/US10 COMB.pcp:\*

6: /cgn2\_6/ptodata/1/paa/US11 COMB.pcp:\*

7: /cgn2\_6/ptodata/1/paa/US12 COMB.pcp:\*

8: /cgn2\_6/ptodata/1/paa/US13 COMB.pcp:\*

9: /cgn2\_6/ptodata/1/paa/US14 COMB.pcp:\*

10: /cgn2\_6/ptodata/1/paa/US15 COMB.pcp:\*

11: /cgn2\_6/ptodata/1/paa/US16 COMB.pcp:\*

12: /cgn2\_6/ptodata/1/paa/US17 COMB.pcp:\*

13: /cgn2\_6/ptodata/1/paa/US18 COMB.pcp:\*

14: /cgn2\_6/ptodata/1/paa/US19 COMB.pcp:\*

15: /cgn2\_6/ptodata/1/paa/US20 COMB.pcp:\*

16: /cgn2\_6/ptodata/1/paa/US21 COMB.pcp:\*

17: /cgn2\_6/ptodata/1/paa/US22 COMB.pcp:\*

18: /cgn2\_6/ptodata/1/paa/US23 COMB.pcp:\*

19: /cgn2\_6/ptodata/1/paa/US24 COMB.pcp:\*

20: /cgn2\_6/ptodata/1/paa/US25 COMB.pcp:\*

21: /cgn2\_6/ptodata/1/paa/US26 COMB.pcp:\*

22: /cgn2\_6/ptodata/1/paa/US27 COMB.pcp:\*

23: /cgn2\_6/ptodata/1/paa/US28 COMB.pcp:\*

24: /cgn2\_6/ptodata/1/paa/US29 COMB.pcp:\*

25: /cgn2\_6/ptodata/1/paa/US30 COMB.pcp:\*

26: /cgn2\_6/ptodata/1/paa/US31 COMB.pcp:\*

27: /cgn2\_6/ptodata/1/paa/US32 COMB.pcp:\*

28: /cgn2\_6/ptodata/1/paa/US33 COMB.pcp:\*

29: /cgn2\_6/ptodata/1/paa/US34 COMB.pcp:\*

30: /cgn2\_6/ptodata/1/paa/US35 COMB.pcp:\*

31: /cgn2\_6/ptodata/1/paa/US36 COMB.pcp:\*

32: /cgn2\_6/ptodata/1/paa/US37 COMB.pcp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1848	100.0	345	1	PCT-US99-22668-7 Sequence 7, Appli

2	1848	100.0	345	17	US-09-304-216-35	Sequence 35, Appl
3	1848	100.0	345	18	US-09-410-349A-7	Sequence 7, Appli
4	1848	100.0	345	19	US-09-540-703-4	Sequence 4, Appli
5	1848	100.0	345	20	US-09-541-752-43	Sequence 43, Appli
6	1848	100.0	345	20	US-09-695-121-4	Sequence 43, Appli
7	1848	100.0	345	21	US-09-706-968-43	Sequence 43, Appli
8	1848	100.0	345	23	US-09-818-943-2	Sequence 2, Appli
9	1848	100.0	345	23	US-09-823-033-4	Sequence 4, Appli
10	1848	100.0	345	23	US-09-852-209-7	Sequence 7, Appli
11	1848	100.0	345	23	US-09-852-209A-7	Sequence 7, Appli
12	1848	100.0	345	27	US-10-131-600-7	Sequence 7, Appli
13	1848	100.0	345	27	US-10-139-583-43	Sequence 43, Appli
14	1848	100.0	345	28	US-10-264-361-4	Sequence 4, Appli
15	1848	100.0	345	29	US-10-303-997B-7	Sequence 7, Appli
16	1667	90.2	345	1	PCT-US01-43523-286	Sequence 286, App
17	1667	90.2	345	1	PCT-US02-24563-386	Sequence 386, App
18	1667	90.2	345	1	PCT-US03-04213-34	Sequence 34, Appli
19	1667	90.2	345	1	PCT-US99-01574-2	Sequence 2, Appli
20	1667	90.2	345	1	PCT-US99-15783-4	Sequence 4, Appli
21	1667	90.2	345	1	PCT-US99-31025-2	Sequence 2, Appli
22	1667	90.2	345	15	US-09-184-216-2	Sequence 2, Appli
23	1667	90.2	345	16	US-09-207-120-2	Sequence 2, Appli
24	1667	90.2	345	16	US-09-223-546-2	Sequence 2, Appli
25	1667	90.2	345	16	US-09-237-705-2	Sequence 2, Appli
26	1667	90.2	345	16	US-09-267-213-2	Sequence 2, Appli
27	1667	90.2	345	17	US-09-304-216-33	Sequence 33, Appli
28	1667	90.2	345	17	US-09-380-138-488	Sequence 488, App
29	1667	90.2	345	18	US-09-458-690A-4	Sequence 4, Appli
30	1667	90.2	345	18	US-09-471-179-2	Sequence 2, Appli
31	1667	90.2	345	19	US-09-540-703-2	Sequence 2, Appli
32	1667	90.2	345	19	US-09-541-752-2	Sequence 2, Appli
33	1667	90.2	345	19	US-09-599-596-2	Sequence 2, Appli
34	1667	90.2	345	20	US-09-662-783-24	Sequence 24, Appli
35	1667	90.2	345	20	US-09-685-330-24	Sequence 24, Appli
36	1667	90.2	345	20	US-09-688-312-51	Sequence 51, Appli
37	1667	90.2	345	20	US-09-695-121-2	Sequence 2, Appli
38	1667	90.2	345	21	US-09-706-968-2	Sequence 2, Appli
39	1667	90.2	345	21	US-09-723-749-2	Sequence 2, Appli
40	1667	90.2	345	22	US-09-795-006A-149	Sequence 149, App
41	1667	90.2	345	22	US-09-796-753-6	Sequence 6, Appli
42	1667	90.2	345	23	US-09-823-033-2	Sequence 2, Appli
43	1667	90.2	345	24	US-09-918-585A-488	Sequence 488, App
44	1667	90.2	345	24	US-09-923-995-4	Sequence 4, Appli
45	1667	90.2	345	24	US-09-929-404-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

PCT-US99-22668-7

; Sequence 7, Application PC/TUS9922668B

; GENERAL INFORMATION:

; APPLICANT: LUDWIG INSTITUTE FOR CANCER RESEARCH

; APPLICANT: HELSINKI UNIVERSITY LICENSING LTD.

; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C,

; TITLE OF INVENTION: THEREFOR, AND USES THEREOF

; FILE REFERENCE: PCT/US99/22669-LUDWIG INST FOR CANCER

; CURRENT APPLICATION NUMBER: PCT/US99/22668B

; CURRENT FILING DATE: 1999-09-30

; EARLIER APPLICATION NUMBER: 60/102,461

; EARLIER FILING DATE: 1998-09-30

; EARLIER APPLICATION NUMBER: 60/108,109

; EARLIER FILING DATE: 1998-11-12

; EARLIER APPLICATION NUMBER: 60/110,749

; EARLIER FILING DATE: 1998-12-03

; EARLIER APPLICATION NUMBER: 60/113,002

; EARLIER FILING DATE: 1998-12-18

; EARLIER APPLICATION NUMBER: 60/135,426

; EARLIER FILING DATE: 1999-05-21

; EARLIER APPLICATION NUMBER: 60/144,022

; NUMBER OF SEQ ID NOS: 39

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 7

LENGTH: 345

TYPE: PR

ORGANISM: Murinae gen. sp.

CT-US99-22668-7

Query Match 100.0%; Score 1848; DB 1; Length 345;  
Best Local Similarity 100.0%; Pred. No. 3.2e-175;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 1 MLLGLLLTSLAGQRTGTRAESNLSSKQLSSDKQNGVQDPRHVRVTTISNGSIHS 60  
DB 1 MLLGLLLTSLAGQRTGTRAESNLSSKQLSSDKQNGVQDPRHVRVTTISNGSIHS 60  
QY 61 PKPHTYPRNMVLRVAVDENVRQLTDFRFGLEDPEDDICKYDFVEVEEPPSDGSLV 120  
DB 61 PKPHTYPRNMVLRVAVDENVRQLTDFRFGLEDPEDDICKYDFVEVEEPPSDGSLV 120  
QY 121 GRWCGSTVPGKQTSKGNHRIIRFVSDYFPPSEPGFCIHYSIIMPQVTTETSPSVLPSS 180  
DB 121 GRWCGSTVPGKQTSKGNHRIIRFVSDYFPPSEPGFCIHYSIIMPQVTTETSPSVLPSS 180  
QY 181 LSLDLNNAVTAFSTLEELIRYLEPDRMQVDLSLYKPTWLLGKAFLYGKSKVNNL 240  
DB 181 LSLDLNNAVTAFSTLEELIRYLEPDRMQVDLSLYKPTWLLGKAFLYGKSKVNNL 240  
QY 241 LKEEVKLYSCTPRNFSVIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPK 300  
DB 241 LKEEVKLYSCTPRNFSVIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPK 300  
QY 301 VTKKHEVLQLRPKTGKGLHLSLTDVALEHHEBCDCVCRNAGG 345  
DB 301 VTKKHEVLQLRPKTGKGLHLSLTDVALEHHEBCDCVCRNAGG 345

## RESULT 2

US-09-304-216-35  
; Sequence 35, Application US/09304216  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4  
; FILE REFERENCE: 99-19X  
; CURRENT FILING DATE: 1999-05-03  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 35  
; LENGTH: 345  
; TYPE: PR  
; ORGANISM: Mus musculus

US-09-304-216-35

Query Match 100.0%; Score 1848; DB 17; Length 345;  
Best Local Similarity 100.0%; Pred. No. 3.2e-175;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTSLAGQRTGTRAESNLSSKQLSSDKQNGVQDPRHVRVTTISNGSIHS 60  
DB 1 MLLGLLLTSLAGQRTGTRAESNLSSKQLSSDKQNGVQDPRHVRVTTISNGSIHS 60  
QY 61 PKPHTYPRNMVLRVAVDENVRQLTDFRFGLEDPEDDICKYDFVEVEEPPSDGSLV 120  
DB 61 PKPHTYPRNMVLRVAVDENVRQLTDFRFGLEDPEDDICKYDFVEVEEPPSDGSLV 120  
QY 121 GRWCGSTVPGKQTSKGNHRIIRFVSDYFPPSEPGFCIHYSIIMPQVTTETSPSVLPSS 180  
DB 121 GRWCGSTVPGKQTSKGNHRIIRFVSDYFPPSEPGFCIHYSIIMPQVTTETSPSVLPSS 180  
QY 181 LSLDLNNAVTAFSTLEELIRYLEPDRMQVDLSLYKPTWLLGKAFLYGKSKVNNL 240

DB 181 LSLDLNNAVTAFSTLEELIRYLEPDRMQVDLSLYKPTWLLGKAFLYGKSKVNNL 240  
QY 241 LKEEVKLYSCTPRNFSVIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPK 300  
DB 241 LKEEVKLYSCTPRNFSVIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPK 300  
QY 301 VTKKHEVLQLRPKTGKGLHLSLTDVALEHHEBCDCVCRNAGG 345  
DB 301 VTKKHEVLQLRPKTGKGLHLSLTDVALEHHEBCDCVCRNAGG 345

## RESULT 3

US-09-410-349A-7  
; Sequence 7, Application US/09410349A  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: AASE, Karin  
; APPLICANT: LEE, Xuri  
; APPLICANT: PONTEN, Annica  
; APPLICANT: UTELA, Marko  
; APPLICANT: ALITALO, Kari  
; APPLICANT: OESTMAN, Arne  
; APPLICANT: HELDIN, Carl-Henrik  
; APPLICANT: BETSHOLTZ, Christer  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING  
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF  
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740  
; CURRENT APPLICATION NUMBER: US/09/410,349A  
; CURRENT FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: 60/108,109  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: 60/110,749  
; PRIOR FILING DATE: 1998-12-03  
; PRIOR APPLICATION NUMBER: 60/113,002  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: 60/135,426  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: 60/144,022  
; PRIOR FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 345  
; TYPE: PR  
; ORGANISM: Murinae gen. sp.

US-09-410-349A-7

Query Match 100.0%; Score 1848; DB 18; Length 345;  
Best Local Similarity 100.0%; Pred. No. 3.2e-175;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTSLAGQRTGTRAESNLSSKQLSSDKQNGVQDPRHVRVTTISNGSIHS 60  
DB 1 MLLGLLLTSLAGQRTGTRAESNLSSKQLSSDKQNGVQDPRHVRVTTISNGSIHS 60  
QY 61 PKPHTYPRNMVLRVAVDENVRQLTDFRFGLEDPEDDICKYDFVEVEEPPSDGSLV 120  
DB 61 PKPHTYPRNMVLRVAVDENVRQLTDFRFGLEDPEDDICKYDFVEVEEPPSDGSLV 120  
QY 121 GRWCGSTVPGKQTSKGNHRIIRFVSDYFPPSEPGFCIHYSIIMPQVTTETSPSVLPSS 180  
DB 121 GRWCGSTVPGKQTSKGNHRIIRFVSDYFPPSEPGFCIHYSIIMPQVTTETSPSVLPSS 180  
QY 181 LSLDLNNAVTAFSTLEELIRYLEPDRMQVDLSLYKPTWLLGKAFLYGKSKVNNL 240  
DB 181 LSLDLNNAVTAFSTLEELIRYLEPDRMQVDLSLYKPTWLLGKAFLYGKSKVNNL 240  
QY 241 LKEEVKLYSCTPRNFSVIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPK 300  
DB 241 LKEEVKLYSCTPRNFSVIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPK 300  
QY 301 VTKKHEVLQLRPKTGKGLHLSLTDVALEHHEBCDCVCRNAGG 345



Db 301 VTKYHEVLQRPKTVGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345

## RESULT 4

US-09-540-703-4

; Sequence 4, Application US/09540703  
; GENERAL INFORMATION:  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Gilbertson, Debra G.  
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,  
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE  
; FILE REFERENCE: 00-12X  
; CURRENT APPLICATION NUMBER: US/09/540,703  
; CURRENT FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-540-703-4

Query Match 100.0%; Score 1848; DB 19; Length 345;  
Best Local Similarity 100.0%; Pred. No. 3.2e-175;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLITLSALAGORTGTRAESNLSSKQLSSDKEQNGVQDPHRRVVTISGNGSIHS 60  
DB 1 MLLGLLLITLSALAGORTGTRAESNLSSKQLSSDKEQNGVQDPHRRVVTISGNGSIHS 60  
QY 61 PKFPHYPRNMLVWRLVAVDENVRIQLTFDRFGLDEPDDICKYDFVEVEEPPSDGSVL 120  
DB 61 PKFPHYPRNMLVWRLVAVDENVRIQLTFDRFGLDEPDDICKYDFVEVEEPPSDGSVL 120  
QY 121 GRWCSGTVPGKQTSKGNHIRIRFVSDVEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180  
DB 121 GRWCSGTVPGKQTSKGNHIRIRFVSDVEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180  
QY 181 LSLDLINNAVTAFTSLLEELIRYLEPDRMQVLDLSLYKPTWQLLGKAFLYGKSKVNNLNL 240  
DB 181 LSLDLINNAVTAFTSLLEELIRYLEPDRMQVLDLSLYKPTWQLLGKAFLYGKSKVNNLNL 240  
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNCACCLHNCNECCVPRK 300  
DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNCACCLHNCNECCVPRK 300  
QY 301 VTKYHEVLQRPKTVGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
DB 301 VTKYHEVLQRPKTVGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345

## RESULT 5

US-09-541-752-43

; Sequence 43, Application US/09541752  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoenaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60C1  
; CURRENT APPLICATION NUMBER: US/09/541,752  
; CURRENT FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 43  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-541-752-43

Query Match 100.0%; Score 1848; DB 19; Length 345;  
Best Local Similarity 100.0%; Pred. No. 3.2e-175;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLITLSALAGORTGTRAESNLSSKQLSSDKEQNGVQDPHRRVVTISGNGSIHS 60  
DB 1 MLLGLLLITLSALAGORTGTRAESNLSSKQLSSDKEQNGVQDPHRRVVTISGNGSIHS 60  
QY 61 PKFPHYPRNMLVWRLVAVDENVRIQLTFDRFGLDEPDDICKYDFVEVEEPPSDGSVL 120  
DB 61 PKFPHYPRNMLVWRLVAVDENVRIQLTFDRFGLDEPDDICKYDFVEVEEPPSDGSVL 120  
QY 121 GRWCSGTVPGKQTSKGNHIRIRFVSDVEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180  
DB 121 GRWCSGTVPGKQTSKGNHIRIRFVSDVEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180  
QY 181 LSLDLINNAVTAFTSLLEELIRYLEPDRMQVLDLSLYKPTWQLLGKAFLYGKSKVNNLNL 240  
DB 181 LSLDLINNAVTAFTSLLEELIRYLEPDRMQVLDLSLYKPTWQLLGKAFLYGKSKVNNLNL 240  
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNCACCLHNCNECCVPRK 300  
DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNCACCLHNCNECCVPRK 300  
QY 301 VTKYHEVLQRPKTVGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
DB 301 VTKYHEVLQRPKTVGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345

## RESULT 6

US-09-695-121-4

; Sequence 4, Application US/09695121  
; GENERAL INFORMATION:  
; APPLICANT: Gilbertson, Debra G.  
; TITLE OF INVENTION: METHOD OF TREATING FIBROSIS  
; FILE REFERENCE: 00-53  
; CURRENT APPLICATION NUMBER: US/09/695,121  
; CURRENT FILING DATE: 2000-10-23  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-695-121-4

Query Match 100.0%; Score 1848; DB 20; Length 345;  
Best Local Similarity 100.0%; Pred. No. 3.2e-175;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLITLSALAGORTGTRAESNLSSKQLSSDKEQNGVQDPHRRVVTISGNGSIHS 60  
DB 1 MLLGLLLITLSALAGORTGTRAESNLSSKQLSSDKEQNGVQDPHRRVVTISGNGSIHS 60  
QY 61 PKFPHYPRNMLVWRLVAVDENVRIQLTFDRFGLDEPDDICKYDFVEVEEPPSDGSVL 120  
DB 61 PKFPHYPRNMLVWRLVAVDENVRIQLTFDRFGLDEPDDICKYDFVEVEEPPSDGSVL 120  
QY 121 GRWCSGTVPGKQTSKGNHIRIRFVSDVEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180  
DB 121 GRWCSGTVPGKQTSKGNHIRIRFVSDVEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180  
QY 181 LSLDLINNAVTAFTSLLEELIRYLEPDRMQVLDLSLYKPTWQLLGKAFLYGKSKVNNLNL 240  
DB 181 LSLDLINNAVTAFTSLLEELIRYLEPDRMQVLDLSLYKPTWQLLGKAFLYGKSKVNNLNL 240  
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNCACCLHNCNECCVPRK 300  
DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGGNCACCLHNCNECCVPRK 300  
QY 301 VTKYHEVLQRPKTVGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
DB 301 VTKYHEVLQRPKTVGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345

301 VTKYHEVLQRPKTVGKGLHKSITDVALEHHEBCDCVCRNAGG 345

Db

RESULT 7

US-09-706-968-43  
; Sequence 43, Application US/09706968  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3  
; FILE REFERENCE: 98-60CI  
; CURRENT APPLICATION NUMBER: US/09/706,968  
; CURRENT FILING DATE: 2000-11-06  
; PRIOR APPLICATION NUMBER: US/09/541,752  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 43  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-706-968-43

Query Match 100.0%; Score 1848; DB 21; Length 345;  
Best Local Similarity 100.0%; Pred. No. 3.2e-175;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTTSALAGORTGTRAESNLSSKLQSSDKQNGVQDPRHVVTTISNGSIHS 60  
Db 1 MLLGLLLTTSALAGORTGTRAESNLSSKLQSSDKQNGVQDPRHVVTTISNGSIHS 60  
QY 61 PKFPHYPRNMVLMVRLVAVDENVRILTDFRFGLEDPEDDICKYDFVEVEPSDGSVL 120  
Db 61 PKFPHYPRNMVLMVRLVAVDENVRILTDFRFGLEDPEDDICKYDFVEVEPSDGSVL 120  
QY 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDYFPPSPGFCIHYSIIMPQVTTTSPSVLPSS 180  
Db 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDYFPPSPGFCIHYSIIMPQVTTTSPSVLPSS 180  
QY 181 LSLDLLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTWLLGKAFLYGKSKVNNL 240  
Db 181 LSLDLLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTWLLGKAFLYGKSKVNNL 240  
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPRK 300  
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPRK 300  
QY 301 VTKYHEVLQRPKTVGKGLHKSITDVALEHHEBCDCVCRNAGG 345  
Db 301 VTKYHEVLQRPKTVGKGLHKSITDVALEHHEBCDCVCRNAGG 345

RESULT 8

US-09-818-943-2  
; Sequence 2, Application US/09818943  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: LI, Xuri  
; APPLICANT: PONTEN, Annica  
; APPLICANT: AASE, Karin  
; APPLICANT: LI, Hong  
; TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMALS EXPRESSING PLATELET-DERIVED GROWTH F  
; FILE REFERENCE: 1064/48487  
; CURRENT APPLICATION NUMBER: US/09/818,943  
; CURRENT FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: US 60/192,507  
; PRIOR FILING DATE: 2000-03-28

; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Murinae gen. sp.  
US-09-818-943-2

Query Match 100.0%; Score 1848; DB 23; Length 345;  
Best Local Similarity 100.0%; Pred. No. 3.2e-175;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTTSALAGORTGTRAESNLSSKLQSSDKQNGVQDPRHVVTTISNGSIHS 60  
Db 1 MLLGLLLTTSALAGORTGTRAESNLSSKLQSSDKQNGVQDPRHVVTTISNGSIHS 60  
QY 61 PKFPHYPRNMVLMVRLVAVDENVRILTDFRFGLEDPEDDICKYDFVEVEPSDGSVL 120  
Db 61 PKFPHYPRNMVLMVRLVAVDENVRILTDFRFGLEDPEDDICKYDFVEVEPSDGSVL 120  
QY 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDYFPPSPGFCIHYSIIMPQVTTTSPSVLPSS 180  
Db 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDYFPPSPGFCIHYSIIMPQVTTTSPSVLPSS 180  
QY 181 LSLDLLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTWLLGKAFLYGKSKVNNL 240  
Db 181 LSLDLLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTWLLGKAFLYGKSKVNNL 240  
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPRK 300  
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPRK 300  
QY 301 VTKYHEVLQRPKTVGKGLHKSITDVALEHHEBCDCVCRNAGG 345  
Db 301 VTKYHEVLQRPKTVGKGLHKSITDVALEHHEBCDCVCRNAGG 345

RESULT 9

US-09-823-033-4  
; Sequence 4, Application US/09823033  
; GENERAL INFORMATION:  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Gilbertson, Debra G.  
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,  
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE  
; FILE REFERENCE: 00-12  
; CURRENT APPLICATION NUMBER: US/09/823,033  
; CURRENT FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-823-033-4

Query Match 100.0%; Score 1848; DB 23; Length 345;  
Best Local Similarity 100.0%; Pred. No. 3.2e-175;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTTSALAGORTGTRAESNLSSKLQSSDKQNGVQDPRHVVTTISNGSIHS 60  
Db 1 MLLGLLLTTSALAGORTGTRAESNLSSKLQSSDKQNGVQDPRHVVTTISNGSIHS 60  
QY 61 PKFPHYPRNMVLMVRLVAVDENVRILTDFRFGLEDPEDDICKYDFVEVEPSDGSVL 120  
Db 61 PKFPHYPRNMVLMVRLVAVDENVRILTDFRFGLEDPEDDICKYDFVEVEPSDGSVL 120  
QY 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDYFPPSPGFCIHYSIIMPQVTTTSPSVLPSS 180  
Db 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDYFPPSPGFCIHYSIIMPQVTTTSPSVLPSS 180  
QY 181 LSLDLLNNAVTAFTLEELIRYLEPDRQVLDLSLYKPTWLLGKAFLYGKSKVNNL 240

```
Db 181 LSLDLLNNAVAFSTLEBELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVVNLNL 240
Qy 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
Qy 301 VTKKYHEVLQRPKTVGKGLHSLTDVALEHHEECDCVCRGNAGG 345
Db 301 VTKKYHEVLQRPKTVGKGLHSLTDVALEHHEECDCVCRGNAGG 345

RESULT 10
US-09-852-209-7
; Sequence 7, Application US/09852209
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: BETSHOLTZ, Christer
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
; CURRENT APPLICATION NUMBER: US/09/852,209
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/144,022
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 345
; TYPE: PRN
; ORGANISM: Murinae gen. sp.
US-09-852-209-7

Query Match 100.0%; Score 1848; DB 23; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.2e-175;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLGLLLLTALAGORTGTGAESNLSSKQLQSSDKQNGVQDPRHVRVTTISGNGSIHS 60
Db 1 MLLGLLLLTALAGORTGTGAESNLSSKQLQSSDKQNGVQDPRHVRVTTISGNGSIHS 60
Qy 61 PKFPHYPRNMVWLWRLVAVDENVRILQTFDRRFGLEDPEDDICKYDFVEVEEPSDGSVL 120
Db 61 PKFPHYPRNMVWLWRLVAVDENVRILQTFDRRFGLEDPEDDICKYDFVEVEEPSDGSVL 120
Qy 121 GRWCSSGTVPGKQTSKGNHIRIRFVSDVEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Db 121 GRWCSSGTVPGKQTSKGNHIRIRFVSDVEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Qy 181 LSLDLLNNAVAFSTLEBELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVVNLNL 240
Db 181 LSLDLLNNAVAFSTLEBELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVVNLNL 240
Qy 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
Qy 301 VTKKYHEVLQRPKTVGKGLHSLTDVALEHHEECDCVCRGNAGG 345
Db 301 VTKKYHEVLQRPKTVGKGLHSLTDVALEHHEECDCVCRGNAGG 345

RESULT 12
US-10-131-600-7
; Sequence 7, Application US/10131600
; GENERAL INFORMATION:
```

```
Db 301 VTKKYHEVLQRPKTVGKGLHSLTDVALEHHEECDCVCRGNAGG 345
Qy 301 VTKKYHEVLQRPKTVGKGLHSLTDVALEHHEECDCVCRGNAGG 345

RESULT 11
US-09-852-209A-7
; Sequence 7, Application US/09852209A
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: BETSHOLTZ, Christer
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
; CURRENT APPLICATION NUMBER: US/09/852,209A
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/144,022
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 345
; TYPE: PRN
; ORGANISM: Murinae gen. sp.
US-09-852-209A-7

Query Match 100.0%; Score 1848; DB 23; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.2e-175;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLGLLLLTALAGORTGTGAESNLSSKQLQSSDKQNGVQDPRHVRVTTISGNGSIHS 60
Db 1 MLLGLLLLTALAGORTGTGAESNLSSKQLQSSDKQNGVQDPRHVRVTTISGNGSIHS 60
Qy 61 PKFPHYPRNMVWLWRLVAVDENVRILQTFDRRFGLEDPEDDICKYDFVEVEEPSDGSVL 120
Db 61 PKFPHYPRNMVWLWRLVAVDENVRILQTFDRRFGLEDPEDDICKYDFVEVEEPSDGSVL 120
Qy 121 GRWCSSGTVPGKQTSKGNHIRIRFVSDVEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Db 121 GRWCSSGTVPGKQTSKGNHIRIRFVSDVEYFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Qy 181 LSLDLLNNAVAFSTLEBELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVVNLNL 240
Db 181 LSLDLLNNAVAFSTLEBELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVVNLNL 240
Qy 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
Db 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
Qy 301 VTKKYHEVLQRPKTVGKGLHSLTDVALEHHEECDCVCRGNAGG 345
Db 301 VTKKYHEVLQRPKTVGKGLHSLTDVALEHHEECDCVCRGNAGG 345

RESULT 12
US-10-131-600-7
; Sequence 7, Application US/10131600
; GENERAL INFORMATION:
```

APPLICANT: ERIKSSON, Ulf  
 APPLICANT: AASE, Karin  
 APPLICANT: LEE, Xuri  
 APPLICANT: PONTEN, Annica  
 APPLICANT: UUTELA, Marko  
 APPLICANT: ALITALO, Kari  
 APPLICANT: OESTMAN, Arne  
 APPLICANT: HELDIN, Carl-Henrik  
 APPLICANT: BERTSHOLTZ, Christel  
 TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING  
 TITLE OF INVENTION: THEREOF, AND USES THEREOF  
 FILE REFERENCE: 09-410349-Eriksson et al-1064-44740  
 CURRENT APPLICATION NUMBER: US/10/131,600  
 PRIOR FILING DATE: 2002-04-25  
 RIOR APPLICATION NUMBER: US/09/410,349  
 RIOR FILING DATE: 1999-09-30  
 RIOR APPLICATION NUMBER: 60/108,109  
 RIOR FILING DATE: 1998-11-12  
 RIOR APPLICATION NUMBER: 60/110,749  
 RIOR FILING DATE: 1998-12-03  
 RIOR APPLICATION NUMBER: 60/113,002  
 RIOR FILING DATE: 1998-12-18  
 RIOR APPLICATION NUMBER: 60/135,426  
 RIOR FILING DATE: 1999-05-21  
 RIOR APPLICATION NUMBER: 60/144,022  
 RIOR FILING DATE: 1999-07-15  
 NUMBER OF SEQ ID NOS: 39  
 SOFTWARE: Patent In Ver. 2.0  
 SEQ ID NO 7  
 LENGTH: 345  
 TYPE: PRT  
 ORGANISM: Murinae gen. sp.  
 -10-131-600-7

Query Match 100.0%; Score 1848; DB 27; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-175;  
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 MLLGLLLTSALAGQRTGTRAESNLSSKLQSSDKEQNGVQDPRHERVVTISGNSIHS 60  
 1 MLLGLLLTSALAGQRTGTRAESNLSSKLQSSDKEQNGVQDPRHERVVTISGNSIHS 60  
 61 PKFPHYPRNNVLRVAVDENVRITQTFDERFGLDEPDDICKYDFVEVEPSDGSVL 120  
 61 PKFPHYPRNNVLRVAVDENVRITQTFDERFGLDEPDDICKYDFVEVEPSDGSVL 120  
 121 GRWCSGTVPGKQTSKGNHIRFVSDYFPSPGFCIHYSIIMPOVTETTSVLPSS 180  
 121 GRWCSGTVPGKQTSKGNHIRFVSDYFPSPGFCIHYSIIMPOVTETTSVLPSS 180  
 181 LSLLNNNAVTAFTSTLEELIRYLEPDRQVLDLSYKPTWQLLKAFLYGKSKVNNL 240  
 181 LSLLNNNAVTAFTSTLEELIRYLEPDRQVLDLSYKPTWQLLKAFLYGKSKVNNL 240  
 241 LKEEVLYSCTPRNFSVSIREEKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300  
 241 LKEEVLYSCTPRNFSVSIREEKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300  
 301 VTKKHEVLQRLPRTGVKGLHKSITDVALEHHEECDCVCRGNAGG 345  
 301 VTKKHEVLQRLPRTGVKGLHKSITDVALEHHEECDCVCRGNAGG 345

RESULT 13  
 US-10-139-583-43  
 ; Sequence 43, Application US/10139583  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gao, Zeren  
 ; APPLICANT: Hart, Charles E.  
 ; APPLICANT: Piddington, Christopher S.  
 ; APPLICANT: Sheppard, Paul O.  
 ; APPLICANT: Shoemaker, Kimberly E.  
 ; APPLICANT: Gilbertson, Debra G.

APPLICANT: West, James W.  
 TITLE OF INVENTION: GROWTH FACTOR HOMOLOGY ZVSQF3  
 FILE REFERENCE: 98-60  
 CURRENT APPLICATION NUMBER: US/10/139,583  
 CURRENT FILING DATE: 2002-05-02  
 PRIOR APPLICATION NUMBER: 09/457,066  
 PRIOR FILING DATE: 1999-12-07  
 NUMBER OF SEQ ID NOS: 50  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 43  
 LENGTH: 345  
 TYPE: PRT  
 ORGANISM: Mus musculus  
 US-10-139-583-43

Query Match 100.0%; Score 1848; DB 27; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-175;  
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 MLLGLLLTSALAGQRTGTRAESNLSSKLQSSDKEQNGVQDPRHERVVTISGNSIHS 60  
 1 MLLGLLLTSALAGQRTGTRAESNLSSKLQSSDKEQNGVQDPRHERVVTISGNSIHS 60  
 61 PKFPHYPRNNVLRVAVDENVRITQTFDERFGLDEPDDICKYDFVEVEPSDGSVL 120  
 61 PKFPHYPRNNVLRVAVDENVRITQTFDERFGLDEPDDICKYDFVEVEPSDGSVL 120  
 121 GRWCSGTVPGKQTSKGNHIRFVSDYFPSPGFCIHYSIIMPOVTETTSVLPSS 180  
 121 GRWCSGTVPGKQTSKGNHIRFVSDYFPSPGFCIHYSIIMPOVTETTSVLPSS 180  
 181 LSLLNNNAVTAFTSTLEELIRYLEPDRQVLDLSYKPTWQLLKAFLYGKSKVNNL 240  
 181 LSLLNNNAVTAFTSTLEELIRYLEPDRQVLDLSYKPTWQLLKAFLYGKSKVNNL 240  
 241 LKEEVLYSCTPRNFSVSIREEKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300  
 241 LKEEVLYSCTPRNFSVSIREEKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPRK 300  
 301 VTKKHEVLQRLPRTGVKGLHKSITDVALEHHEECDCVCRGNAGG 345  
 301 VTKKHEVLQRLPRTGVKGLHKSITDVALEHHEECDCVCRGNAGG 345

RESULT 14  
 US-10-264-361-4  
 ; Sequence 4, Application US/10264361  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gilbertson, Debra G.  
 ; TITLE OF INVENTION: METHOD OF TREATING FIBROSIS  
 ; FILE REFERENCE: 00-53  
 ; CURRENT APPLICATION NUMBER: US/10/264,361  
 ; CURRENT FILING DATE: 2002-10-03  
 ; PRIOR APPLICATION NUMBER: US/09/695,121  
 ; PRIOR FILING DATE: 2000-10-23  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 4  
 ; LENGTH: 345  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-10-264-361-4

Query Match 100.0%; Score 1848; DB 28; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-175;  
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 MLLGLLLTSALAGQRTGTRAESNLSSKLQSSDKEQNGVQDPRHERVVTISGNSIHS 60  
 1 MLLGLLLTSALAGQRTGTRAESNLSSKLQSSDKEQNGVQDPRHERVVTISGNSIHS 60  
 61 PKFPHYPRNNVLRVAVDENVRITQTFDERFGLDEPDDICKYDFVEVEPSDGSVL 120

Db 61 PKPHTYPRNMVLRVAVDENVRIOQLTFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120  
QY 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDYFFSEPGFCIHYSIIMPQVTTETSPSVLPSS 180  
Db 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDYFFSEPGFCIHYSIIMPQVTTETSPSVLPSS 180  
QY 181 LSLDLLNNAVTAFTLEBLIRYLEPDRWQVDLSLYKPTWQLLGKAFLYGKSKVYNLNL 240  
Db 181 LSLDLLNNAVTAFTLEBLIRYLEPDRWQVDLSLYKPTWQLLGKAFLYGKSKVYNLNL 240  
QY 241 LKEEVKLYSCTPRNFSVSIRELKKTDTFWPGCLLVKRCGNCACCLHNCNECCVPRK 300  
Db 241 LKEEVKLYSCTPRNFSVSIRELKKTDTFWPGCLLVKRCGNCACCLHNCNECCVPRK 300  
QY 301 VTKKYHEVLQLRPKTGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKKYHEVLQLRPKTGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345

## RESULT 15

US-10-303-997B-7  
; Sequence 7, Application US/10303997B  
; GENERAL INFORMATION:  
; APPLICANT: LI, Xuri  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: CARMELIET, Peter  
; APPLICANT: COLLUM, Desire  
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR MODULATING VASCULOGENESIS AND ANGIOGEN  
; FILE REFERENCE: 029065.44740C3  
; CURRENT APPLICATION NUMBER: US/10/303,997B  
; CURRENT FILING DATE: 2002-11-26  
; PRIOR APPLICATION NUMBER: US 09/410,349  
; PRIOR FILING DATE: 1999-09-30  
; PRIOR APPLICATION NUMBER: US 60/102,461  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: US 60/108,109  
; PRIOR FILING DATE: 1998-11-12  
; PRIOR APPLICATION NUMBER: US 60/110,749  
; PRIOR FILING DATE: 1998-12-03  
; PRIOR APPLICATION NUMBER: US 60/113,002  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: US 60/135,426  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: US 60/144,022  
; PRIOR FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Murinae gen. sp.  
US-10-303-997B-7

Query Match 100.0%; Score 1848; DB 29; Length 345;  
Best Local Similarity 100.0%; Pred. No. 3.2e-175;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLLGLLLLTALAGQRTGTRAESNLSSKLQSSDKQNGQDPRHERVVTISNGSIHS 60  
Db 1 MLLGLLLLTALAGQRTGTRAESNLSSKLQSSDKQNGQDPRHERVVTISNGSIHS 60  
QY 61 PKPHTYPRNMVLRVAVDENVRIOQLTFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120  
Db 61 PKPHTYPRNMVLRVAVDENVRIOQLTFDERFGLDEPDDICKYDFVEVEEPSDGSVL 120  
QY 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDYFFSEPGFCIHYSIIMPQVTTETSPSVLPSS 180  
Db 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDYFFSEPGFCIHYSIIMPQVTTETSPSVLPSS 180  
QY 181 LSLDLLNNAVTAFTLEBLIRYLEPDRWQVDLSLYKPTWQLLGKAFLYGKSKVYNLNL 240  
Db 181 LSLDLLNNAVTAFTLEBLIRYLEPDRWQVDLSLYKPTWQLLGKAFLYGKSKVYNLNL 240

QY 241 LKEEVKLYSCTPRNFSVSIRELKKTDTFWPGCLLVKRCGNCACCLHNCNECCVPRK 300  
Db 241 LKEEVKLYSCTPRNFSVSIRELKKTDTFWPGCLLVKRCGNCACCLHNCNECCVPRK 300  
QY 301 VTKKYHEVLQLRPKTGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKKYHEVLQLRPKTGKGLHKSLLTDVALEHHEECDCVCRGNAGG 345

Search completed: November 25, 2003, 21:14:50  
Job time : 170.753 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 21:02:59 ; Search time 13.6905 Seconds  
(without alignments)  
1293.384 Million cell updates/sec

Title: US-09-852-209A-7  
Perfect score: 1848  
Sequence: 1 MLLGLLLTTSALAGQRTGT.....DVALEHHEEDCVCKGNAGG 345

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 271250 seqs, 51324744 residues

Total number of hits satisfying chosen parameters: 271250

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents AA New.\*  
1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pcp.\*  
2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pcp.\*  
3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pcp.\*  
4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pcp.\*  
5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pcp.\*  
6: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pcp.\*  
7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1848	100.0	345	5	US-09-457-066-43
2	1848	100.0	345	5	US-09-876-813-35
3	1667	90.2	345	1	PCT-US03-26491-191
4	1667	90.2	345	5	US-09-457-066-2
5	1667	90.2	345	5	US-09-876-813-33
6	1667	90.2	345	6	US-10-648-593-191
7	1667	90.2	345	6	US-10-471-221-1
8	1667	90.2	345	7	US-60-487-610-1644
9	1667	90.2	345	7	US-60-485-450-1042
10	1659	89.8	345	5	US-09-830-320A-12
11	1267.5	68.6	282	6	US-10-471-221-5
12	1204.5	65.2	303	5	US-09-876-813-57
13	1200.64	64.9	302	5	US-09-876-813-54
14	1077.5	58.3	305	1	PCT-US00-28803-7
15	1035.5	56.0	317	5	US-09-876-813-56
16	1019	55.1	316	5	US-09-876-813-55
17	752	40.7	370	5	US-09-457-066-37
18	752	40.7	370	5	US-09-876-813-2
19	752	40.7	370	6	US-10-321-962-4
20	752	40.7	370	6	US-10-606-055-2
21	746.5	40.4	370	5	US-09-876-813-53
22	746.5	40.4	370	6	US-10-321-962-8
23	746.5	40.4	370	6	US-10-606-055-4
24	720	39.0	167	6	US-10-471-221-6
25	549	29.7	111	6	US-10-471-221-2
26	440.5	23.8	261	6	US-10-321-962-10

27	324.5	17.6	132	6	US-10-321-962-6	Sequence 6, Appli
28	312.5	16.9	154	6	US-10-321-962-12	Sequence 12, Appl
29	191	10.3	110	6	US-10-321-962-14	Sequence 14, Appl
30	190	10.3	823	7	US-60-495-114-2259	Sequence 2259, Ap
31	190	10.3	823	7	US-60-495-114-2266	Sequence 2266, Ap
32	190	10.3	823	7	US-60-495-114-2267	Sequence 2267, Ap
33	188	10.2	726	7	US-60-495-114-2251	Sequence 2251, Ap
34	185	10.0	1015	7	US-60-495-114-1841	Sequence 1841, Ap
35	183.5	9.9	730	5	US-09-830-320A-12	Sequence 12, Appl
36	183.5	9.9	730	7	US-60-495-114-2257	Sequence 2257, Ap
37	183.5	9.9	730	7	US-60-495-114-2260	Sequence 2260, Ap
38	183.5	9.9	730	7	US-60-495-114-2268	Sequence 2268, Ap
39	181	9.8	466	7	US-60-495-114-2262	Sequence 2262, Ap
40	181	9.8	717	7	US-60-495-114-2252	Sequence 2252, Ap
41	181	9.8	717	7	US-60-495-114-2253	Sequence 2253, Ap
42	181	9.8	717	7	US-60-495-114-2253	Sequence 2253, Ap
43	181	9.8	986	6	US-10-474-794-242	Sequence 242, App
44	181	9.8	986	7	US-60-495-114-2254	Sequence 2254, Ap
45	181	9.8	986	7	US-60-495-114-2264	Sequence 2264, Ap

ALIGNMENTS

RESULT 1  
US-09-457-066-43  
; Sequence 43, Application US/09457066  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Zeren  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Piddington, Christopher S.  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Shoemaker, Kimberly E.  
; APPLICANT: Gilbertson, Debra G.  
; APPLICANT: West, James W.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVGF3  
; FILE REFERENCE: 98-60  
; CURRENT APPLICATION NUMBER: US/09/457,066  
; CURRENT FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 43  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-457-066-43

Query Match	100.0%;	Score 1848;	DB 5;	Length 345;
Best Local Similarity	100.0%;	Pred. No. 3.3e-152;		
Matches 345;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MLLGLLLTTSALAGQRTGTGTRAESNLSSKLQSSDKQNGVODPRHVVVTISGNSIHS	60	
Db	1	MLLGLLLTTSALAGQRTGTGTRAESNLSSKLQSSDKQNGVODPRHVVVTISGNSIHS	60	
QY	61	PKFPHTYPNNMVLVRLVAVDENVRIQLTFDRFGLDEPDDICKYDFVEVEPPSGSVL	120	
Db	61	PKFPHTYPNNMVLVRLVAVDENVRIQLTFDRFGLDEPDDICKYDFVEVEPPSGSVL	120	
QY	121	GRWCSGTVPKGQTSKGNHIRIRFVSDEYFPBPFGPCIHYSIMPQVTTTSPVLPSS	180	
Db	121	GRWCSGTVPKGQTSKGNHIRIRFVSDEYFPBPFGPCIHYSIMPQVTTTSPVLPSS	180	
QY	181	LSLDLNNVATFAFTEELIRYLEPDRQVODLSLYKPTWQLLGKFLYKSKVNNLNL	240	
Db	181	LSLDLNNVATFAFTEELIRYLEPDRQVODLSLYKPTWQLLGKFLYKSKVNNLNL	240	
QY	241	LKEEVKLYSCTPRNFSVSIREELKRTDTTFWFGCLLVKRCGNCACCLHNCNCCQVPRK	300	
Db	241	LKEEVKLYSCTPRNFSVSIREELKRTDTTFWFGCLLVKRCGNCACCLHNCNCCQVPRK	300	
QY	301	VTKKHYEVLQLPKTCVGLHKSLLTDVALEHHEBCDCVCRNAGG	345	

```
Db      301 VTKYHEVLQRLPKTGVKGLHKSLLTDVALEHHEECDCVCRGNAGG 345

RESULT 2
US-09-876-813-35
; Sequence 35, Application US/09876813
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/876,813
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US/09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US/09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US/60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US/60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-876-813-35

Query Match      100.0%; Score 1848; DB 5; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.3e-152;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLLGLLLTTSALAGORTGTRAESNLSSKQLQSSDKQNGVQDPHRRVVTISGNGSIHS 60
Db      1 MLLGLLLTTSALAGORTGTRAESNLSSKQLQSSDKQNGVQDPHRRVVTISGNGSIHS 60
QY      61 PKFPHTYPRNMVLMVRLVAVDENVRILQTFDERFGLDEDDICKYDFVEVEEPPSGSVL 120
Db      61 PKFPHTYPRNMVLMVRLVAVDENVRILQTFDERFGLDEDDICKYDFVEVEEPPSGSVL 120
QY      121 GRWCGSGTVPKGKQTSKGNHIRIRFVSDEYFPPSPGFCIHYSIIMPQVTTTSPSVLPSS 180
Db      121 GRWCGSGTVPKGKQTSKGNHIRIRFVSDEYFPPSPGFCIHYSIIMPQVTTTSPSVLPSS 180
QY      181 LSDDLNNAVTAFSTLEELIRYLEPDRWQVDLSLYKPTWLLGKAFLYGKSKVNLNL 240
Db      181 LSDDLNNAVTAFSTLEELIRYLEPDRWQVDLSLYKPTWLLGKAFLYGKSKVNLNL 240
QY      241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPRK 300
Db      241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPRK 300
QY      301 VTKYHEVLQRLPKTGVKGLHKSLLTDVALEHHEECDCVCRGNAGG 345
Db      301 VTKYHEVLQRLPKTGVKGLHKSLLTDVALEHHEECDCVCRGNAGG 345

RESULT 3
PCT-US03-26491-191
; Sequence 191, Application PC/TUS0326491
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
; FILE REFERENCE: D0273 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/26491
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 60/406,385
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 557
```

```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 191
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-26491-191

Query Match      90.2%; Score 1667; DB 1; Length 345;
Best Local Similarity 87.0%; Pred. No. 1.5e-136;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY      1 MLLGLLLTTSALAGORTGTRAESNLSSKQLQSSDKQNGVQDPHRRVVTISGNGSIHS 60
Db      1 MSLFGLLLTTSALAGORTGTRAESNLSSKQLQSSDKQNGVQDPHRRVVTISGNGSIHS 60
QY      61 PKFPHTYPRNMVLMVRLVAVDENVRILQTFDERFGLDEDDICKYDFVEVEEPPSGSVL 120
Db      61 PRFPHTYPRNTVLVWRLVAVDENVRILQTFDERFGLDEDDICKYDFVEVEEPPSGTIL 120
QY      121 GRWCGSGTVPKGKQTSKGNHIRIRFVSDEYFPPSPGFCIHYSIIMPQVTTTSPSVLPSS 180
Db      121 GRWCGSGTVPKGKQTSKGNHIRIRFVSDEYFPPSPGFCIHYSIIMPQVTTTSPSVLPSS 180
QY      181 LSDDLNNAVTAFSTLEELIRYLEPDRWQVDLSLYKPTWLLGKAFLYGKSKVNLNL 240
Db      181 LPDLNNAITAFSTLEELIRYLEPDRWQVDLSLYKPTWLLGKAFVFGKSRVVDLNL 240
QY      241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPRK 300
Db      241 LTEEVLVYSCPTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPSK 300
QY      301 VTKYHEVLQRLPKTGVKGLHKSLLTDVALEHHEECDCVCRGNAGG 345
Db      301 VTKYHEVLQRLPKTGVKGLHKSLLTDVALEHHEECDCVCRGSTGG 345

RESULT 4
US-09-457-066-2
; Sequence 2, Application US/09457066
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-457-066-2

Query Match      90.2%; Score 1667; DB 5; Length 345;
Best Local Similarity 87.0%; Pred. No. 1.5e-136;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY      1 MLLGLLLTTSALAGORTGTRAESNLSSKQLQSSDKQNGVQDPHRRVVTISGNGSIHS 60
Db      1 MSLFGLLLTTSALAGORTGTRAESNLSSKQLQSSDKQNGVQDPHRRVVTISGNGSIHS 60
QY      61 PKFPHTYPRNMVLMVRLVAVDENVRILQTFDERFGLDEDDICKYDFVEVEEPPSGSVL 120
Db      61 PRFPHTYPRNTVLVWRLVAVDENVRILQTFDERFGLDEDDICKYDFVEVEEPPSGTIL 120
QY      121 GRWCGSGTVPKGKQTSKGNHIRIRFVSDEYFPPSPGFCIHYSIIMPQVTTTSPSVLPSS 180
Db      121 GRWCGSGTVPKGKQTSKGNHIRIRFVSDEYFPPSPGFCIHYSIIMPQVTTTSPSVLPSS 180
```

Db 121 GRWCGGTVPGKQISKGNIQIRIRFVSDVFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPA 180  
Qy 181 LSLDLNNAVTAFSTLEELIRYLEPRQVQLDSLYKPTWQLLKGAFLYGKSKVYNLNL 240  
Db 181 LPLDLNNAITAFSTLEDLIRYLEPRQVQLDSLYKPTWQLLKGAFVFGKRSRVVDLNL 240  
Qy 241 LKEEVKLYSCTPRNFSVIRELKEKTDITFPGCLLVKRCGNCACCLHNCNECCVPRK 300  
Db 241 LTEEVRLYSCTPRNFSVIRELKEKTDITFPGCLLVKRCGNCACCLHNCNECCVPRK 300  
Qy 301 VTKKYHEVLQRLPKTGVRGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKKYHEVLQRLPKTGVRGLHKSLLTDVALEHHEECDCVCRGNAGG 345

## RESULT 5

US-09-876-813-33  
; Sequence 33, Application US/09876813  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4  
; FILE REFERENCE: 99-19  
; CURRENT APPLICATION NUMBER: US/09/876,813  
; PRIOR FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: US/09/564,595  
; PRIOR FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: US/09/304,216  
; PRIOR FILING DATE: 1999-05-03  
; PRIOR APPLICATION NUMBER: US/60/164,463  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: US/60/180,169  
; PRIOR FILING DATE: 2000-02-04  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 33  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-876-813-33

Query Match 90.2%; Score 1667; DB 5; Length 345;  
Best Local Similarity 87.0%; Pred. No. 1.5e-136;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MLLGLLLLTALAGORTGTRAESNLSSKQLQSSDKQNGVODPRHRVVTISGNGSIHS 60  
Db 1 MSLFGLLLLTALAGORQGTQAESNLSSKQFSSNKQNGVODPQHERIITVSTNGSIHS 60  
Qy 61 PKFPHYPRNVMVLRVAVDENVRIOITFDRFGLGLEDDEDDICKYDFVEVEEPPSDGVL 120  
Db 61 PRFPHYPRNTVLVWRLVAVENVMIOITFDRFGLGLEDDEDDICKYDFVEVEEPPSDGVL 120  
Qy 121 GRWCGGTVPGKQISKGNIQIRIRFVSDVFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180  
Db 121 GRWCGGTVPGKQISKGNIQIRIRFVSDVFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPA 180  
Qy 181 LSLDLNNAVTAFSTLEELIRYLEPRQVQLDSLYKPTWQLLKGAFLYGKSKVYNLNL 240  
Db 181 LPLDLNNAITAFSTLEDLIRYLEPRQVQLDSLYKPTWQLLKGAFVFGKRSRVVDLNL 240  
Qy 241 LKEEVKLYSCTPRNFSVIRELKEKTDITFPGCLLVKRCGNCACCLHNCNECCVPRK 300  
Db 241 LTEEVRLYSCTPRNFSVIRELKEKTDITFPGCLLVKRCGNCACCLHNCNECCVPRK 300  
Qy 301 VTKKYHEVLQRLPKTGVRGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKKYHEVLQRLPKTGVRGLHKSLLTDVALEHHEECDCVCRGNAGG 345

## RESULT 6

US-10-648-593-191

; Sequence 191, Application US/10648593  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THE  
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR  
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS  
; FILE REFERENCE: D0273 NP  
; CURRENT APPLICATION NUMBER: US/10/648,593  
; PRIOR FILING DATE: 2003-08-26  
; PRIOR APPLICATION NUMBER: 60/406,385  
; PRIOR FILING DATE: 2002-08-27  
; NUMBER OF SEQ ID NOS: 557  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 191  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-648-593-191

Query Match 90.2%; Score 1667; DB 6; Length 345;  
Best Local Similarity 87.0%; Pred. No. 1.5e-136;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MLLGLLLLTALAGORTGTRAESNLSSKQLQSSDKQNGVODPRHRVVTISGNGSIHS 60  
Db 1 MSLFGLLLLTALAGORQGTQAESNLSSKQFSSNKQNGVODPQHERIITVSTNGSIHS 60  
Qy 61 PKFPHYPRNVMVLRVAVDENVRIOITFDRFGLGLEDDEDDICKYDFVEVEEPPSDGVL 120  
Db 61 PRFPHYPRNTVLVWRLVAVENVMIOITFDRFGLGLEDDEDDICKYDFVEVEEPPSDGVL 120  
Qy 121 GRWCGGTVPGKQISKGNIQIRIRFVSDVFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180  
Db 121 GRWCGGTVPGKQISKGNIQIRIRFVSDVFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPA 180  
Qy 181 LSLDLNNAVTAFSTLEELIRYLEPRQVQLDSLYKPTWQLLKGAFLYGKSKVYNLNL 240  
Db 181 LPLDLNNAITAFSTLEDLIRYLEPRQVQLDSLYKPTWQLLKGAFVFGKRSRVVDLNL 240  
Qy 241 LKEEVKLYSCTPRNFSVIRELKEKTDITFPGCLLVKRCGNCACCLHNCNECCVPRK 300  
Db 241 LTEEVRLYSCTPRNFSVIRELKEKTDITFPGCLLVKRCGNCACCLHNCNECCVPRK 300  
Qy 301 VTKKYHEVLQRLPKTGVRGLHKSLLTDVALEHHEECDCVCRGNAGG 345  
Db 301 VTKKYHEVLQRLPKTGVRGLHKSLLTDVALEHHEECDCVCRGNAGG 345

## RESULT 7

US-10-471-221-1  
; Sequence 1, Application US/10471221  
; GENERAL INFORMATION:  
; APPLICANT: Janssen Pharmaceutica N.V.  
; TITLE OF INVENTION: Modulation Of Smooth Muscle Cell Proliferation  
; FILE REFERENCE: JAB 1687  
; CURRENT APPLICATION NUMBER: US/10/471,221  
; PRIOR FILING DATE: 2003-09-05  
; PRIOR APPLICATION NUMBER: US/60/274901  
; PRIOR FILING DATE: 2001-03-09  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-471-221-1

Query Match 90.2%; Score 1667; DB 6; Length 345;  
Best Local Similarity 87.0%; Pred. No. 1.5e-136;  
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MLLGLLLLTALAGORTGTRAESNLSSKQLQSSDKQNGVODPRHRVVTISGNGSIHS 60  
Db 1 MSLFGLLLLTALAGORQGTQAESNLSSKQFSSNKQNGVODPQHERIITVSTNGSIHS 60



1	MSIFGLLLTSALAGQGGTQAE	NSL	ASK	FS	SNKE	QNG	QVD	PO	HE	RI	I	I	V	T	N	G	S	T	H	S	60	
61	PKPFHTYPRNMVLVRLVAV	DEN	YRI	Q	L	T	P	F	R	E	G	L	E	D	P	E	D	I	C	K	Y	120
61	PRPFHTYPRNTVLVRLVAV	EEN	VWI	Q	L	T	P	F	R	E	G	L	E	D	P	E	D	I	C	K	Y	120
121	GRWCGSTVPCKONSKGNH	IRI	R	F	V	S	D	R	F	P	S	E	P	G	F	C	I	H	S	I	M	180
121	GRWCGSTVPFGQISKGNQ	IRI	R	F	V	S	D	R	F	P	S	E	P	G	F	C	I	H	S	I	M	180
181	LSLDLLNNAVTAFTSEL	BEL	I	R	L	E	P	D	R	Q	V	D	L	S	L	Y	K	P	T	Q	L	240
181	LPDLNNAITAFSTLED	LIR	L	E	P	R	Q	V	D	L	E	L	Y	R	P	T	Q	L	L	G	K	240
241	LKEVKLYSCCTPRNFS	V	S	I	R	E	L	K	T	D	T	I	F	M	P	G	C	L	L	V	R	300
241	LTEEVRLYSCCTPRNFS	V	S	I	R	E	L	K	T	D	T	I	F	M	P	G	C	L	L	V	R	300
301	VTKKYHEVLQLRPTK	VG	K	L	H	K	S	L	T	D	V	A	L	E	H	E	E	C	D	C	V	345
301	VTKKYHEVLQLRPTK	VG	K	L	H	K	S	L	T	D	V	A	L	E	H	E	E	C	D	C	V	345

```

RESULT 8
US-60-487-610-1644
; Sequence 1644, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: HUANG, Hongjin
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; FILE REFERENCE: CLO01469
; CURRENT APPLICATION NUMBER: US/60/487,610
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1644
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-487-610-1644

```

Query Match	90.2%	Score 1667;	DB 7;	Length 345;
Best Local Similarity	87.0%;	Pred. No. 1.5e-136;		
Matches	300;	Conservative 27;	Mismatches 18;	Indels 0; Gaps 0;
Qy	1	MLLGLLLLSALAGQTGTAE	NSLASKLQSSDKQNGVQD	PRHERVVTISGNGSIHS 60
Db	1	MSLFGLLLSALAGQGTQAE	NSLASKFQSSNKQNGVQD	PQHERIIIVTNGSIHS 60
Qy	61	PKFHPTTPRNMVLVWRLVAV	DENVRIQLTDFERFGLDEP	DDICKYDFVEVEEESDGSVL 120
Db	61	PRFHPTTPRNTLVWRLVAVE	NVWIIQLTDFERFGLDEP	DDICKYDFVEVEEESDGTIL 120
Qy	121	GRWCGSGTVPGKQKTSKGNH	IRIRFVSDEYFPFSEPGFC	HIHSIIMPQVTTETTSPSVLPPSS 180
Db	121	GRWCGSGTVPGKQISKGNQ	IRIRFVSDEYFPFSEPGFC	HIHNVIMPQTEAVSPSVLPSSA 180
Qy	181	LSLQLLNNAVTAFTSLIEL	IRYLEPDRDWQVLDLSLYK	PTWOLLGKAFLYGKKSKVNNL 240
Db	181	LPQLLLNNAITAFSTLED	ILIRYLEPERWQLOLED	LIYRPTWOLLGKAFVFGRRKSRVDNL 240
Qy	241	LKEEVKLYSCTPRNFVSIR	EELKRTDTIIFWPGCLLVK	RCGNCACCLHNCNEQCQVPVK 300
Db	241	LTEEVRLYSCTPRNFVSIR	EELKRTDTIIFWPGCLLVK	RCGNCACCLHNCNEQCQVPVK 300
Qy	301	VTKKYHEVLQRPKTVGVL	HKHSITDVALEHHEECDC	VCVRNAGG 345
Db	301	VTKKYHEVLQRPKTVGVL	HKHSITDVALEHHEECDC	VCVRSTGG 345

## RESULT 9

```

US-60-485-450-1042
; Sequence 1042, Application US/60485450
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: CHANG, Sheng-Yung
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001470
; CURRENT APPLICATION NUMBER: US/60/485,450
; CURRENT FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 47859
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1042
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-485-450-1042

Query Match          90.2%;   Score 1667;   DB 7;   Length 345;
Best Local Similarity 87.08;   Pred No. 1.5e-136;
Matches 300;   Conservative 27;   Mismatches 18;   Indels 0;   Gaps 0

Qy      1  MLLGLGLLLTSALAGQRTGTGAESNLSSKLQLSSDKEQNGVDPRHRVVTISNGSIHS 60
Db      1  MSLFGLGLLLTSALAGQRTGTGAESNLSSKFKQSSNKEQNGVDQPOHERIITVSTNGSIHS 60

Qy      61  PKPHITYPRNMVLVRLVAVDENVRIOLTDEREGLEDPEDDICKYDFVEVEEPSDGSVL 120
Db      61  PRFPHITYPRNTVLVRLVAVDENVRWIOLTDEREGLEDPEDDICKYDFVEVEEPSDGTIL 120

Qy      121  GRWCGSGTVPGKQTSKGNHRIIRFVSDEYFPSEPGFCIHYSIIMPQVTTETSPSVLPSS 180
Db      121  GRWCGSGTVPGKQISKGNQRIIRFVSDEYFPSEPGFCIHINIVMPQFTEAVSPSVLPSSA 180

Qy      181  LSLDLLANNAVTAFTSLBELIRYLEBPDRAQVDLDLSLYKPTWOLLGKAFUYGKKSKVYNL 240
Db      181  LPLDLLANNAVTAFTSLBELIRYLEBPERWQLDLEDLYRPTWOLLGKAFYVFGKRSRYVDL 240

Qy      241  LKEBVKLYSCTPRNFSYSIREELKRTDTIIFWPGCLLVKRCGNCACCLHNCNEQCQVPRK 300
Db      241  LTBEBVLYSCTPRNFSYSIREELKRTDTIIFWPGCLLVKRCGNCACCLHNCNEQCQVPSK 300

Qy      301  VTKYKHYEVLQLRPKTGVKGLHKSITDVALEHHEHCDCVCRGNAGG 345
Db      301  VTKYKHYEVLQRPKTVGRGLHKSITDVALEHHEHCDCVCRGSTGG 345

```

```

RESULT 10
US-09-830-320A-4
; Sequence 4, Application US/09830320A
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: TANG, Y. Tom
; APPLICANT: YUE, Henry
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: CORLEY, Neil C.
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: AU-YOUNG, Janice K.
; TITLE OF INVENTION: GROWTH FACTOR RELATED MOLECULES
; FILE REFERENCE: PF-0627 USN
; CURRENT APPLICATION NUMBER: US/09/830,320A
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: PCT/US99/25458
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 60/183,024
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 60/155,216
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/172,233
; PRIOR FILING DATE: 1999-05-17

```

```
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No.: 4163378CD1
US-09-830-320A-4

Query Match      89.8%; Score 1659; DB 5; Length 345;
Best Local Similarity 86.7%; Pred. No. 7.6e-136;
Matches 299; Conservative 27; Mismatches 19; Indels 0; Gaps 0;

QY 1 MLLGLLLTSLALAGTQTTRAESNLSSKLQSSDKQNGVQDPHRRVVTISGNGSIHS 60
DB 1 MSLFGLLLTSLALAGTQTTRAESNLSSKQFSSNKEQYGVQDPQHERIITVSTNGSIHS 60
QY 61 PRPHTYPRNMVLVWRLVAVDENVRQLTFDERFGLDEDDICKYDFVEVEEPPSGSVL 120
DB 61 PRPHTYPRNTVLVWRLVAVDENVRQLTFDERFGLDEDDICKYDFVEVEEPPSGDTIL 120
QY 121 GRWCGSGTVPKGKQISKGNQIRIRFVSDYFPPSPGFCIHYNIVMPQTEAVSPSVLPSS 180
DB 121 GRWCGSGTVPKGKQISKGNQIRIRFVSDYFPPSPGFCIHYNIVMPQTEAVSPSVLPSSA 180
QY 181 LSLDLNNAVTAFTSTLEELIRYLEPDRWQVLDLSLYKPTWQLLGKAFLYGKSKVNNLN 240
DB 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVGRKSRVVDNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPK 300
DB 241 LEEVRLYSCTPRNFVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNECQCVPK 300
QY 301 VTKKHYEVLQRPKTCVKGKGLHSLTDVALEHHEECDCVCRGNAGG 345
DB 301 VTKKHYEVLQRPKTCVGRGLHSLTDVALEHHEECDCVCRGSGG 345

RESULT 11
US-10-471-221-5
; Sequence 5, Application US/10471221
; GENERAL INFORMATION:
; APPLICANT: Janssen Pharmaceutica N.V.
; FILE OF INVENTION: Modulation Of Smooth Muscle Cell Proliferation
; CURRENT APPLICATION NUMBER: US/10/471,221
; PRIOR FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: US 60/274901
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-471-221-5

Query Match      68.6%; Score 1267.5; DB 6; Length 282;
Best Local Similarity 69.3%; Pred. No. 4.6e-102;
Matches 239; Conservative 26; Mismatches 17; Indels 63; Gaps 1;

QY 1 MLLGLLLTSLALAGTQTTRAESNLSSKLQSSDKQNGVQDPHRRVVTISGNGSIHS 60
DB 1 MSLFGLLLTSLALAGTQTTRAESNLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
QY 61 PRPHTYPRNMVLVWRLVAVDENVRQLTFDERFGLDEDDICKYDFVEVEEPPSGSVL 120
DB 61 PRPHTYPRNTVLVWRLVAVDENVRQLTFDERFGLDEDDICKYDFVEVEEPPSGDTIL 120
QY 121 GRWCGSGTVPKGKQISKGNHIRIRFVSDYFPPSPGFCIHYSIIMPQVTTTSPSVLPSS 180
DB 121 GRWCGSGTVPKGKQISKGNHIRIRFVSDYFPPSPGFCIHYSIIMPQVTTTSPSVLPSS 180

RESULT 12
US-09-876-813-57
; Sequence 57, Application US/09876813
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles B.
; APPLICANT: Sheppard, Paul O.
; FILE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; CURRENT APPLICATION NUMBER: US/09/876,813
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US/09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-876-813-57

Query Match      65.2%; Score 1204.5; DB 5; Length 303;
Best Local Similarity 71.3%; Pred. No. 1.5e-96;
Matches 216; Conservative 42; Mismatches 40; Indels 5; Gaps 3;

QY 47 ERVVTISGNSIHSKPKPHTYPRNMVLVWRLVAVDENVRQLTFDERFGLDEDDICKY 106
DB 2 DETIQVKGNGYVQSPPFNPSYPRNLLLTWRLHS-QENTRIQLVFDNQFGLAEADICRY 60
QY 107 DFVEVEEPPSGSVL--GRWCGSGTVPKGKQISKGNHIRIRFVSDYFPPSPGFCIHYSI 163
DB 61 DFVEVEDISETTIIRGRWCGHKEVPPRIKSRNTQIKITFKSDDYFVAKPGFKIYSLLE 120
QY 164 -MPQVTTTSPSVLPSSLSLDLNNNAVTAFTSTLEELIRYLEPDRWQVLDLSLYKPTW 222
DB 121 DFQPAASVSPSVLPSSALPLDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQL 180
QY 223 LKAFLYGKSKVNNLNLLKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCG 282
DB 181 LKAFVGRKSRVVDNLNLLTEEVRLYSCTPRNFVSIREELKRTDTTFWPGCLLVKRCG 240
QY 283 NCACCLHNCNECQCVPKVTYKHYEVLQRPKTCVKGKGLHSLTDVALEHHEECDCVCRGN 342
DB 241 NCACCLHNCNECQCVPKVTYKHYEVLQRPKTCVGRGLHSLTDVALEHHEECDCVCRGS 300
QY 343 AGG 345
DB 301 TGG 303
```

RESULT 13  
US-09-876-813-54  
; Sequence 54, Application US/09876813  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Shepard, Paul O.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4  
; FILE REFERENCE: 99-19  
; CURRENT APPLICATION NUMBER: US/09/876,813  
; CURRENT FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: US/09/564,595  
; PRIOR FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: US 09/304,216  
; PRIOR FILING DATE: 1999-05-03  
; PRIOR APPLICATION NUMBER: US 60/164,463  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: US 60/180,169  
; PRIOR FILING DATE: 2000-02-04  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 54  
; LENGTH: 302  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: fusion polypeptide  
US-09-876-813-54  
Query Match 64.9%; Score 1200; DB 5; Length 302;  
Best Local Similarity 72.4%; Pred. No. 3.6e-96;  
Matches 215; Conservative 35; Mismatches 43; Indels 4; Gaps 2;  
QY 46 HERVVTISNGSIHSPKPPHYPRNMLVWRLVAVDENVRIOITFDERFGLEDPEDDICK 105  
DB 1 HERITVSTNGSIHSPKPPHYPRNMLVWRLVAVDENVRIOITFDERFGLEDPEDDICK 60  
QY 106 YDFVEVEEPPSDGSLGRWCGSGTVPKGKQIRIRFVSDVEFPSEPGFCIHYSIIMP 165  
DB 61 YDFVEVEEPPSDGSLGRWCGSGTVPKGKQIRIRFVSDVEFPSEPGFCIHYSIIMP 120  
QY 166 QVTETTSVLPSPSSLSLDLNNNAVTAFTSTLEELIRLYLEPDRMQVDLSLYKPTWOLLGK 225  
DB 121 QTEAVSPSVLPSPSALPLDLNNNAVTAFTSTLEELIRLYLEPDRMQVDLSLYKPTWOLLGK 180  
QY 226 AFLVKGKSKVNNLLKEEVKLYSCTPRNFSVSIREELKSTDTIFWPGCLLVKCGCNCA 285  
DB 181 AFVFGKRSR-VLDRLNDADAKRYSCTPRNVSVNIREELKLANVVFPRCLLVQRCGNGC 239  
QY 286 CCLHNCNECQVPRKVKKKHEVLQLRP---KTGVKGLHKSITDVALEHHEECDCVC 339  
DB 240 CGTVNWRSCNCSGKTVKKYHEVLQFEPGHIKRRGRAKTMAVLDIQLDHERCDIC 296  
RESULT 14  
PCT-US00-28803-7  
; Sequence 7, Application PC/TUS0028803  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Donoho, Gregory  
; APPLICANT: Nehls, Michael  
; APPLICANT: Hilbun, Erin  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: Novel Human Proteins and Polynucleotides  
; FILE REFERENCE: LEX-0070-PCT  
; CURRENT APPLICATION NUMBER: PCT/US00/28803  
; CURRENT FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: US 60/160,106  
; PRIOR FILING DATE: 1999-10-18  
; PRIOR APPLICATION NUMBER: US 60/162,547  
; PRIOR FILING DATE: 1999-10-29

; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 305  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US00-28803-7  
Query Match 58.3%; Score 1077.5; DB 1; Length 305;  
Best Local Similarity 75.7%; Pred. No. 1.5e-85;  
Matches 203; Conservative 27; Mismatches 35; Indels 3; Gaps 1;  
QY 1 MLLGLLLTTSALAGQRTGTAESNLSSKQLSDSKKONGVQDPRHVRVTSNGSIHS 60  
DB 1 MSLFGLLLTTSALAGQRTGTAESNLSSKQLSDSKKONGVQDPRHVRVTSNGSIHS 60  
QY 61 PKFPHTYPRNMLVWRLVAVDENVRIOITFDERFGLEDPEDDICKYDFVEVEEPPSDGSLV 120  
DB 61 PRFPHTYPRNMLVWRLVAVDENVRIOITFDERFGLEDPEDDICKYDFVEVEEPPSDGSLV 120  
QY 121 GRWCGSGTVPKGKQIRIRFVSDVEFPSEPGFCIHYSIIMPQVTETTSVLPSPSS 180  
DB 121 GRWCGSGTVPKGKQIRIRFVSDVEFPSEPGFCIHYSIIMPQVTETTSVLPSPSS 180  
QY 181 LSLDLNNNAVTAFTSTLEELIRLYLEPDRMQVDLSLYKPTWOLLGKAFVFGKSKVNNLL 240  
DB 181 LPLDLNNNAVTAFTSTLEELIRLYLEPDRMQVDLSLYKPTWOLLGKAFVFGKSKVNNLL 240  
QY 241 ---LKEEVKLYSCTPRNFSVSIREELK 265  
DB 241 EKNLKNFVKYLAEGNFFNIIVKLFFK 268  
RESULT 15  
US-09-876-813-56  
; Sequence 56, Application US/09876813  
; GENERAL INFORMATION:  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Hart, Charles E.  
; APPLICANT: Shepard, Paul O.  
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4  
; FILE REFERENCE: 99-19  
; CURRENT APPLICATION NUMBER: US/09/876,813  
; CURRENT FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: US/09/564,595  
; PRIOR FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: US 09/304,216  
; PRIOR FILING DATE: 1999-05-03  
; PRIOR APPLICATION NUMBER: US 60/164,463  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: US 60/180,169  
; PRIOR FILING DATE: 2000-02-04  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 56  
; LENGTH: 317  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: fusion polypeptide  
US-09-876-813-56  
Query Match 56.0%; Score 1035.5; DB 5; Length 317;  
Best Local Similarity 60.2%; Pred. No. 6.7e-82;  
Matches 192; Conservative 47; Mismatches 57; Indels 23; Gaps 6;  
QY 47 ERVVTISNGSIHSPKPPHYPRNMLVWRLVAVDENVRIOITFDERFGLEDPEDDICKY 106  
DB 2 DETIQKNGYVQSPRPNFNSVPRNMLLTLWRLHS-QENTRIQLVFNQGLGEAENDICRY 60  
QY 107 DFVEVEEPPSDGSLV--GRWCGSGTVPKGKQIRIRFVSDVEFPSEPGFCIHYSI- 163  
DB 61 DFVEVEDISETITIRGRWCWGKHEVPPRIKSRTNQIKITFKSDDDYFAKPGFKIYSLLE 120

Qy	164	--MPQVTETT-----SPSVLPSPSSLSLNNNAVTAFTLBEELIRYLEPD	206
Db	121	DFQPAARSETWESVTSSISGVSNPSVTDp-TLJADALDKIAEFDTVEDLLKYFNPE	179
Qy	207	RWQVDLSLYKPTWQLGKAFLYGKSKVNLNLLKEEVKLYSCTPRNFSVSIREELKRT	266
Db	180	SWQEDLENNMYLDTPRYGRSY-HDRKSKVDNLNLTTEEVRLYSCTPRNFSVSIREELKRT	238
Qy	267	DTIFWPGCLLVKRCGNCACCLHNCNECQVPRKVTKKYHEVLQRPKTGVKGLHKS LTD	326
Db	239	DTIFWPGCLLVKRCGNCACCLHNCNECQVPSKVKYHEVLQRPKTGVKGLHKS LTD	298
Qy	327	VALEHHEECDCVCRGNAGG	345
Db	299	VALEHHEECDCVCRGSTGG	317

Search completed: November 25, 2003, 21:15:41  
Job time : 14.6905 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 20:59:34 ; Search time 14.7173 Seconds  
(without alignments)  
2254.373 Million cell updates/sec

Title: US-09-852-209A-7

Perfect score: 1848

Sequence: 1 MLLGLLLTSLAQRTGT.....DVALEHHERCVCVRNAGG 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:\*\*

1: pir1:\*\*

2: pir2:\*\*

3: pir3:\*\*

4: pir4:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	754	40.8	370	2 JC7592	spinal cord-derive
2	753	40.7	370	2 JC7591	spinal cord-derive
3	191	10.3	707	2 JC2218	procollagen C-endo
4	140	10.3	823	1 A58788	procollagen C-endo
5	183.5	9.9	730	1 BMH1	procollagen C-endo
6	183.5	9.9	927	1 JQ0948	A5 antigen precurs
7	181	9.8	986	1 B58788	procollagen C-endo
8	181	9.8	991	2 I49540	procollagen C-endo
9	174.5	9.4	3623	2 T09456	intrinsic factor-B
10	160	8.7	3623	2 T08618	intrinsic factor-B
11	158	8.5	449	2 A55362	procollagen I C-pr
12	153	8.3	1057	1 A39288	dorsal-ventral pat
13	147.5	8.0	1524	2 T30337	polyprotein - Afri
14	145.5	7.9	686	1 A59271	Ra-reactive factor
15	144	7.8	699	1 I54763	Ra-reactive factor
16	143.5	7.8	597	2 S71352	metalloproteinase
17	141.5	7.7	1070	2 T31069	tolloid-BMP-1 like
18	140.5	7.6	3871	2 T22812	hypothetical prote
19	139	7.5	1594	2 T30349	hensin - rabbit
20	137.5	7.4	705	1 C1HURB	complement subcomp
21	135.5	7.3	1464	2 S58984	development protei
22	133.5	7.2	402	2 JH0403	procollagen I C-pr
23	128	6.9	277	2 A41735	hyaluronate-bindin
24	127	6.9	419	2 S69207	vascular endotheli
25	126.5	6.8	579	2 JC7629	membrane-type friz
26	125.5	6.8	245	1 TVCTSS	platelet-derived g
27	125.5	6.8	767	2 T30018	hypothetical prote
28	123	6.7	275	2 JC6506	tumor necrosis fac
29	122.5	6.6	2403	2 A59386	sanko - human

30	119.5	6.5	2083	2 T42721	CRP-ductin-alpha p
31	117.5	6.4	276	2 A47290	TSG-6 homolog PS4
32	117.5	6.4	1290	2 A57190	ebnerin precursor
33	114.5	6.2	200	2 I51551	platelet-derived g
34	114.5	6.2	215	2 S08220	platelet-derived g
35	114.5	6.2	226	2 I51550	platelet-derived g
36	113	6.1	695	1 S05008	complement subcomp
37	112.5	6.1	241	1 PFHUG2	platelet-derived g
38	111.5	6.0	226	1 TVMVSS	PDGF-related trans
39	109	5.9	694	2 JC6554	complement subcomp
40	108.5	5.9	148	2 D48530	16K vascular endot
41	107	5.8	321	2 T33161	hypothetical prote
42	104	5.6	319	2 I51569	UVS.2 protein - Af
43	103.5	5.6	225	2 S25097	platelet-derived g
44	103	5.6	196	2 B28964	platelet-derived g
45	103	5.6	211	1 PFHUG1	platelet-derived g

## ALIGNMENTS

### RESULT 1

JC7592

spinal cord-derived growth factor-B precursor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 24-Aug-2001

C;Accession: JC7592

R;Hamada, T.; Ui-Tei, K.; Imaki, J.; Miyata, Y.

Biochem. Biophys. Res. Commun. 280: 733-737, 2001

A;Title: Molecular cloning of SCDGF-B, a novel growth factor homologous to SCDGF/PDGF-

A;Reference number: JC7591; MUID:21092670; PMID:11162582

A;Contents: Fetal brain

A;Accession: JC7592

A;Molecule type: mRNA

A;Residues: 1-370 <HAM>

A;Cross-references: DDBJ:AB052170

C;Genetics:

A;Gene: scdgf-B

F;1-17/Domain: secretory signal sequence #status predicted <SIG>

F;18-370/Product: spinal cord-derived growth factor-B #status predicted <SIG>

F;52-170/Region: CUB domain #status predicted

F;272-370/Region: homologous to platelet-derived growth factor/vascular endothelial gr

F;294-308/Region: conserved motif #status predicted

Query Match	40.8%;	Score	754;	DB	2;	Length	370;
Best Local Similarity	46.2%;	Pred. No.	1.4e-55;				
Matches	151;	Conservative	62;	Mismatches	86;	Indels	28;
Gaps	10;						
QY	37	EQNGVQD-PRHERVVTISNGSIHSPKPHPTYPNNMVLVRLVAVDENVRILQTFDERFG	95				
Db	42	ESNHLTLVRRDENIRVTGTGHVQSPRFPNLSYPRNLLLTWRLHS-QBKTRIQIAFDHQFG	100				
QY	96	LEPEDDICKYDFVEVEERSDGS--VLGRWCGSTGVPGKOTSGNHRIRFVSPDEYRPSSE	153				
Db	101	LEAENDICRYDFVEVEDVESSTVVRGRWCGHKEIPRITRTNQIKITFQSDDYFVAK	160				
QY	154	PGFCIHYSII---MPQ-----VTET-----TSPSVLPFSSSLDLLNNAVTAFT	195				
Db	161	PGFKIYVSFVEDFQPEAASINNESVTSSFGVSYHSPSVN-DSTLTADALDKAIAEFTD	219				
QY	196	LEELIYLEPDRQVLDLSLYKFTWQLLQKAFYLGKSKVNNLNLKEFKVLSCTPRNF	255				
Db	220	VEDLLKYFPASQDDLENLYMDTPYRGSRV-HERKSK-VLDRLNDVVKRYSCSTPRNH	277				
QY	256	SVSIRELKRDTDFWPGCLLVKRCGNCACCLHNCNCCVPRKVTYKKYHEVLQLRP--	313				
Db	278	SVNLRELKLTNAVFFPRCLLVQRCGNCGCCGTLLNWKSCCTCSSGKTVKKYHEVLKFEFGH	337				
QY	314	-KTGVKGLHKSITDVALEHHEECDCVC	339				
Db	338	FKERGAKNALVDIQIDHHERCDCIC	364				

```
RESULT 2
JC7591
spinal cord-derived growth factor-B precursor - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 24-Aug-2001
C:Accession: JC7591
R:Hamada, T.; Uti-Tei, K.; Imaki, J.; Miyata, Y.
Biochem. Biophys. Res. Commun. 280, 733-737, 2001
A:Title: Molecular cloning of SCDFP-B, a novel growth factor homologous to SCDFP/PDGF-C/
A:Reference number: JC7591; MUID:21092670; PMID:11162582
A:Accession: JC7591
A:Molecule type: DNA
A:Residues: 1-370 <HAM>
A:Cross-references: DDBJ:AB033832
C:Genetics:
A:Gene: scdgp-B
F:1-17/Domain: secretory signal sequence #status predicted <SIG>
F:18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>
F:52-170/Region: CUB domain #status predicted
F:272-370/Region: homologous to platelet-derived growth factor/vascular endothelial growth factor
F:294-308/Region: conserved motif #status predicted
Query Match 40.7%; Score 753; DB 2; Length 370;
Best Local Similarity 45.3%; Pred. No. 1.7e-55;
Matches 148; Conservative 59; Mismatches 92; Indels 28; Gaps 9;
QY 37 EQNGVQD-PRHERVVTISNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRQLTDFDERFG 95
DB 42 ESNHLDLYRDETQVKNGYVQSPFPNSYPRNLLTWLHS-QENTRIQLVFNQFG 100
QY 96 LEDPEDICKYDFVEEESDGSVL--GRWCGSGTVPKGQTSKGNHIRFVSDYFPPE 153
DB 101 LBEAENDICRYDFVEDISSETIIRGWCHEVPPRIKSTNQIKITFKSDDYFAK 160
QY 154 PGFCIHYSII--MPQVTEI-----SPSVLPSSLSLNLNNAVTAFT 195
DB 161 PGKIIYISLLEDFQPAASSTNVESTSISGVSYNSPSTDP-TLIADLDKKIAEFD 219
QY 196 LBEILRYLPDRQVLDLSLYKPTQLLQKAFYLGKSKVYNLLKEEYKLYSCTPRNF 255
DB 220 VEDLLKYFNPESQWEDLENMILTTPRYGRSY-HSRKSK-VDLRLNDDAKRYSCTPRNY 277
QY 256 SVSIREELKRTDTFMPGCLLVKRCGNCACCLHNCNCCVPRKVTYKHYVQLRPP-- 313
DB 278 SVNIREELKLANVFFPRCLLVQRCGNCGCGTNNRSCCTNSGKTIVKHYVQLPEPGH 337
QY 314 -KTGVKGLHSLTDVALEHHEECDCVC 339
DB 338 IKRGRKTKTALVDIQLDHERCDDIC 364
RESULT 3
JC2218
procollagen C-endopeptidase (EC 3.4.24.19) - African clawed frog (clone 22AN)
N:Alternate names: Bone morphogenetic protein 1
C:Species: Xenopus laevis (African clawed frog)
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Sep-1999
C:Accession: JC2218
R:Maeno, M.; Xue, Y.; Wood, T.I.; Ong, R.C.; Kung, H.
Gene 134, 257-261, 1993
A:Title: Cloning and expression of cDNA encoding Xenopus laevis bone morphogenetic prote
A:Reference number: JC2218; MUID:94085787; PMID:8262384
A:Accession: JC2218
A:Molecule type: mRNA
A:Residues: 1-707 <MAE>
A:Cross-references: GB:L12249; NID:G406540; PIDN:AAA16313.1; PID:G406541
C:Comment: This protein induces ectopic cartilage formation in vivo.
C:Superfamily: procollagen C-endopeptidase; ascatin homology; C1r/C1s repeat homology; zinc
C:Keywords: beta-hydroxyasparagine; glycoprotein; hydrolase; metalloproteinase; zinc
F:93-284/Domain: ascatin homology <AST>
F:285-397/Region: complement 1r/1s-like repeat
F:285-394/Domain: C1r/C1s repeat homology <C1R1>
F:398-510/Region: complement 1r/1s-like repeat
```

```
F:398-507/Domain: C1r/C1s repeat homology <C1R2>
F:514-550/Domain: EGF homology <EGF>
F:554-666/Region: complement 1r/1s-like repeat
F:554-663/Domain: C1r/C1s repeat homology <C1R3>
F:62,105,295,326/Binding site: carboxydrate (Asn) (covalent) #status predicted
F:176,180,186,235/Binding site: zinc (His, His, His, Tyr) #status predicted
F:177/Active site: Glu #status predicted
F:528/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
Query Match 10.3%; Score 191; DB 2; Length 707;
Best Local Similarity 45.2%; Pred. No. 6.7e-08;
Matches 47; Conservative 16; Mismatches 33; Indels 8; Gaps 5;
QY 55 NGSIIHSPKFPHTYPRNMVLVWRLVAVDENVRQLTDFDERFGLDEPDDICKYDFVEVEE- 113
DB 562 NGSINSPGWPKPEYPPNKNCIWQVAPTQ-YRISLKFQD---FETEGNDVCKYDFVEVRSG 617
QY 114 -PSDGSVLGRWCGSGTVPKGQTSKGNHIRFVSDYFPPEPGF 156
DB 618 L7SDSKLHGKFCGS-ELPAVITSQYNNMRIFKSDNTV-SKKGF 659
RESULT 4
AS8788
procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form HIS - human
N:Alternate names: bone morphogenic protein splice form BMP-1/HIS
C:Species: Homo sapiens (man)
C:Date: 28-Mar-1998 #sequence_revision 09-Apr-1998 #text_change 18-Jun-1999
C:Accession: A37278; AS8788
R:Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.; He
Science 242, 1528-1534, 1998
A:Title: Novel regulators of bone formation: molecular clones and activities.
A:Reference number: A37278; MUID:89072730; PMID:3201241
A:Accession: A37278
A:Molecule type: mRNA
A:Residues: 1-702, EKRALQPPRGPHQLKRVQKRNTPQ' <WOZ>
A:Cross-references: GB:M22488; NID:G179499; PIDN:AAA51833.1; PID:G179500
R:Takahara, K.; Lyons, G.E.; Greenspan, D.S.
J. Biol. Chem. 269, 32572-32578, 1994
A:Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld) are enc
A:Reference number: AS8788; MUID:95096114; PMID:7798260
A:Accession: AS8788
A:Molecule type: mRNA
A:Residues: 703-823 <TAK>
A:Cross-references: GB:L35278; NID:G619423; PIDN:AAC41703.1; PID:G619424
C:Genetics:
A:Gene: GDB:BMP1; BMP-1
A:Cross-references: GDB:125203; OMIM:112264
A:Map position: 8p21-8p21
C:Function:
A:Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen ty
C:Superfamily: procollagen C-endopeptidase; ascatin homology; C1r/C1s repeat homology;
C:Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication;
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-823/Product: procollagen C-endopeptidase splice form HIS #status predicted <MAT>
F:130-321/Domain: ascatin homology <AST>
F:322-431/Domain: C1r/C1s repeat homology <C1R1>
F:435-544/Domain: C1r/C1s repeat homology <C1R2>
F:551-587/Domain: EGF homology <EGF>
F:591-700/Domain: C1r/C1s repeat homology <C1R3>
F:738-752/Region: histidine-rich
F:91,142,332,363,599/Binding site: carboxydrate (Asn) (covalent) #status predicted
F:163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-6
F:213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted
F:214/Active site: Glu #status predicted
F:565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
Query Match 10.3%; Score 190; DB 1; Length 823;
Best Local Similarity 36.0%; Pred. No. 9.9e-08;
Matches 54; Conservative 20; Mismatches 48; Indels 28; Gaps 7;
QY 55 NGSIIHSPKFPHTYPRNMVLVWRLVAVDENVRQLTDFDERFGLDEPDDICKYDFVEVEE- 113
```







A:Cross-references: FlyBase:FBgn0003719  
C:Superfamily: dorsal-ventral patterning protein tolloid; astacin homology; C1r/C1s ref  
C:Keywords: duplication; hydrolase; metalloproteinase; zinc  
F:136-329/Domain: astacin homology <AST>  
F:352-464/Domain: C1r/C1s repeat homology <C1R1>  
F:468-578/Domain: C1r/C1s repeat homology <C1R2>  
F:585-620/Domain: EGF homology <EG1>  
F:624-740/Domain: C1r/C1s repeat homology <C1R3>  
F:747-782/Domain: EGF homology <EG2>  
F:787-896/Domain: C1r/C1s repeat homology <C1R4>  
F:900-1013/Domain: C1r/C1s repeat homology <C1R5>  
F:221,225,231,280/Binding site: zinc (His, His, Tyr) #status predicted  
F:222/Active site: Glu #status predicted

Query Match 8.3%; Score 153; DB 1; Length 1057;  
Best Local Similarity 33.3%; Pred. No. 0.00018;  
Matches 47; Conservative 28; Mismatches 54; Indels 12; Gaps 7;

Qy 13 LAGORTGTAESENISLKKQLSSDKEQNGVQDPRHERV----VTISGNGSIHSPKPPHTYP 68  
Db :  
432 VSGEVIITQTSMLLNVNRNAAGYRGFK-ARFEVVCGGLTKDQSIDSNPYPMYM 490  
Qy 69 RNMVLVRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE--PSDSGVLRWCGS 126  
Db :  
491 PDKECVWRITAPD-NHQVALKF-QSFLE--KHDDGCAYDFVEIRDGNHSDSRILGRFCGD 546  
Qy 127 GTVPKGKTSKGNHIRIRFVSD 147  
Db :  
547 KLPNIKT-RSQMWIRFVSD 566

RESULT 13  
T30337  
Polyprotein - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C>Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 03-Feb-2003  
C:Accession: T30337  
R:Yang, J.C.; Lindsay, L.L.; Hedrick, J.L.  
submitted to the EMBL Data Library, March 1998  
A:Description: cDNA cloning of ovocytinase, a chymotrypsin-like protease released from y  
A:Reference number: Z20829  
A:Accession: T30337  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-1524 <YAN>  
C:Cross-references: EMBL:U81290; NID:g2981640; PID:g2981641; PIDN:AAC24717.1  
C:Superfamily: tryosin related polyprotein; trypsin homology

Query Match 8.0%; Score 147.5; DB 2; Length 1524;  
Best Local Similarity 28.7%; Pred. No. 0.00082;  
Matches 54; Conservative 34; Mismatches 73; Indels 27; Gaps 10;

Qy 56 GSIIHPKFPPTYPRNMVLVRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEV-EEP 114  
Db 439 GMIVSPNPDPYPLKTCSW-IIEAPENHIVKLAFED-FNVEYGHG-CIYDAVEVYDGA 494  
Qy 115 SDGSVLGRWCSGTVPGKQTSKGNHIRFVSDRYFFSEPGCFCHYSIMFQ-----VT 168  
Db :  
495 EEKQILIARQY-TLPLPISSPENTMILRFKTD-MENSYPGKVKFSVPVKEKQFSLPVD 552  
Qy 169 ETTPSPSVLPSSLSDLNNNA-VTAFSTLEEILRYLEPD---RWQVDL-----DS 214  
Db :  
553 DTPTISMHLRAIALDVCGMAFTPKWWLPRIVGEEASPNWPMPVOIFFLRTFHCHEGA 612  
Qy 215 LYKETWOL 222  
Db :  
613 IISPQWIL 620

RESULT 14  
A59271  
Ra-reactive factor (EC 3.4.21.-) 2 precursor - human  
N:Alternate names: mannose binding protein-associated serine proteinase 2 (MABSD-2)

C:Species: Homo sapiens (man)  
 C:Date: 19-May-2000 #sequence\_revision 19-May-2000 #text\_change 16-Jun-2000  
 C:Accession: A59271  
 R:Thiel, S.; Vorup-Jensen, T.; Stover, C.M.; Schwaible, W.J.; Laursen, S.B.; Poulsen, K.  
 Nature 386, 506-510, 1997  
 A:Title: A second serine protease associated with mannan-binding lectin that activates complement factor F1-17/Domains: signal sequence #status predicted <SIG>  
 A:Reference number: A59271; MUID:97242412; PMID:9087411  
 A:Accession: A59271  
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-686 <JEN>  
 A:Cross-references: GB:Y09926; NID:94007626; PIDN:CAA71059.1; PID:94007627  
 A:Experimental source: tissue liver  
 A:Note: submitted to GenBank, December 1996  
 A:Note: parts of this sequence, including the amino end of the mature protein, were determined by mass spectrometry  
 C:Genetics:  
 A:Gene: GDB:MASP2  
 A:Cross-references: GDB:6071500  
 A:Map position: lp36.2-1p36.3  
 C:Superfamily: complement subcomponent C1r; C1r/C1s repeat homology; complement factor H repeat homology  
 C:Keywords: beta-hydroxyasparagine; complement pathway; duplication; hydrolase; serine protease  
 F:1-15/Domains: signal sequence #status predicted <SIG>  
 F:16-444, 445-686/Product: Ra-reactive factor 2 #status predicted <MAT>  
 F:19-134/Domains: C1r/C1s repeat homology <C1R1>  
 F:142-180/Domains: EGF homology <EGF>  
 F:184-293/Domains: C1r/C1s repeat homology <C1R2>  
 F:300-361/Domains: complement factor H repeat homology <FH1>  
 F:366-430/Domains: complement factor H repeat homology <FH2>  
 F:445-679/Domains: trypsin homology <TRY>  
 F:72-90, 142-156, 152-165, 167-180, 184-211, 241-259, 300-348, 328-361, 366-412, 396-430, 434-552, 552-553, 554-555, 556-557, 558-559, 560-561, 562-563, 564-565, 566-567, 568-569, 570-571, 572-573, 574-575, 576-577, 578-579, 580-581, 582-583, 584-585, 586-587, 588-589, 590-591, 592-593, 594-595, 596-597, 598-599, 600-601, 602-603, 604-605, 606-607, 608-609, 610-611, 612-613, 614-615, 616-617, 618-619, 620-621, 622-623, 624-625, 626-627, 628-629, 630-631, 632-633, 634-635, 636-637, 638-639, 640-641, 642-643, 644-645, 646-647, 648-649, 650-651, 652-653, 654-655, 656-657, 658-659, 660-661, 662-663, 664-665, 666-667, 668-669, 670-671, 672-673, 674-675, 676-677, 678-679, 680-681, 682-683, 684-685, 686-687, 688-689, 690-691, 692-693, 694-695, 696-697, 698-699, 700-701, 702-703, 704-705, 706-707, 708-709, 710-711, 712-713, 714-715, 716-717, 718-719, 720-721, 722-723, 724-725, 726-727, 728-729, 730-731, 732-733, 734-735, 736-737, 738-739, 740-741, 742-743, 744-745, 746-747, 748-749, 750-751, 752-753, 754-755, 756-757, 758-759, 760-761, 762-763, 764-765, 766-767, 768-769, 770-771, 772-773, 774-775, 776-777, 778-779, 780-781, 782-783, 784-785, 786-787, 788-789, 790-791, 792-793, 794-795, 796-797, 798-799, 800-801, 802-803, 804-805, 806-807, 808-809, 810-811, 812-813, 814-815, 816-817, 818-819, 820-821, 822-823, 824-825, 826-827, 828-829, 830-831, 832-833, 834-835, 836-837, 838-839, 840-841, 842-843, 844-845, 846-847, 848-849, 850-851, 852-853, 854-855, 856-857, 858-859, 860-861, 862-863, 864-865, 866-867, 868-869, 870-871, 872-873, 874-875, 876-877, 878-879, 880-881, 882-883, 884-885, 886-887, 888-889, 890-891, 892-893, 894-895, 896-897, 898-899, 900-901, 902-903, 904-905, 906-907, 908-909, 910-911, 912-913, 914-915, 916-917, 918-919, 920-921, 922-923, 924-925, 926-927, 928-929, 930-931, 932-933, 934-935, 936-937, 938-939, 940-941, 942-943, 944-945, 946-947, 948-949, 950-951, 952-953, 954-955, 956-957, 958-959, 960-961, 962-963, 964-965, 966-967, 968-969, 970-971, 972-973, 974-975, 976-977, 978-979, 980-981, 982-983, 984-985, 986-987, 988-989, 990-991, 992-993, 994-995, 996-997, 998-999, 1000-1001, 1002-1003, 1004-1005, 1006-1007, 1008-1009, 1010-1011, 1012-1013, 1014-1015, 1016-1017, 1018-1019, 1020-1021, 1022-1023, 1024-1025, 1026-1027, 1028-1029, 1030-1031, 1032-1033, 1034-1035, 1036-1037, 1038-1039, 1040-1041, 1042-1043, 1044-1045, 1046-1047, 1048-1049, 1050-1051, 1052-1053, 1054-1055, 1056-1057, 1058-1059, 1060-1061, 1062-1063, 1064-1065, 1066-1067, 1068-1069, 1070-1071, 1072-1073, 1074-1075, 1076-1077, 1078-1079, 1080-1081, 1082-1083, 1084-1085, 1086-1087, 1088-1089, 1090-1091, 1092-1093, 1094-1095, 1096-1097, 1098-1099, 1100-1101, 1102-1103, 1104-1105, 1106-1107, 1108-1109, 1110-1111, 1112-1113, 1114-1115, 1116-1117, 1118-1119, 1120-1121, 1122-1123, 1124-1125, 1126-1127, 1128-1129, 1130-1131, 1132-1133, 1134-1135, 1136-1137, 1138-1139, 1140-1141, 1142-1143, 1144-1145, 1146-1147, 1148-1149, 1150-1151, 1152-1153, 1154-1155, 1156-1157, 1158-1159, 1160-1161, 1162-1163, 1164-1165, 1166-1167, 1168-1169, 1170-1171, 1172-1173, 1174-1175, 1176-1177, 1178-1179, 1180-1181, 1182-1183, 1184-1185, 1186-1187, 1188-1189, 1190-1191, 1192-1193, 1194-1195, 1196-1197, 1198-1199, 1200-1201, 1202-1203, 1204-1205, 1206-1207, 1208-1209, 1210-1211, 1212-1213, 1214-1215, 1216-1217, 1218-1219, 1220-1221, 1222-1223, 1224-1225, 1226-1227, 1228-1229, 1230-1231, 1232-1233, 1234-1235, 1236-1237, 1238-1239, 1240-1241, 1242-1243, 1244-1245, 1246-1247, 1248-1249, 1250-1251, 1252-1253, 1254-1255, 1256-1257, 1258-1259, 1260-1261, 1262-1263, 1264-1265, 1266-1267, 1268-1269, 1270-1271, 1272-1273, 1274-1275, 1276-1277, 1278-1279, 1280-1281, 1282-1283, 1284-1285, 1286-1287, 1288-1289, 1290-1291, 1292-1293, 1294-1295, 1296-1297, 1298-1299, 1300-1301, 1302-1303, 1304-1305, 1306-1307, 1308-1309, 1310-1311, 1312-1313, 1314-1315, 1316-1317, 1318-1319, 1320-1321, 1322-1323, 1324-1325, 1326-1327, 1328-1329, 1330-1331, 1332-1333, 1334-1335, 1336-1337, 1338-1339, 1340-1341, 1342-1343, 1344-1345, 1346-1347, 1348-1349, 1350-1351, 1352-1353, 1354-1355, 1356-1357, 1358-1359, 1360-1361, 1362-1363, 1364-1365, 1366-1367, 1368-1369, 1370-1371, 1372-1373, 1374-1375, 1376-1377, 1378-1379, 1380-1381, 1382-1383, 1384-1385, 1386-1387, 1388-1389, 1390-1391, 1392-1393, 1394-1395, 1396-1397, 1398-1399, 1400-1401, 1402-1403, 1404-1405, 1406-1407, 1408-1409, 1410-1411, 1412-1413, 1414-1415, 1416-1417, 1418-1419, 1420-1421, 1422-1423, 1424-1425, 1426-1427, 1428-1429, 1430-1431, 1432-1433, 1434-1435, 1436-1437, 1438-1439, 1440-1441, 1442-1443, 1444-1445, 1446-1447, 1448-1449, 1450-1451, 1452-1453, 1454-1455, 1456-1457, 1458-1459, 1460-1461, 1462-1463, 1464-1465, 1466-1467, 1468-1469, 1470-1471, 1472-1473, 1474-1475, 1476-1477, 1478-1479, 1480-1481, 1482-1483, 1484-1485, 1486-1487, 1488-1489, 1490-1491, 1492-1493, 1494-1495, 1496-1497, 1498-1499, 1500-1501, 1502-1503, 1504-1505, 1506-1507, 1508-1509, 1510-1511, 1512-1513, 1514-1515, 1516-1517, 1518-1519, 1520-1521, 1522-1523, 1524-1525, 1526-1527, 1528-1529, 1530-1531, 1532-1533, 1534-1535, 1536-1537, 1538-1539, 1540-1541, 1542-1543, 1544-1545, 1546-1547, 1548-1549, 1550-1551, 1552-1553, 1554-1555, 1556-1557, 1558-1559, 1560-1561, 1562-1563, 1564-1565, 1566-1567, 1568-1569, 1570-1571, 1572-1573, 1574-1575, 1576-1577, 1578-1579, 1580-1581, 1582-1583, 1584-1585, 1586-1587, 1588-1589, 1590-1591, 1592-1593, 1594-1595, 1596-1597, 1598-1599, 1600-1601, 1602-1603, 1604-1605, 1606-1607, 1608-1609, 1610-1611, 1612-1613, 1614-1615, 1616-1617, 1618-1619, 1620-1621, 1622-1623, 1624-1625, 1626-1627, 1628-1629, 1630-1631, 1632-1633, 1634-1635, 1636-1637, 1638-1639, 1640-1641, 1642-1643, 1644-1645, 1646-1647, 1648-1649, 1650-1651, 1652-1653, 1654-1655, 1656-1657, 1658-1659, 1660-1661, 1662-1663, 1664-1665, 1666-1667, 1668-1669, 1670-1671, 1672-1673, 1674-1675, 1676-1677, 1678-1679, 1680-1681, 1682-1683, 1684-1685, 1686-1687, 1688-1689, 1690-1691, 1692-1693, 1694-1695, 1696-1697, 1698-1699, 1700-1701, 1702-1703, 1704-1705, 1706-1707, 1708-1709, 1710-1711, 1712-1713, 1714-1715, 1716-1717, 1718-1719, 1720-1721, 1722-1723, 1724-1725, 1726-1727, 1728-1729, 1730-1731, 1732-1733, 1734-1735, 1736-1737, 1738-1739, 1740-1741, 1742-1743, 1744-1745, 1746-1747, 1748-1749, 1750-1751, 1752-1753, 1754-1755, 1756-1757, 1758-1759, 1760-1761, 1762-1763, 1764-1765, 1766-1767, 1768-1769, 1770-1771, 1772-1773, 1774-1775, 1776-1777, 1778-1779, 1780-1781, 1782-1783, 1784-1785, 1786-1787, 1788-1789, 1790-1791, 1792-1793, 1794-1795, 1796-1797, 1798-1799, 1800-1801, 1802-1803, 1804-1805, 1806-1807, 1808-1809, 1810-1811, 1812-1813, 1814-1815, 1816-1817, 1818-1819, 1820-1821, 1822-1823, 1824-1825, 1826-1827, 1828-1829, 1830-1831, 1832-1833, 1834-1835, 1836-1837, 1838-1839, 1840-1841, 1842-1843, 1844-1845, 1846-1847, 1848-1849, 1850-1851, 1852-1853, 1854-1855, 1856-1857, 1858-1859, 1860-1861, 1862-1863, 1864-1865, 1866-1867, 1868-1869, 1870-1871, 1872-1873, 1874-1875, 1876-1877, 1878-1879, 1880-1881, 1882-1883, 1884-1885, 1886-1887, 1888-1889, 1890-1891, 1892-1893, 1894-1895, 1896-1897, 1898-1899, 1900-1901, 1902-1903, 1904-1905, 1906-1907, 1908-1909, 1910-1911, 1912-1913, 1914-1915, 1916-1917, 1918-1919, 1920-1921, 1922-1923, 1924-1925, 1926-1927, 1928-1929, 1930-1931, 1932-1933, 1934-1935, 1936-1937, 1938-1939, 1940-1941, 1942-1943, 1944-1945, 1946-1947, 1948-1949, 1950-1951, 1952-1953, 1954-1955, 1956-1957, 1958-1959, 1960-1961, 1962-1963, 1964-1965, 1966-1967, 1968-1969, 1970-1971, 1972-1973, 1974-1975, 1976-1977, 1978-1979, 1980-1981, 1982-1983, 1984-1985, 1986-1987, 1988-1989, 1990-1991, 1992-1993, 1994-1995, 1996-1997, 1998-1999, 2000-2001, 2002-2003, 2004-2005, 2006-2007, 2008-2009, 2010-2011, 2012-2013, 2014-2015, 2016-2017, 2018-2019, 2020-2021, 2022-2023, 2024-2025, 2026-2027, 2028-2029, 2030-2031, 2032-2033, 2034-2035, 2036-2037, 2038-2039, 2040-2041, 2042-2043, 2044-2045, 2046-2047, 2048-2049, 2050-2051, 2052-2053, 2054-2055, 2056-2057, 2058-2059, 2060-2061, 2062-2063, 2064-2065, 2066-2067, 2068-2069, 2070-2071, 2072-2073, 2074-2075, 2076-2077, 2078-2079, 2080-2081, 2082-2083, 2084-2085, 2086-2087, 2088-2089, 2090-2091, 2092-2093, 2094-2095, 2096-2097, 2098-2099, 2100-2101, 2102-2103, 2104-2105, 2106-2107, 2108-2109, 2110-2111, 2112-2113, 2114-2115, 2116-2117, 2118-2119, 2120-2121, 2122-2123, 2124-2125, 2126-2127, 2128-2129, 2130-2131, 2132-2133, 2134-2135, 2136-2137, 2138-2139, 2140-2141, 2142-2143, 2144-2145, 2146-2147, 2148-2149, 2150-2151, 2152-2153, 2154-2155, 2156-2157, 2158-2159, 2160-2161, 2162-2163, 2164-2165, 2166-2167, 2168-2169, 2170-2171, 2172-2173, 2174-2175, 2176-2177, 2178-2179, 2180-2181, 2182-2183, 2184-2185, 2186-2187, 2188-2189, 2190-2191, 2192-2193, 2194-2195, 2196-2197, 2198-2199, 2200-2201, 2202-2203, 2204-2205, 2206-2207, 2208-2209, 2210-2211, 2212-2213, 2214-2215, 2216-2217, 2218-2219, 2220-2221, 2222-2223, 2224-2225, 2226-2227, 2228-2229, 2230-2231, 2232-2233, 2234-2235, 2236-2237, 2238-2239, 2240-2241, 2242-2243, 2244-2245, 2246-2247, 2248-2249, 2250-2251, 2252-2253, 2254-2255, 2256-2257, 2258-2259, 2260-2261, 2262-2263, 2264-2265, 2266-2267, 2268-2269, 2270-2271, 2272-2273, 2274-2275, 2276-2277, 2278-2279, 2280-2281, 2282-2283, 2284-2285, 2286-2287, 2288-2289, 2290-2291, 2292-2293, 2294-2295, 2296-2297, 2298-2299, 2300-2301, 2302-2303, 2304-2305, 2306-2307, 2308-2309, 2310-2311, 2312-2313, 2314-2315, 2316-2317, 2318-2319, 2320-2321, 2322-2323, 2324-2325, 2326-2327, 2328-2329, 2330-2331, 2332-2333, 2334-2335, 2336-2337, 2338-2339, 2340-2341, 2342-2343, 2344-2345, 2346-2347, 2348-2349, 2350-2351, 2352-2353, 2354-2355, 2356-2357, 2358-2359, 2360-2361, 2362-2363, 2364-2365, 2366-2367, 2368-2369, 2370-2371, 2372-2373, 2374-2375, 2376-2377, 2378-2379, 2380-2381, 2382-2383, 2384-2385, 2386-2387, 2388-2389, 2390-2391, 2392-2393, 2394-2395, 2396-2397, 2398-2399, 2400-2401, 2402-2403, 2404-2405, 2406-2407, 2408-2409, 2410-2411, 2412-2413, 2414-2415, 2416-2417, 2418-2419, 2420-2421, 2422-2423, 2424-2425, 2426-2427, 2428-2429, 2430-2431, 2432-2433, 2434-2435, 2436-2437, 2438-2439, 2440-2441, 2442-2443, 2444-2445, 2446-2447, 2448-2449, 2450-2451, 2452-2453, 2454-2455, 2456-2457, 2458-2459, 2460-2461, 2462-2463, 2464-2465, 2466-2467, 2468-2469, 2470-2471, 2472-2473, 2474-2475, 2476-2477, 2478-2479, 2480-2481, 2482-2483, 2484-2485, 2486-2487, 2488-2489, 2490-2491, 2492-2493, 2494-2495, 2496-2497, 2498-2499, 2500-2501, 2502-2503, 2504-2505, 2506-2507, 2508-2509, 2510-2511, 2512-2513, 2514-2515, 2516-2517, 2518-2519, 2520-2521, 2522-2523, 2524-2525, 2526-2527, 2528-2529, 2530-2531, 2532-2533, 2534-2535, 2536-2537, 2538-2539, 2540-2541, 2542-2543, 2544-2545, 2546-2547, 2548-2549, 2550-2551, 2552-2553, 2554-2555, 2556-2557, 2558-2559, 2560-2561, 2562-2563, 2564-2565, 2566-2567, 2568-2569, 2570-2571, 2572-2573, 2574-2575, 2576-2577, 2578-2579, 2580-2581, 2582-2583, 2584-2585, 2586-2587, 2588-2589, 2590-2591, 2592-2593, 2594-2595, 2596-2597, 2598-2599, 2600-2601, 2602-2603, 2604-2605, 2606-2607, 2608-2609, 2610-2611, 2612-2613, 2614-2615, 2616-2617, 2618-2619, 2620-2621, 2622-2623, 2624-2625, 2626-2627, 2628-2629, 2630-2631, 2632-2633, 2634-2635, 2636-2637, 2638-2639, 2640-2641, 2642-2643, 2644-2645, 2646-2647, 2648-2649, 2650-2651, 2652-2653, 2654-2655, 2656-2657, 2658-2659, 2660-2661, 2662-2663, 2664-2665, 2666-2667, 2668-2669, 2670-2671, 2672-2673, 2674-2675, 2676-2677, 2678-2679, 2680-2681, 2682-2683, 2684-2685, 2686-2687, 2688-2689, 2690-2691, 2692-2693, 2694-2695, 2696-2697, 26

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 20:55:48 ; Search time 8.55655 Seconds  
(without alignments)  
1896.117 Million cell updates/sec

Title: US-09-852-209A-7

Perfect score: 1848

Sequence: 1 MLLGLLLTSLALAGQRTGT.....DVALEHHECDVCVRGNAGG 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	191	10.3	707	1 BMP1_XENLA	P98070 xenopus lae
2	183.5	9.9	928	1 NRPI_XENLA	P28824 xenopus lae
3	181	9.8	986	1 BMP1_HUMAN	P13497 homo sapien
4	181	9.8	991	1 BMP1_MOUSE	P98063 mus musculus
5	176	9.5	923	1 NRPI_HUMAN	O14786 homo sapien
6	174	9.4	1022	1 TLD_BRARE	O57460 brachydanio
7	172	9.3	922	1 NRPI_RAT	Q9cwj9 rattus norv
8	169	9.1	923	1 NRPI_MOUSE	P97333 mus musculus
9	167	9.0	914	1 NRPI_CHICK	P79795 gallus gall
10	163.5	8.8	616	1 SPAN_STRPU	P97995 strongyloce
11	158	8.5	449	1 PCO1_HUMAN	Q15113 homo sapien
12	155.5	8.4	925	1 NRP2_RAT	O35276 rattus norv
13	155.5	8.4	931	1 NRP2_HUMAN	O60462 homo sapien
14	155.5	8.4	931	1 NRP2_MOUSE	O35375 mus musculus
15	153.5	8.3	326	1 VEGD_RAT	O35251 rattus norv
16	153	8.3	1057	1 TLD_DROME	P25723 drosophila
17	147.5	8.0	704	1 CEAR_MOUSE	P98064 mus musculus
18	145.5	7.9	686	1 MAS2_HUMAN	O00187 homo sapien
19	144.5	7.8	597	1 BP10_PARLI	P42674 paracentrot
20	144	7.8	699	1 CEAR_HUMAN	P48740 h complemen
21	137.5	7.4	705	1 CLAR_HUMAN	P00736 rattus norv
22	136.5	7.4	458	1 PCO1_RAT	O08628 rattus norv
23	136	7.4	354	1 VEGD_HUMAN	O43915 homo sapien
24	135.5	7.3	358	1 VEGD_MOUSE	P97946 mus musculus
25	133.5	7.2	468	1 PCO1_MOUSE	Q61398 mus musculus
26	132	7.1	415	1 VGCC_MOUSE	P97953 mus musculus
27	130	7.0	639	1 BMPH_STRPU	P98069 strongyloce
28	128	6.9	277	1 TSG6_HUMAN	P98066 homo sapien
29	127	6.9	419	1 VEGC_HUMAN	P49767 homo sapien
30	125.5	6.8	245	1 PDGB_FELCA	P12919 felis silve
31	123	6.7	275	1 TSG6_MOUSE	O08859 mus musculus
32	117.5	6.4	276	1 TSG6_RABIT	P98065 oryctolagus
33	114.5	6.2	226	1 PDGA_XENLA	P13698 xenopus lae

## RESULT 1

ID	BMP1_XENLA	STANDARD;	PRT;	707 AA.
AC	P98070;			
DT	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Bone morphogenetic protein 1 precursor (EC 3.4.24.-) (BMP-1).			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;			
OC	Xenopodinae; Xenopus.			
OK	NCBI_TaxID=8355;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Embryo;			
RX	MEDLINE=94085787; PubMed=8262384;			
RA	Maeno M., Xue Y., Wood T.I., Ong R.C., Kung H.F.;			
RT	"Cloning and expression of cDNA encoding Xenopus laevis bone			
RT	morphogenetic protein-1 during early embryonic development.";			
RL	Gene 134:257-261(1993).			
CC	-!- FUNCTION: INVOLVED IN PATTERN FORMATION IN GASTRULA AND LATER			
CC	DIFFERENTIATION OF DEVELOPING ORGANS.			
CC	-!- DEVELOPMENTAL STAGE: BLASTULA, EARLY GASTRULA AND HATCHED			
CC	TADPOLES; LITTLE OR NO EXPRESSION IN MORULA AND LATE GASTRULA.			
CC	-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.			
CC	-!- SIMILARITY: Contains 1 EGF-like domain.			
CC	-!- SIMILARITY: Contains 3 CUB domains.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
EMBL	L12249; AAA16313.1; -			
PIR	JC2218; JC2218.			
DR	HSSP; P00736; 1APO.			
DR	MEROPS; M12.005; -			
DR	InterPro; IPR001506; Astacin.			
DR	InterPro; IPR000152; Abx_hydroxyl.			
DR	InterPro; IPR000859; CUB domain.			
DR	InterPro; IPR001881; EGF Ca.			
DR	InterPro; IPR006209; EGF-like.			
DR	InterPro; IPR006026; Nzn_Mtpeptidase.			
DR	InterPro; IPR006025; Zn_Mtpeptidase.			
DR	Pfam; PF01400; Astacin; 1.			
DR	Pfam; PF00431; CUB; 3.			
DR	Pfam; PF00008; EGF; 1.			
DR	PRINTS; PR00480; ASTACIN.			
DR	SMART; SM00042; CUB; 3.			
DR	SMART; SM00179; EGF_CA; 1.			
DR	SMART; SM00235; ZnMC; 1.			
DR	PROSITE; PS00142; ZINC_PROTEASE; 1.			

34	113	6.1	695	1	CASP_MESAU	P15156 mesocricetu
35	112.5	6.1	241	1	PDGB_HUMAN	P01127 homo sapien
36	111.5	6.0	164	1	VEGA_CAVPO	P26617 cavia porce
37	111.5	6.0	226	1	TSIS_SMSAV	P01128 simian sarc
38	109	5.9	855	1	STI4_HUMAN	Q9y5y6 homo sapien
39	108.5	5.9	148	1	VEGH_HRFN7	P52585 orf virus (
40	105.5	5.7	207	1	VEGH_HUMAN	P49765 homo sapien
41	104	5.6	514	1	UVS2_XENLA	P42664 xenopus lae
42	103.5	5.6	207	1	VEGB_BOVIN	Q9xe49 bos taurus
43	103.5	5.6	225	1	PDGB_RAT	Q05028 rattus norv
44	103.5	5.6	241	1	PDGB_SHEEP	Q95229 ovis aries
45	103	5.6	211	1	PDGA_HUMAN	P04085 homo sapien

## ALIGNMENTS

```

DR PROSITE; PS01180; CUB; 3.
DR PROSITE; PS00010; ASX HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
KW Growth factor; Cytokine; Repeat; Bone; Cartilage; Hydrolase; Protease;
KW Metalloprotease; EGF-like domain; Zinc; Calcium; Signal;
KW Glycoprotein.
FT SIGNAL 1 ? POTENTIAL.
FT PROPEP ? 83
FT CHAIN 84 707 POTENTIAL.
FT DOMAIN 84 284 BONE MORPHOGENETIC PROTEIN 1.
FT DOMAIN 285 397 METALLOPROTEASE.
FT DOMAIN 398 509 CUB 1.
FT DOMAIN 510 551 CUB 2.
FT DOMAIN 554 666 EGF-LIKE, CALCIUM-BINDING (POTENTIAL).
FT METAL 176 177 CUB 3.
FT ACT SITE 177 177 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 180 180 BY SIMILARITY.
FT METAL 186 186 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 146 149 ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID 514 526 BY SIMILARITY.
FT DISULFID 522 535 BY SIMILARITY.
FT DISULFID 537 550 BY SIMILARITY.
FT CARBOHYD 62 62 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 105 105 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 326 326 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 562 562 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 707 AA; 80673 MW; 1B6980D716DC9B8D CRC64;

Query Match 10.3%; Score 191; DB 1; Length 707;
Best Local Similarity 45.2%; Pred. No. 6.9e-08;
Matches 47; Conservative 16; Mismatches 33; Indels 8; Gaps 5;

QY 55 NGSIIHSPKPHPTYPNNVLVWELVAVDENVRQLTFDERFGLDEDDICKYDFVEVER- 113
DB 562 NGSINSPGPKPYPPNKNKINQVLVPTQ-YRISLAKFDQ---PETGNDVCKYDFVEVRSG 617
QY 114 -PSDGSVLGRWCGSGTVPGKQSKGNHIRFVSDYFPSPGPF 156
DB 618 LTSDSKLHGKFGS-ELPAVITSQNNMIEFKSDNTV-SKKG 659

RESULT 2
NRPI_XENLA
ID NRPI_XENLA STANDARD; PRT; 928 AA.
AC P28824;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neupilin-1 precursor (A5 protein) (A5 antigen).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=91337458; PubMed=1908252;
RA Takagi S., Hirata T., Agata K., Mochii M., Eguchi G., Fujisawa H.;
RT "The A5 antigen, a candidate for the neuronal recognition molecule,
RT has homologues to complement components and coagulation factors.";
RL Neuron 7:295-307(1991).
CC -!- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE
CC CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF
CC CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS
CC SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SENAPHORINS (BY
CC SIMILARITY). PRESUMED TO BE INVOLVED IN THE NEURONAL RECOGNITION
CC BETWEEN THE OPTIC NERVE FIBERS AND THE VISUAL CENTERS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: RETINAL GANGLION CELLS AND VISUAL CENTER

```

```

CC NEURONS.
CC -!- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
CC -!- SIMILARITY: Contains 2 CUB domains.
CC -!- SIMILARITY: Contains 2 F5/8 type C domains.
CC -!- SIMILARITY: Contains 1 MAM domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D10467; BAA01260.1; -.
CC HSSP; P12259; 1CZT
CC InterPro; IPR000859; CUB domain.
CC InterPro; IPR000421; FA58_C.
CC InterPro; IPR000998; MAM_domain.
CC Pfam; PF00431; CUB; 2.
CC Pfam; PF00754; F5_F8_type_C; 2.
CC Pfam; PF00629; MAM; 1.
CC PRINTS; PR00020; MAMDOMAIN.
CC SMART; SM00042; CUB; 2.
CC SMART; SM00231; FA58C; 2.
CC SMART; SM00137; MAM; 1.
CC PROSITE; PS01180; CUB; 2.
CC PROSITE; PS01285; FA58C_1; 2.
CC PROSITE; PS01286; FA58C_2; 2.
CC PROSITE; PS00022; FA58C_3; 2.
CC PROSITE; PS00740; MAM 1; 1.
CC PROSITE; PS00060; MAM 2; 1.
KW Angiogenesis; Transmembrane; Glycoprotein; Neurone; Signal; Repeat;
KW Receptor; Antigen.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 928 NEUROPILIN-1.
FT DOMAIN 22 860 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 861 883 POTENTIAL.
FT DOMAIN 884 928 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 27 141 CUB 1.
FT DOMAIN 147 265 CUB 2.
FT DOMAIN 275 424 F5/8 TYPE C 1.
FT DOMAIN 431 584 F5/8 TYPE C 2.
FT DOMAIN 646 812 MAM.
FT DISULFID 27 54 PROBABLE.
FT DISULFID 82 104 PROBABLE.
FT DISULFID 147 173 PROBABLE.
FT DISULFID 206 228 PROBABLE.
FT DISULFID 275 424 BY SIMILARITY.
FT DISULFID 431 584 BY SIMILARITY.
FT CARBOHYD 150 150 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 523 523 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 844 844 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 928 AA; 103416 MW; AF6B323B0A4C789D CRC64;

Query Match 9.9%; Score 183.5; DB 1; Length 928;
Best Local Similarity 30.7%; Pred. No. 4e-07;
Matches 55; Conservative 34; Mismatches 65; Indels 25; Gaps 9;

QY 50 VTISNGSIHSPKPHPTYPNNVLVWELVAVDENVRQLTFDERFGLDEDDICKYDFV 109
DB 31 IKITSPLTSAGYPSHSPPSQRCWLQAPHYQRIIMFNPHFDLEDR---CKYDIV 87
QY 110 EV--EPPDGSVLGRWCGSGTVPGKQSKGNHIRFVSDYFPSPGPGCIHYSIM--P 165
DB 88 EVIDGDNAGNQLLGKYGK-IAPSPLVSTGSPSIFIRFVSDYETPG-AGFSIYEVFKTGP 145
QY 166 QVTE--TTSPLVLP-----PSSLSLDLNNVATATSTLELIRYLEPDRQVLDLS 214
DB 146 ECRNFTSSNGVIGPKYKPKYNALECYTIIFA----PKMQEIV--LEFSEFLEADS 198

```

```
RESULT 3
ID -BMP1_HUMAN STANDARD; PRT; 986 AA.
AC P13497; Q13872; Q14874; Q99421; Q99422; Q99423; Q99438;
DT 01-JAN-1990 (Rel. 13, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bone morphogenetic protein 1 precursor (EC 3.4.24.19) (BMP-1)
DE (Procollagen C-proteinase) (PCP) (Mammalian tolloid protein) (mTld).
GN BMP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM BMP1-3).
RC TISSUE=Skin;
RX MEDLINE=96209868; PubMed=8643539;
RA Li S.W., Sieron A.L., Fertala A., Hojima Y., Arnold W.V.,
RA Prockop D.J.;
RT "The C-proteinase that processes procollagens to fibrillar collagens
RT is identical to the protein previously identified as bone morphogenic
RT protein-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:5127-5130(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM BMP1-1).
RX MEDLINE=89072730; PubMed=3201241;
RA Wozney J.M., Rosen V., Celeste A.J., Mitscock L.M., Whitters M.J.,
RA Kriz R.W., Hewick R.M., Wang E.A.;
RT "Novel regulators of bone formation: molecular clones and
RT activities.";
RL Science 242:1528-1534(1988).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS BMP1-4; BMP1-5 AND BMP1-6).
RC TISSUE=Placenta;
RX MEDLINE=96160316; PubMed=9500680;
RA Janitz M., Heiser V., Boettcher U., Landt O., Lauster R.;
RT "Three alternatively spliced variants of the gene coding for the human
RT bone morphogenetic protein-1.";
RL J. Mol. Med. 76:141-146(1998).
RN [4]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS BMP1-3 AND BMP1-7).
RC TISSUE=Placenta;
RX MEDLINE=95096114; PubMed=7798260;
RA Takahara K., Lyons G.E., Greenspan D.S.;
RT "Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld)
RT are encoded by alternatively spliced transcripts which are
RT differentially expressed in some tissues.";
RL J. Biol. Chem. 269:32572-32578(1994).
RN [5]
RP DISULFIDE BOND IN METALLOPROTEASE DOMAIN.
RX MEDLINE=21336528; PubMed=11283002;
RA Garrigue-Antar L., Barker C., Kadler K.E.;
RT "Identification of amino acid residues in bone morphogenetic
RT protein-1 important for procollagen C-proteinase activity.";
RL J. Biol. Chem. 276:26237-26242(2001).
CC -!- FUNCTION: CLEAVES THE C-TERMINAL PROPEPTIDES OF PROCOLLAGEN I, II
CC AND II. INDUCES CARTILAGE AND BONE FORMATION.
CC -!- CATALYTIC ACTIVITY: Cleavage of the C-terminal propeptide at
CC Ala--Asp in type I and II procollagens and at Arg--Asp in type
CC III.
CC COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -!- ENZYME REGULATION: ACTIVITY IS INCREASED BY THE PROCOLLAGEN C-
CC ENDOPEPTIDASE ENHANCER PROTEIN.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=7;
CC Name=BMP1-3;
CC IsoId=P13497-1; Sequence=Displayed;
CC Name=BMP1-1;
CC IsoId=P13497-2; Sequence=VSP_005461, VSP_005462;
CC Name=BMP1-2;
CC IsoId=P13497-7; Sequence=Not described;
```

```
CC CC Name=BMP1-4;
CC CC IsoId=P13497-3; Sequence=VSP_005463, VSP_005464;
CC CC Name=BMP1-5;
CC CC IsoId=P13497-4; Sequence=VSP_005465, VSP_005466;
CC CC Name=BMP1-6;
CC CC IsoId=P13497-5; Sequence=VSP_005467, VSP_005468;
CC CC Name=BMP1-7;
CC CC IsoId=P13497-6; Sequence=VSP_005469, VSP_005470;
CC CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.
CC CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC CC -!- SIMILARITY: Contains 5 CUB domains.
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U50330; AAA93462.1; -
CC EMBL; M22488; AAA51833.1; -
CC EMBL; Y08723; CAA69973.1; -
CC EMBL; Y08724; CAA69974.1; -
CC EMBL; Y08725; CAA69975.1; -
CC EMBL; L35278; AAC41703.1; -
CC EMBL; L35279; AAC41710.1; -
CC PIR; A37278; B58788.
CC HSRF; P00736; IAPQ.
CC MEROPS; M12.005; -.
CC Genew; HGNC:1067; BMP1.
CC MIM; 112264; -.
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0008237; F:metalloproteinase activity; NAS.
CC GO; GO:0001502; P:cartilage condensation; TAS.
CC GO; GO:0007275; P:development; TAS.
CC InterPro; IPR001506; Astacin.
CC InterPro; IPR000152; Asx hydroxyl.
CC InterPro; IPR000859; CUB domain.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR006209; EGF_like.
CC InterPro; IPR006026; Ntn_Mrptdse.
CC InterPro; IPR006025; Zn_Mrptdse.
CC Pfam; PF01400; Astacin; 1.
CC Pfam; PF00431; CUB; 5.
CC Pfam; PF00008; EGF; 2.
CC PRINTS; PR00480; ASTACIN.
CC SMART; SM00042; CUB; 5.
CC SMART; SM00179; EGF_CA; 2.
CC SMART; SM00235; ZnMG; 1.
CC PROSITE; PS00142; ZINC_PROTEASE; 1.
CC PROSITE; PS01180; CUB; 5.
CC PROSITE; PS00010; ASX_HYDROXYL; 2.
CC PROSITE; PS00022; EGF_1; FALSE_NEG.
CC PROSITE; PS01186; EGF_2; 2.
CC PROSITE; PS01187; EGF_CA; 2.
CC Growth factor; Cytokine; Repeat; Bone; Cartilage; Hydrolase;
CC Metalloprotease; EGF-like domain; Zinc; Calcium; Signal;
CC Glycoprotein; Zymogen; Alternative splicing.
CC SIGNAL 1 22
CC PROPEP 23 120
CC CHAIN 121 986
CC DOMAIN 121 321
CC DOMAIN 322 434
CC DOMAIN 435 546
CC DOMAIN 547 588
CC DOMAIN 591 703
CC DOMAIN 704 743
CC DOMAIN 747 859
CC DOMAIN 860 976
CC METAL 213 213
CC ACT_SITE 214 214
```





GO; GO:0007267; P:cell-cell signaling; TAS.  
GO; GO:0007397; P:histogenesis and organogenesis; TAS.  
GO; GO:0008284; P:positive regulation of cell proliferation; TAS.  
GO; GO:0007165; P:signal transduction; TAS.  
InterPro; IPR000859; CUB domain.  
InterPro; IPR000421; FAS5 C.  
InterPro; IPR000998; MAM domain.  
Pfam; PF00431; CUB; 2.  
Pfam; PF00754; F5\_F8\_type\_C; 2.  
Pfam; PF00629; MAM; 1.  
PRINTS; PR00020; MAMDOMAIN.  
SMART; SM00042; CUB; 2.  
SMART; SM00231; FAS5C; 2.  
SMART; SM00137; MAM; 1.  
PROSITE; PS01180; CUB; 2.  
PROSITE; PS01285; FAS5C; 1; 2.  
PROSITE; PS01286; FAS5C; 2.  
PROSITE; PS00022; FAS5C; 2.  
PROSITE; PS00740; MAM; 1; 1.  
PROSITE; PS00600; MAM; 2; 1.  
Angiogenesis; Transmembrane; Glycoprotein; Neuron; Signal; Repeat;  
Receptor; Alternative splicing; 3D-structure.  
CHAIN 1 21  
FT CHAIN 22 923 NEUROFILIN-1.  
FT DOMAIN 22 856 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 857 879 POTENTIAL.  
FT DOMAIN 880 923 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 27 141 CUB 1.  
FT DOMAIN 147 265 CUB 2.  
FT DOMAIN 275 424 F5/8 TYPE C 1.  
FT DOMAIN 431 583 F5/8 TYPE C 2.  
FT DOMAIN 645 811 MAM.  
FT DISULFID 27 54 PROBABLE.  
FT DISULFID 82 104 PROBABLE.  
FT DISULFID 147 173 PROBABLE.  
FT DISULFID 206 228 PROBABLE.  
FT DISULFID 275 424 BY SIMILARITY.  
FT DISULFID 431 583 BY SIMILARITY.  
FT CARBOHYD 150 150 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 261 261 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 300 300 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 522 522 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 842 842 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT VARSPLIC 642 644 EFP -> GIK (in isoform 2).  
FT VARSPLIC 645 923 Missing (in isoform 2).  
FT VARSPLIC 645 923 Missing (in isoform 2).  
FT CONFLICT 26 26 K -> E (IN REF. 1).  
FT CONFLICT 749 749 D -> H (IN REF. 2).  
FT CONFLICT 855 855 E -> D (IN REF. 2).  
SQ SEQUENCE 923 AA; 103120 MW; ADEADC4A849B5D57 CRC64;  
  
Query Match 9.5%; Score 176; DB 1; Length 923;  
Best Local Similarity 32.6%; Pred. No. 1.6e-06;  
Matches 57; Conservative 24; Mismatches 68; Indels 26; Gaps 9;  
  
QY 50 VTISNGSHSPKFFHYPRNMLVRLVAVDENVRILQTFDERFLEDPEDDICKYDFV 109  
Db 31 IKIESPGYLTSGYSHVHPSEKCEWLQAPDPYQIRIMNFPHFLEDRD---CKYDIV 87  
QY 110 EV--EPPSGVLRWCGSGTVPKQTSKGNHIRFVSDEYFPPEPFCIHYSIM--P 165  
Db 88 EYFDGENENHGRFKGCGK-IAPPPVSSGPFIFKIFVSD-YETHGAGFSIRYIFKRGF 145  
QY 166 QYTE--TTSFSLP-----PSSLSLDLNNATVAFSTLEELRY----LEPD 206  
Db 146 ECSQNYTPSPGVIKSPGFPEKYPNSLECTYI---VFAPKXSEILFEFSFDLEPD 197  
  
RESULT 6  
TLD\_BRARE  
ID TLD\_BRARE  
AC 057460; PRT; 1022 AA.

DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Dorsal-ventral patterning tolloid protein precursor (BC 3.4.24.-)  
DE (Mini fin protein).  
GN TOLLOID OR TLD OR MFN.  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_taxid=7955;  
RN [1]  
RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.  
RC TISSUE=Gastrula;  
RX MEDLINE=98057457; PubMed=9395394;  
RA Blader P., Raasteg S., Fischer N., Straehle U.;  
RT "Cleavage of the BMP-4 antagonist chordin by zebrafish Tolloid.";  
RL Science 278:1937-1940 (1997).  
RN [2]  
RP FUNCTION, AND TISSUE SPECIFICITY.  
RX MEDLINE=99107076; PubMed=10375503;  
RA Connors S.A., Trout J., Ekker M., Mullins M.C.;  
RT "The role of tolloid/mini fin in dorsoventral pattern formation of the zebrafish embryo.";  
RL Development 126:3119-3130 (1999).  
CC -!- FUNCTION: Required for patterning ventral tissues of the tail. May increase bone morphogenetic protein (BMP) activity at the end of gastrulation by proteolytic cleavage of chordin and release of BMP from inactive complexes.  
CC -!- TISSUE SPECIFICITY: During gastrulation, accumulates around the closing blastopore with greater expression ventrally. At the animal pole, expressed in the ectoderm flanking the anterior neural plate. At the 10-somite stage, expressed in the developing tailbud and cranial neural crest. At the 20-somite stage, also expressed in the hematopoietic system.  
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.  
CC -!- SIMILARITY: Contains 2 EGF-like domains.  
CC -!- SIMILARITY: Contains 5 CUB domains.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; AF027596; AAC60304.1; --  
CC HSSP; P35555; IEMN.  
CC MEROPS; M12.016; --  
CC ZFIN; ZDB-GENE-990415-265; tolloid.  
DR InterPro; IPR001506; Astacin.  
DR InterPro; IPR000152; Asx hydroxyl.  
DR InterPro; IPR000859; CUB domain.  
DR InterPro; IPR001861; EGF\_Ca.  
DR InterPro; IPR006209; EGF like.  
DR InterPro; IPR006026; Nzn Mtpetpds.  
DR InterPro; IPR006025; Zn Mtpetpds.  
DR Pfam; PF01400; Astacin; 1.  
DR Pfam; PF00431; CUB; 5.  
DR Pfam; PF00008; EGF; 2.  
DR PRINTS; PR00480; ASTACIN.  
DR SMART; SM00042; CUB; 5.  
DR SMART; SM00179; EGF\_Ca; 2.  
DR SMART; SM00235; ZMNC; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 2.  
DR PROSITE; PS01180; CUB; 5.  
DR PROSITE; PS00022; EGF 1; FALSE\_NEG.  
DR PROSITE; PS01186; EGF 2; 2.  
DR PROSITE; PS01187; EGF\_Ca; 2.  
DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
KW Developmental protein; Hydrolase; Protease; Metalloprotease; Zinc;  
KW Metal-binding; Calcium; EGF-like domain; Repeat; Signal; Glycoprotein;



```
KW Zymogen. 1 32
FT SIGNAL 33 156
FT PROPEP 157 1022
FT CHAIN 157 1022
FT DOMAIN 157 357
FT DOMAIN 358 470
FT DOMAIN 471 583
FT DOMAIN 583 624
FT DOMAIN 627 739
FT DOMAIN 739 779
FT DOMAIN 783 895
FT DOMAIN 896 1012
FT METAL 249 249
FT ACT SITE 250 250
FT METAL 253 253
FT METAL 259 259
FT METAL 358 384
FT DISULFID 411 433
FT DISULFID 471 497
FT DISULFID 524 546
FT DISULFID 587 599
FT DISULFID 595 608
FT DISULFID 610 623
FT DISULFID 627 653
FT DISULFID 680 702
FT DISULFID 743 754
FT DISULFID 750 763
FT DISULFID 765 778
FT DISULFID 783 809
FT DISULFID 836 858
FT DISULFID 896 926
FT DISULFID 953 975
FT CARBOHYD 129 129
FT CARBOHYD 178 178
FT CARBOHYD 368 368
FT CARBOHYD 399 399
FT CARBOHYD 635 635
SQ SEQUENCE 1022 AA; A68CALD0E41793F9 CRC64;

Query Match 9.4%; Score 174; DB 1; Length 1022;
Best Local Similarity 41.7%; Pred. No. 2.7e-06;
Matches 45; Conservative 20; Mismatches 35; Indels 8; Gaps 6;

Qy 55 NGSIHSPKFFHTYPRNMVLRVAVDENVRITQTFDERFGLDEPDICKYDFVEVEE- 113
Db 635 NGTITFGWPKEYPFNKNCVQVAPTQ-YRISMQF-EAFLEG--NEVCYDYVEVRSG 690

Qy 114 -PSDGSVLGRWCGSGTVPKGKTSKNHIRIRFVSDEYFPSPGFCIH 160
Db 691 LSSDSKLHGKCYGT-EVEVITVSQNNNRIBFKSDNTV-SKKGPKAHF 736

RESULT 7
NRPI_RAT STANDARD; PRT; 922 AA.
AC Q9QWJ9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropilin-1 precursor (Vascular endothelial cell growth factor 165 receptor).
GN NRPI.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=97433085; PubMed=9288754;
```

```
RA Kolodkin A.L., Levengood D.V., Rowe E.G., Tai Y.-T., Giger R.J.,
RA Ginty D.D.;
RT "Neuropilin is a semaphorin III receptor.";
RL Cell 90:753-762(1997).
CC -!- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE
CC CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF
CC CERTAIN NEURONAL CIRCUITS AND IN ORGANOREGULATION OF THE NERVOUS
CC SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS. IT
CC BINDS TO SEMAPHORIN 3A, THE PLGF-2 ISOFORM OF PGF, THE VEGF-165
CC ISOFORM OF VEGF AND VEGF-B. COEXPRESSION WITH KDR RESULTS IN
CC INCREASED VEGF-165 BINDING TO KDR AS WELL AS INCREASED CHEMOTAXIS.
CC IT MAY REGULATE VEGF-INDUCED ANGIOGENESIS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC -!- TISSUE SPECIFICITY: FOUND IN THE EMBRYONIC NERVOUS SYSTEM.
CC -!- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
CC -!- SIMILARITY: Contains 2 CUB domains.
CC -!- SIMILARITY: Contains 2 F5/8 type C domains.
CC -!- SIMILARITY: Contains 1 MAM domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR HSSP; AF016296; AAC53337.1; -.
DR InterPro; IPR000859; CUB domain.
DR InterPro; IPR000421; FAS8_C.
DR InterPro; IPR000998; MAM_domain.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00754; F5_F8 type C; 2.
DR PRINTS; PR000629; MAM; 1.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00231; FAS8C; 2.
DR SMART; SM00137; MAM; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01285; FAS8C_1; 2.
DR PROSITE; PS01286; FAS8C_2; 2.
DR PROSITE; PS00022; FAS8C_3; 2.
DR PROSITE; PS00740; MAM_1; 1.
DR PROSITE; PS00060; MAM_2; 1.
KW Angiogenesis; Transmembrane; Glycoprotein; Neuron; Signal; Repeat;
KW Receptor.
FT SIGNAL 1 21
FT CHAIN 22 922
FT DOMAIN 22 855
FT TRANSMEM 856 880
FT DOMAIN 881 922
FT DOMAIN 27 141
FT DOMAIN 147 265
FT DOMAIN 275 424
FT DOMAIN 431 583
FT DOMAIN 645 811
FT DISULFID 27 54
FT DISULFID 82 104
FT DISULFID 147 173
FT DISULFID 206 228
FT DISULFID 275 424
FT DISULFID 431 583
FT CARBOHYD 150 150
FT CARBOHYD 261 261
FT CARBOHYD 300 300
FT CARBOHYD 522 522
FT CARBOHYD 841 841
SQ SEQUENCE 922 AA; 103082 MW; CC6F82AD098B0F2E CRC64;

Query Match 9.3%; Score 172; DB 1; Length 922;
Best Local Similarity 31.5%; Pred. No. 3.4e-06;
Matches 56; Conservative 21; Mismatches 67; Indels 34; Gaps 8;
```

Qy 2 LLLGLLLTSALAGORTCTRAESNLSKQLQLSDKEQNGVQDPRHVRVVTISGNGSIHSP 61  
 Db 7 LCATLALALAG-----AFRSKCGG-----TKIENPGYLTSP 42  
 Qy 62 KFPHTYPRNMLVRLVAVDENVRILTDFRFGLEDPEDDICKYDFVEV--EBPSDGSV 119  
 Db 43 GYPHSYHSEKCEWLIQAEPYQRIINFNPHFDLEDRLD---CKDYVEVIDGENEGRL 99  
 Qy 120 LGRWCGSTVGKQTSKGNHRIKRVSDYEPSPGFCIHYSIIM--PQVET-TSPS 174  
 Db 100 WKGFCGK-IAPSPVSSGPFLLFIKFSVD-YETHGAGFSIRYEIFKRGPECSQNYTAPT 155

RESULT 8  
 NRPI\_MOUSE STANDARD; PRT; 923 AA.  
 ID NRPI\_MOUSE 1 21  
 AC P97333; NEUROFILIN-1.  
 DT 01-NOV-1997 (Rel. 35, Created) EXTRACELLULAR (POTENTIAL).  
 DT 01-NOV-1997 (Rel. 35, Last sequence update) POTENTIAL.  
 DT 28-FEB-2003 (Rel. 41, Last annotation update) CYTOPLASMIC (POTENTIAL).  
 DE Neupilin-1 precursor (A5 protein).  
 GN NRPI OR NRP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]

SEQUENCE FROM N.A.  
 RP STRAIN=BAUB/C; TISSUE=Embryonic brain;  
 RC MEDLINE=96353149; PubMed=8748368;  
 RA Kawakami A., Kitukawa T., Takagi S., Fujisawa H.;  
 RA "Developmentally regulated expression of a cell surface protein,  
 RT neupilin, in the mouse nervous system.";  
 RL J. Neurobiol. 29:1-17(1996).

CC -!- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE  
 CC CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF  
 CC CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS  
 CC SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS. IT  
 CC BINDS TO SEMAPHORIN 3A, THE PLGF-2 ISOFORM OF EGF, THE VEGF-165  
 CC ISOFORM OF VEGF AND VEGF-B. COEXPRESSION WITH KDR RESULTS IN  
 CC INCREASED VEGF-165 BINDING TO KDR AS WELL AS INCREASED CHEMOTAXIS.  
 CC IT MAY REGULATE VEGF-INDUCED ANGIOGENESIS (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- TISSUE SPECIFICITY: NERVOUS SYSTEM.  
 CC -!- SIMILARITY: BELONGS TO THE NEUROFILIN FAMILY.  
 CC -!- SIMILARITY: Contains 2 CUB domains.  
 CC -!- SIMILARITY: Contains 2 F5/8 type C domains.  
 CC -!- SIMILARITY: Contains 1 MAM domain.

CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
 DR EMBL; D50086; BAA08789.1; -.  
 DR HSSP; P12259; 1CZT.  
 DR MGD; MGI:106206; Nrp.  
 DR InterPro; IPR000859; CUB domain.  
 DR InterPro; IPR000421; FA58\_C.  
 DR InterPro; IPR000998; MAM\_domain.  
 DR Pfam; PF00431; CUB; 2.  
 DR Pfam; PF00754; F5\_F8\_type\_C; 2.  
 DR Pfam; PF00629; MAM; 1.  
 DR PRINTS; PR00020; MAMDOMAIN.  
 DR SMART; SM00042; CUB; 2.  
 DR SMART; SM00231; FA58C; 2.  
 DR SMART; SM00137; MAM; 1.  
 DR PROSITE; PS01180; CUB; 2.  
 DR PROSITE; PS01285; FA58C\_1; 2.

DR PROSITE; PS01286; FA58C\_2; 2.  
 DR PROSITE; PS00222; FA58C\_3; 2.  
 DR PROSITE; PS00740; MAM\_1; 1.  
 DR PROSITE; PS00600; MAM\_2; 1.  
 KW Angiogenesis; Transmembrane; Glycoprotein; Neurone; Signal; Repeat;  
 KW Receptor.  
 FT SIGNAL 1 21 POTENTIAL.  
 FT CHAIN 22 923 NEUROFILIN-1.  
 FT DOMAIN 22 856 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 857 879 POTENTIAL.  
 FT DOMAIN 880 923 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 27 141 CUB 1.  
 FT DOMAIN 147 265 CUB 2.  
 FT DOMAIN 275 424 F5/8 TYPE C 1.  
 FT DOMAIN 431 583 F5/8 TYPE C 2.  
 FT DOMAIN 645 811 MAM.  
 FT DISULFID 27 54 PROBABLE.  
 FT DISULFID 82 104 PROBABLE.  
 FT DISULFID 147 173 PROBABLE.  
 FT DISULFID 206 228 PROBABLE.  
 FT DISULFID 275 424 BY SIMILARITY.  
 FT DISULFID 431 583 BY SIMILARITY.  
 FT CARBOHYD 150 150 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 261 261 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 300 300 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 522 522 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 842 842 N-LINKED (GLCNAC. .) (POTENTIAL).  
 SQ SEQUENCE 923 AA; 103020 MW; 0644B8A170796808 CRC64;

Query Match 9.1%; Score 169; DB 1; Length 923;  
 Best Local Similarity 31.5%; Pred. No. 6e-06;  
 Matches 56; Conservative 21; Mismatches 67; Indels 34; Gaps 8;  
 Qy 2 LLLGLLLTSALAGORTCTRAESNLSKQLQLSDKEQNGVQDPRHVRVVTISGNGSIHSP 61  
 Db 7 LCATLALALAG-----AFRSKCGG-----TKIENPGYLTSP 42  
 Qy 62 KFPHTYPRNMLVRLVAVDENVRILTDFRFGLEDPEDDICKYDFVEV--EBPSDGSV 119  
 Db 43 GYPHSYHSEKCEWLIQAEPYQRIINFNPHFDLEDRLD---CKDYVEVIDGENEGRL 99  
 Qy 120 LGRWCGSTVGKQTSKGNHRIKRVSDYEPSPGFCIHYSIIM--PQVET-TSPS 174  
 Db 100 WKGFCGK-IAPSPVSSGPFLLFIKFSVD-YETHGAGFSIRYEIFKRGPECSQNYTAPT 155

RESULT 9  
 NRPI\_CHICK STANDARD; PRT; 914 AA.  
 ID NRPI\_CHICK 1 21  
 AC P97955;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neupilin-1 precursor (A5 protein).  
 GN NRPI OR NRP.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus  
 OX NCBI\_TaxID=9031;  
 RN [1]

SEQUENCE FROM N.A.  
 RP STRAIN=White leghorn; TISSUE=Embryonic brain;  
 RC MEDLINE=95324761; PubMed=7601310;  
 RA Takagi S., Kasuya Y., Shimizu M., Matsuura T., Tsuboi M., Kawakami A.,  
 RA Fujisawa H.;  
 RT "Expression of a cell adhesion molecule, neupilin, in the  
 RT developing chick nervous system.";  
 RL Dev. Biol. 170:207-222(1995).  
 CC -!- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE  
 CC CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF  
 CC CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS  
 CC SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS (BY

```

CC SIMILARITY). SEEMS TO HAVE CALCIUM-INDEPENDENT CELL ADHESION
CC PROPERTIES.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: DEVELOPING NERVOUS SYSTEM; OPTIC TECTUM
CC (LAYERS D AND E OF SGFS), AMACRINE CELLS OF RETINA, NEURITES OF
CC DORSAL ROOT GANGLIA. ALSO EXPRESSED IN NONNEURONAL CELLS, E.G.
CC BLOOD VESSELS IN THE ENTIRE EMBRYO.
CC -1- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
CC -1- SIMILARITY: Contains 2 CUB domains.
CC -1- SIMILARITY: Contains 2 F5/8 type C domains.
CC -1- SIMILARITY: Contains 1 MAM domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D45416; BAA08256.1; -.
CC HSPF; P12259; LC2T.
CC InterPro; IPR000859; CUB domain.
CC InterPro; IPR000421; FAS8_C.
CC InterPro; IPR000998; MAM_domain.
CC Pfam; PF00431; CUB; 2.
CC Pfam; PF00754; F5_F8_type_C; 2.
CC Pfam; PF00629; MAM; 1.
CC PRINTS; PR00020; MAMDOMAIN.
CC SMART; SM00042; CUB; 2.
CC SMART; SM00231; FAS8C; 2.
CC SMART; SM00137; MAM; 1.
CC PROSITE; PS01180; CUB; 2.
CC PROSITE; PS01285; FAS8C_1; 2.
CC PROSITE; PS01286; FAS8C_2; 2.
CC PROSITE; PS00022; FAS8C_3; 2.
CC PROSITE; PS00740; MAM_1; 1.
CC PROSITE; PS00060; MAM_2; 1.
CC Angiogenesis; Transmembrane; Glycoprotein; Neuron; Signal; Repeat;
CC Receptor; Cell adhesion.
CC SIGNAL 1 18 POTENTIAL.
CC CHAIN 19 914 NEUROPILIN-1.
CC DOMAIN 20 847 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 848 870 POTENTIAL.
CC DOMAIN 871 914 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 25 139 CUB 1.
CC DOMAIN 145 263 CUB 2.
CC DOMAIN 273 422 F5/8 TYPE C 1.
CC DOMAIN 429 581 F5/8 TYPE C 2.
CC DOMAIN 636 801 MAM.
CC DISULFID 25 52 PROBABLE.
CC DISULFID 80 102 PROBABLE.
CC DISULFID 145 171 PROBABLE.
CC DISULFID 204 226 PROBABLE.
CC DISULFID 273 422 BY SIMILARITY.
CC DISULFID 429 581 BY SIMILARITY.
CC SEQUENCE 914 AA; 102480 MW; DD2EE6D6F0CBB68C CRC64;
CC
CC Query Match 9.0%; Score 167; DB 1; Length 914;
CC Best Local Similarity 28.8%; Pred. No. 8.6e-06;
CC Matches 51; Conservative 31; Mismatches 65; Indels 30; Gaps 9;
CC
CC 50 VTISNGSHSPKPHYPRNNVLRVAVDENVRILQTFORFGLDEPDIDICKYDFV 109
CC : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CC 29 IKILSPYLTSQYQSYHPSKCEWLIQAPPYQRIIMNFPHFLEDRD---CKYDV 85
CC : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CC 110 EV--EPPSGSVLGRWCGSGTVPGKTSKGNHIRFVSDYPPSPGFCIHYSIIM--P 165
CC : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CC 86 EVIDGNABEGLWGYCKGK-IAPPLVSSGPLYLFKIFVSD-YETHGAGFSIRYEVKRGF 143
CC : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CC 166 QYTE--TTSFSLP-----PSSLSLDL-----LNAVTAFTLEILRYLEPD 206
CC : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CC 144 ECSRNFTSSGMKSPGFPEKYPNSLECTYIIAPKMSRIILEFESFE-----LEPD 195
CC : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

## RESULT 10

```

SPAN_STRPU SPAN_STRPU STANDARD; PRT; 616 AA.
ID SPAN_STRPU
AC P98068;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE SPAN protein precursor (EC 3.4.24.-).
GN SPAN.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92315921; PubMed=1618141;
RA Reynolds S.D., Angerer L.M., Palis J., Nasir A., Angerer R.C.;
RT "Early mRNAs, spatially restricted along the animal-vegetal axis of
RT sea urchin embryos, include one encoding a protein related to tolloid
RT and BMP-1."; 114:769-786 (1992).
RL Development
CC -1- TISSUE SPECIFICITY: ASYMMETRICALLY ALONG THE ANIMAL-VEGETAL AXIS
CC OF THE BLASTULA.
CC -1- DEVELOPMENTAL STAGE: VERY EARLY BLASTULA (BETWEEN 16-CELL STAGE
CC AND HATCHING).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
CC -1- SIMILARITY: Contains 2 CUB domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M84144; AAA30072.1; -.
CC HSPF; P28925; IIAF.
CC InterPro; IPR001506; Astacin.
CC InterPro; IPR000859; CUB domain.
CC InterPro; IPR006209; EGF-like.
CC InterPro; IPR006210; IEGF.
CC InterPro; IPR006026; Nzn_Mtpeptdse.
CC InterPro; IPR006025; Zn_Mtpeptdse.
CC Pfam; PF01400; Astacin; 1.
CC Pfam; PF00431; CUB; 2.
CC PRINTS; PR00480; ASTACIN.
CC SMART; SM00042; CUB; 2.
CC SMART; SM00181; EGF; 1.
CC SMART; SM00235; ZmC; 1.
CC PROSITE; PS00142; ZINC_PROTEASE; 1.
CC PROSITE; PS01180; CUB; 2.
CC PROSITE; PS00022; EGF_1; 1.
CC PROSITE; PS01186; EGF_2; FALSE_NEG.
CC Developmental protein; Repeat; Hydrolase; Protease; Zinc; Embryo;
CC Metalloprotease; EGF-like domain; Signal.
CC SIGNAL 1 16 POTENTIAL.
CC PROPEP 17 93 ACTIVATION PEPTIDE (POTENTIAL).
CC CHAIN 94 616 SPAN PROTEIN.
CC DOMAIN 89 93 ARG/LYS-RICH (BASIC).
CC DOMAIN 295 329 METALLOPROTEASE.
CC DOMAIN 340 450 EGF-LIKE.
CC DOMAIN 451 502 CUB 1.
CC DOMAIN 503 614 THR-RICH.
CC DOMAIN 190 190 CUB 2.
CC METAL 190 190 ZINC (CATALYTIC) (BY SIMILARITY).
CC ACT_SITE 191 191 BY SIMILARITY.
CC METAL 194 194 ZINC (CATALYTIC) (BY SIMILARITY).

```

```

FT METAL          200      200      ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID       299      315
FT DISULFID       305      317      BY SIMILARITY.
FT DISULFID       319      328      BY SIMILARITY.
SQ SEQUENCE       616 AA; 67902 MW; 397CD923FFB9EB98 CRC64;
Query Match      8.8%; Score 163.5; DB 1; Length 616;
Best Local Similarity 28.0%; Pred. No. 1e-05;
Matches 63; Conservative 30; Mismatches 85; Indels 47; Gaps 11;

QY 9 LTSALAGQRTG-TRAESNLSSKLQSSDKE-----QNGVQDPRIHVV--TISGN- 55
Db 269 LNSRL-GORTLSAADIELANIEYEDCDVEDCSNDECLNGYHDADCDVCPSSVSGDL 327
QY 56 -----GSIHSKPPHYPRNVLVWELVADEVNVRQLQTFDERF 94
Db 328 CDGGPTVRPDCSVRFTEMTGEITSPNPSYEDNTACVIEG-PYGSTIELTF--L 383
QY 95 GLEDPEDDICKYDFVEEPPSPGVLGRWCGSGTVPGKQTSKGNHIRIFVSDYFPPS-- 152
Db 384 DMEIETETLCRYDAVEVRKDDINSIGKPCGN-TLPPVQISSNQMVSTSD---PSIT 439
QY 133 EPGFCHHSIIMPQVT--ETTSFSLVPPSSLSLDLNNAVTAFST 195
Db 440 RGFKATYVILIIQTTFVSTFTTLQTPPSTTTTLQTNPNSTTLQT 484

RESULT 11
PCOI_HUMAN
ID PCOI_HUMAN STANDARD; PRT; 449 AA.
AC Q15113; O14550;
DC 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Procollagen C-proteinase enhancer protein precursor (PCPE) (Type I
DE procollagen COOH-terminal proteinase enhancer) (type 1 procollagen C-
DE proteinase enhancer protein).
GN PCOLCE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=95014462; PubMed=7523404;
RA Takahara K., Kessler E., Binianinov L., Brusel M., Eddy R.L.,
RA Jani-Sait S., Shows T.B., Greenspan D.S.;
RT "Type I procollagen COOH-terminal proteinase enhancer protein:
RT identification, primary structure, and chromosomal localization of the
RT cognate human gene (PCOLCE).";
RL J. Biol. Chem. 269:26280-26285(1994).
RN [2]
RP REVISIONS TO 56; 154 AND 373.
RA Kessler E.;
RL Unpublished observations (FEB-2000).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Hirahara I., Syoufuda K., Harada K., Tomita M., Urakami K., Terai H.,
RA Morisaki N., Saito Y.;
RT "Smooth muscle cell derived procollagen C-protease enhancer protein.";
RL Cell Struct. Funct. 21:662-662(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=99018118; PubMed=9799793;
RA Gloeckner G., Scherer S., Schattevoy R., Boright A.P., Weber J.,
RA Tsui L.-C., Rosenthal A.;
RT "Large-scale sequencing of two regions in human chromosome 7q22:
RT analysis of 650 kb of genomic sequence around the EPO and CUTL1 loci
RT reveals 17 genes.";
RL Genome Res. 8:1060-1073(1998).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=99134301; PubMed=9933570;
RA Scott I.C., Clark T.G., Takahara K., Hoffman G.G., Greenspan D.S.;
RT "Structural organization and expression patterns of the human and
RT mouse genes for the type I procollagen COOH-terminal proteinase
RT enhancer protein.";
RL Genomics 55:229-234(1999).
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altshuler S.F., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klatner R.D., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP PARTIAL SEQUENCE, AND CHARACTERIZATION OF INHIBITORY ACTIVITY.
RX MEDLINE=20092317; PubMed=10625689;
RA Mott J.D., Thomas C.I., Rosenbach M.T., Takahara K., Greenspan D.S.,
RA Banda M.J.;
RT "Post-translational proteolytic processing of procollagen C-terminal
RT proteinase enhancer releases a metalloproteinase inhibitor.";
RL J. Biol. Chem. 275:1384-1390(2000).
CC -!- FUNCTION: BINDS TO THE COOH-TERMINAL PROPEPTIDE OF TYPE I
CC PROCOLLAGEN AND ENHANCES PROCOLLAGEN C-PROTEINASE ACTIVITY.
CC -!- FUNCTION: C-TERMINAL PROCESSED PART OF PCPE (CT-PCPE) MAY HAVE AN
CC METALLOPROTEINASE INHIBITORY ACTIVITY.
CC -!- SUBCELLULAR LOCATION: Secreted
CC -!- PTM: C-TERMINALLY PROCESSED AT MULTIPLE POSITIONS.
CC -!- SIMILARITY: Contains 2 CUB domains.
CC -!- SIMILARITY: Contains 1 NTR domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL; L33799; AAA61949.1; ALT SEQ.
CC EMBL; AB008549; BAA32281.1; -
CC EMBL; AF033356; AAC78800.1; -
CC EMBL; AF083655; AAD16041.1; -
CC EMBL; BC000574; AAH00574.1; -
CC EMBL; BC033205; AAH33205.1; -
CC EMBL; HGNC:8738; PCOLCE.
CC MIM; 600270; -
CC GO; GO:0008151; P:cell growth and/or maintenance; TAS.
CC GO; GO:0007275; P:development; TAS.
CC InterPro; IPR000859; CUB domain.
CC InterPro; IPR001134; Netrin_C.
CC Pfam; PF00431; CUB; 2.
CC Pfam; PF01759; NTR; 1.
CC SMART; SM00643; C345C; 1.
CC SMART; SM00042; CUB; 2.

```

```
DR PROSITE; PS01180; CUB; 2.
KW Glycoprotein; Repeat; Signal.
FT SIGNAL 1 25
FT CHAIN 26 449
FT DOMAIN 37 149
FT DOMAIN 159 273
FT DOMAIN 329 438
FT SITE 287 288
FT SITE 288 289
FT SITE 293 294
FT SITE 299 300
FT SITE 303 304
FT CARBOHYD 29 29
FT CARBOHYD 431 431
SQ SEQUENCE 449 AA; 47972 MW; 3D88430158648796 CRC64;

Query Match 8.5%; Score 158; DB 1; Length 449;
Best Local Similarity 34.5%; Pred. No. 1.9e-05;
Matches 48; Conservative 21; Mismatches 50; Indels 20; Gaps 9;

QY 56 GSIHSPKPHHT-YPRNMLVWRLVAVDENVRIQLTFDERFGLDEPDDICKYDFVEV--- 111
Db 168 GILTPNWPESDYPPGISCWHIAPPQV-IALTF-EKPLE--PDYICRIDSVSFENG 223
QY 112 EEPDGSGLGRCGSGTVPKGQTKGNHRIKRVSDYFPPSEPGFCIHYSIIM----- 164
Db 224 AVSDSRRLGRKFGCD-AVPGSISSEGNELLVQVSDLSVTAD-GFSASYKTLPRGTAKEX 281
QY 165 --PQWETTSFVS-LPPSS 180
Db 282 QGPGKRGTEPKVKLPPKS 300

RESULT 12
NRP2_RAT STANDARD; PRT; 925 AA.
AC O35276;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neupilin-2 precursor (Vascular endothelial cell growth factor 165 receptor 2).
GN NRP2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=97433085; PubMed=9288754;
RA Kolodkin A.L., Levengood D.V., Rowe E.G., Tai Y.-T., Giger R.J., Ginty D.D.;
RT "Neupilin is a semaphorin III receptor.";
RL Cell 90:753-762(1997).
CC -!- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165 AND VEGF-145 ISOFORMS OF VEGF, AND THE PLGF-2 ISOFORM OF PGF.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: FOUND IN CERTAIN NEURONAL POPULATIONS OF THE CNS AND IN OTHER NONNEURONAL TISSUES INCLUDING MESENCHYMAL TISSUE LINING IN THE RIBS.
CC -!- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
CC -!- SIMILARITY: Contains 2 CUB domains.
CC -!- SIMILARITY: Contains 2 F5/8 type C domains.
CC -!- SIMILARITY: Contains 1 MAM domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/)
```

```
CC or send an email to license@isb-sib.ch.
CC EMBL; AF016297; AAC53338.1; -.
DR HSSP; P12259; 1CZT.
DR InterPro; IPR000859; CUB domain.
DR InterPro; IPR000421; FAS8_C.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00754; F5_F8 type C; 2.
DR Pfam; PF00629; MAM; 1.
DR PRINTS; PR00020; MAMDOMAIN.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00231; FAS8C; 2.
DR SMART; SM01137; MAM; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01285; FAS8C_1; 2.
DR PROSITE; PS01286; FAS8C_2; 2.
DR PROSITE; PS00222; FAS8C_3; 2.
DR PROSITE; PS50060; MAM_2; 1.
KW Transmembrane; Glycoprotein; Neutrone; Signal; Repeat; Receptor.
FT SIGNAL 1 22
FT CHAIN 23 925
FT DOMAIN 23 858
FT DOMAIN 859 883
FT DOMAIN 884 925
FT DOMAIN 28 142
FT DOMAIN 149 267
FT DOMAIN 277 427
FT DOMAIN 434 592
FT DOMAIN 642 802
FT DISULFID 28 55
FT DISULFID 83 105
FT DISULFID 149 175
FT DISULFID 208 230
FT DISULFID 277 427
FT DISULFID 434 592
FT CARBOHYD 152 152
FT CARBOHYD 157 157
FT CARBOHYD 629 629
FT CARBOHYD 833 833
FT CARBOHYD 834 834
SQ SEQUENCE 925 AA; 103896 MW; 3BF62903F644851C CRC64;

Query Match 8.4%; Score 155.5; DB 1; Length 925;
Best Local Similarity 33.3%; Pred. No. 7.5e-05;
Matches 41; Conservative 19; Mismatches 56; Indels 7; Gaps 4;

QY 42 QDPRHVVVTISGSGSIHSPKPHHTYPRNMLVWRLVAVDENVRIQLTFDERFGLDEPDP 101
Db 24 QDPPCGRLNSKDAGYITSPGYPDYPSHQNCWVYVAPENPQKIVLNFNPFIEKH-D- 82
QY 102 DICKYDFVEEPEPSDGS--VLGRWCGSGTVPKGQTKGNHRIKRVSDYFPPSEPGFCIH 159
Db 83 --CKYDFIEIRDGDSADLLQKHCN-IAPTTIISGSLVLYIKTSD-YARQAGGFSLR 138
QY 160 YSI 162
Db 139 YEI 141

RESULT 13
NRP2_HUMAN STANDARD; PRT; 931 AA.
AC O60462; O14820; O14821;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neupilin-2 precursor (Vascular endothelial cell growth factor 165 receptor 2).
GN NRP2 OR VEGF165R2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

NCBI\_TaxID=9606;  
[1] SEQUENCE FROM N.A. (ISOFORMS A0 AND A17).  
RX MEDLINE=97470888; PubMed=9331348;  
RA Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.;  
RT "Neuropilin-2, a novel member of the neuropilin family, is a high  
RT affinity receptor for the semaphorins Sema E and Sema IV but not Sema  
RT III.";  
RL Neuron 19:547-559(1997).  
RN [2]  
RN SEQUENCE FROM N.A. (ISOFORM A22).  
RP TISSUE=Brain;  
RC  
RX MEDLINE=98180099; PubMed=9529250;  
RA Soker S., Takashima S., Miao H.-Q., Neufeld G., Klagesbrun M.;  
RT "Neuropilin-1 is expressed by endothelial and tumor cells as an  
RT isoform-specific receptor for vascular endothelial growth factor.";  
RT Cell 92:735-745(1998).  
RN [3]  
RN CHARACTERIZATION.  
RP MEDLINE=20309748; PubMed=10748121;  
RA Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;  
RT "Neuropilin-2 and neuropilin-1 are receptors for the 165-amino acid  
RT form of vascular endothelial growth factor (VEGF) and of placenta  
RT growth factor-2, but only neuropilin-2 functions as a receptor for  
RT the 145-amino acid form of VEGF.";  
RL J. Biol. Chem. 275:18040-18045(2000).  
CC -!- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165  
CC AND VEGF-145 ISOFORMS OF VEGF, AND THE PLGF-2 ISOFORM OF PGF.  
CC -!- SUBUNIT: NEUROFILIN-2 PROBABLY FORMS AN HETEROMERIC COMPLEX WITH  
CC NEUROFILIN-1 IN ORDER TO BE A FUNCTIONAL SEMAPHORIN 3C RECEPTOR.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=3;  
CC Name=A22;  
CC IsoId=060462-1; Sequence=Displayed;  
CC Name=A0;  
CC IsoId=060462-2; Sequence=VSP\_004342;  
CC Name=A17;  
CC IsoId=060462-3; Sequence=VSP\_004341;  
CC -!- SIMILARITY: BELONGS TO THE NEUROFILIN FAMILY.  
CC -!- SIMILARITY: Contains 2 CUB domains.  
CC -!- SIMILARITY: Contains 2 F5/8 type C domains.  
CC -!- SIMILARITY: Contains 1 MAM domain.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; AF022859; AAC51788.1; -;  
CC EMBL; AF022860; AAC51789.1; -;  
CC EMBL; AF016098; AAC12922.1; -;  
CC HSRF; P12259; IC2T.  
CC Genew; HGNC:8005; NRP2.  
CC MIN; 602070; -;  
CC GO; GO:0005624; C:membrane fraction; TAS.  
CC GO; GO:0004872; F:receptor activity; TAS.  
CC GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; TAS.  
CC GO; GO:0007411; F:axon guidance; TAS.  
CC InterPro; IPR000859; CUB\_domain.  
CC InterPro; IPR000421; FA58\_C.  
CC InterPro; IPR000998; MAM\_domain.  
CC Pfam; PF00431; CUB; 2.  
CC Pfam; PF00754; F5 F8 type\_C; 2.  
CC Pfam; PF00629; MAM; 1.  
CC PRINTS; PR00020; MAMDOMAIN.  
CC SMART; SM00042; CUB; 2.  
CC SMART; SM00231; FA58C; 2.  
CC SMART; SM00137; MAM; 1.  
CC PROSITE; PS01180; CUB; 2.

DR PROSITE; PS01285; FA58C\_1; 2.  
DR PROSITE; PS01286; FA58C\_2; 2.  
DR PROSITE; PS04022; FA58C\_3; 2.  
DR PROSITE; PS05060; MAM\_2; 1.  
KW Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor;  
FT SIGNAL 1 20 OR 22 (POTENTIAL).  
FT CHAIN 21 931 NEUROFILIN-2.  
FT DOMAIN 21 864 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 865 889 POTENTIAL.  
FT DOMAIN 890 931 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 28 142 CUB 1.  
FT DOMAIN 149 267 CUB 2.  
FT DOMAIN 277 427 F5/8 TYPE C 1.  
FT DOMAIN 434 592 F5/8 TYPE C 2.  
FT DOMAIN 642 802 MAM.  
FT DOMAIN 671 674 POLY-SER.  
FT DISULFID 28 55 BY SIMILARITY.  
FT DISULFID 83 105 BY SIMILARITY.  
FT DISULFID 149 175 BY SIMILARITY.  
FT DISULFID 208 230 BY SIMILARITY.  
FT DISULFID 277 427 BY SIMILARITY.  
FT DISULFID 434 592 BY SIMILARITY.  
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 839 839 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARSPLIC 809 813 Missing (in isoform A17).  
FT VARSPLIC 809 830 Missing (in isoform A0).  
FT CONFLICT 602 602 /FTID=VSP\_004342.  
FT SEQUENCE 931 AA; 104830 MW; 270CBAB69A0A797C CRC64;  
Query Match 8.4%; Score 155.5; DB 1; Length 931;  
Best Local Similarity 32.1%; Pred. No. 7.6e-05;  
Matches 42; Conservative 20; Mismatches 62; Indels 7; Gaps 4;  
QY 34 SDKQNGVQDPRHVRVVTISNGSIHSPKFTHTYPRNVLVAVDENVRILQTFEDER 93  
Db 16 SRHQVRGQDPPCGRLNSKDAGYITSGYQDYPHONCEWTVYAPENQKIVLNFPH 75  
QY 94 FGLEDPEDDICKDYDFVEVEPESDGS--VLGRWCGSGTVFGKQTSKGNHIRIFVSDYFP 151  
Db 76 FEIEKHD--CKYDFIEIRDGSEADLGRKCGN-IAPPTIISGSMYIKFTSD-YAR 130  
QY 152 SEPGFCHYSI 162  
Db 131 QGAGFSURYEI 141  
RESULT 14  
NRP2\_MOUSE  
ID NRP2\_MOUSE STANDARD; PRT; 931 AA.  
AC O35375; O35373; O35374; O35376; O35377; O35378;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Neuropilin-2 precursor (Vascular endothelial cell growth factor 165  
DE receptor 2).  
GN NRP2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS A0; A17; A22; A5; B0 AND B5).  
RC STRAIN=BALB/C;  
RA MEDLINE=97470888; PubMed=9331348;  
RX Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.;  
RT "Neuropilin-2, a novel member of the neuropilin family, is a high  
RT affinity receptor for the semaphorins Sema E and Sema IV but not Sema  
RT III.";



Search completed: November 25, 2003, 21:02:52  
Job time : 9.55655 secs

Query Match	8.3%;	Score 153.5;	DB 1;	Length 326;
Best Local Similarity	27.7%;	Pred. No. 3e-05;		
Matches	56;	Conservative	28;	Mismatches 81; Indels 37; Gaps 9;
Qy	155	GFCIHYSIIMPQVTTETSPSVLPSSLSLDLNNAVTAFSTLELIRYLEPDRMQV----	210	
Db	21	GFSTEHRAVKDVLSERSRSVLERS-----EQIRAASTLELLQVAHSEDKMLWR	73	
Qy	211	-----DLDSLYKPTWOLGKAFLYGKKSQVNNLLKKEVKLYSCTPRNFVSIREL	263	
Db	74	LKLKSLANVDGRSTSHRSTREPAATFYDTET----	129	
Qy	264	-KRTDITFPWPGCLAVKRCGCACCLHNCNEQCVPK-----VTKKYHEVLQRPKTVGK	319	
Db	130	GKTINTFKPCVNVFRCGG---CC--NEESVMCMNTSTSVISKQLFEISV--PLTSV--	180	
Qy	320	LHKSLTVDVALEHHBEEDCVCVRG	341	
Db	181	--PELVVPVKIANHTGCKCLPTG	200	



Result No.	Score	Query Match	Length	DB	ID	Description
1	1848	100.0	345	11	Q9Y71	Q9y71 mus musculus
2	1846	99.9	345	11	Q8C119	Q8ci19 mus musculus
3	1819	98.4	345	11	Q9JHv8	Q9jhv8 mus musculus
4	1801	97.5	345	11	Q9EQX6	Q9eqx6 mus musculus
5	1667	90.2	345	4	Q3UL22	Q3ul22 homo sapien
6	1664	90.0	345	4	Q3NR41	Q3nr41 homo sapien
7	1552	84.0	345	13	Q3I946	Q3i946 gallus gall
8	1375	74.4	258	11	Q8K429	Q8k429 gallus gall
9	754	40.8	370	11	Q9EQT1	Q9eqt1 rattus norv
10	752	40.7	370	4	Q3GZP0	Q3gzp0 homo sapien
11	750.5	40.6	364	4	Q3BwV5	Q3bwv5 homo sapien
12	746.5	40.4	370	11	Q92517	Q925i7 mus musculus
13	440.5	23.8	261	11	Q8K213	Q8k213 mus musculus
14	201	10.9	923	13	Q8QFX6	Q8qfx6 brachydanio
15	201	10.9	923	13	Q8AXP1	Q8axp1 brachydanio
16	192.5	10.4	691	13	O57658	O57658 gallus gall

```

DR EMBL; AK033734; BAC28455.1; --
DR EMBL; AK042767; BAC31358.1; --
DR EMBL; AK052947; BAC35216.1; --
DR MGD; MGI:1859631; PgGfc.
DR InterPro; IPR000859; CUB_domain.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF 2; 1.
DR PROSITE; PS0278; PDGF 2; 1.
SQ SEQUENCE 345 AA; 38741 MW; 3A58A1F701B84EA2 CRC64;

Query Match 100.0%; Score 1848; DB 11; Length 345;
Best Local Similarity 100.0%; Pred. No. 2.2e-166;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGLLLTSLALAGORTGTRAESNLSSKQLSSDKEQNGVQDPHERVVTISGNGSIHS 60
DB 1 MLLGLLLTSLALAGORTGTRAESNLSSKQLSSDKEQNGVQDPHERVVTISGNGSIHS 60
QY 61 PKFPHYPRNMVWRLVAVDENVRITLTFDERFGLDEDDICKYDFVEVEEPPSDGSVL 120
DB 61 PKFPHYPRNMVWRLVAVDENVRITLTFDERFGLDEDDICKYDFVEVEEPPSDGSVL 120
QY 61 PKFPHYPRNMVWRLVAVDENVRITLTFDERFGLDEDDICKYDFVEVEEPPSDGSVL 120
DB 61 PKFPHYPRNMVWRLVAVDENVRITLTFDERFGLDEDDICKYDFVEVEEPPSDGSVL 120
QY 121 GRWCSTGTPGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
DB 121 GRWCSTGTPGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
QY 121 GRWCSTGTPGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
DB 121 GRWCSTGTPGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
QY 121 GRWCSTGTPGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
DB 121 GRWCSTGTPGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
QY 181 LSLDLINNAVTAFTLEELIRYLEPRDQVLDLSLYKPTWQLLGKAFYKKSQVNNLNL 240
DB 181 LSLDLINNAVTAFTLEELIRYLEPRDQVLDLSLYKPTWQLLGKAFYKKSQVNNLNL 240
QY 181 LSLDLINNAVTAFTLEELIRYLEPRDQVLDLSLYKPTWQLLGKAFYKKSQVNNLNL 240
DB 181 LSLDLINNAVTAFTLEELIRYLEPRDQVLDLSLYKPTWQLLGKAFYKKSQVNNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPRK 300
DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPRK 300
QY 301 VTKKYHEVLQRPKTVGKGLHSLTDVALEHHEECDCVCRGNAGG 345
DB 301 VTKKYHEVLQRPKTVGKGLHSLTDVALEHHEECDCVCRGNAGG 345

RESULT 3
Q9JHV8 PRELIMINARY; PRT; 345 AA.
AC Q9JHV8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Platelet-derived growth factor C.
GN PDGFC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss-Webster/NIH;
RX MEDLINE=20417814; PubMed=10960785;
RA Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.;
RT "The mouse pdgfc gene: dynamic expression in embryonic tissues during
organogenesis.";
RL Mech. Dev. 96:209-213(2000).
CC -I- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AF286725; AAF91483.1; -.
DR MGD; MGI:1859631; PdGfc.
DR InterPro; IPR000859; CUB domain.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF 2; 1.
DR PROSITE; PS0278; PDGF 2; 1.
SQ SEQUENCE 345 AA; 38886 MW; FA1486BED6D362F8 CRC64;

Query Match 98.4%; Score 1819; DB 11; Length 345;
Best Local Similarity 98.8%; Pred. No. 1.2e-163;
Matches 341; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MLLGLLLTSLALAGORTGTRAESNLSSKQLSSDKEQNGVQDPHERVVTISGNGSIHS 60
DB 1 MLLGLLLTSLALAGORTGTRAESNLSSKQLSSDKEQNGVQDPHERVVTISGNGSIHS 60
QY 61 PKFPHYPRNMVWRLVAVDENVRITLTFDERFGLDEDDICKYDFVEVEEPPSDGSVL 120
DB 61 PKFPHYPRNMVWRLVAVDENVRITLTFDERFGLDEDDICKYDFVEVEEPPSDGSVL 120
QY 121 GRWCSTGTPGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
DB 121 GRWCSTGTPGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
QY 121 GRWCSTGTPGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
DB 121 GRWCSTGTPGKQTSKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
QY 181 LSLDLINNAVTAFTLEELIRYLEPRDQVLDLSLYKPTWQLLGKAFYKKSQVNNLNL 240
DB 181 LSLDLINNAVTAFTLEELIRYLEPRDQVLDLSLYKPTWQLLGKAFYKKSQVNNLNL 240
QY 181 LSLDLINNAVTAFTLEELIRYLEPRDQVLDLSLYKPTWQLLGKAFYKKSQVNNLNL 240
DB 181 LSLDLINNAVTAFTLEELIRYLEPRDQVLDLSLYKPTWQLLGKAFYKKSQVNNLNL 240
QY 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPRK 300
DB 241 LKEEVKLYSCTPRNFSVSIREELKRTDTTFWPGCLLVKRCGNCACCLHNCNCCQVPRK 300

```

```
Db 241 LKEEVKLYSCTPRNFSVIRELKRKTDTFRWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
QY 301 VTKKHEVQLRPKTKGVKGLHSLTDVALEHHEEDCVCGRNAGG 345
Db 301 VTKKHEVQLRPKTKGVKGLHSLTDVALEHHEEDCVCGRNAGG 345

RESULT 4
Q9E0X6 PRELIMINARY; PRT; 345 AA.
AC Q9E0X6;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE Spinal cord-derived growth factor.
GN RSCDGF.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Kidney;
RX MEDLINE=21092670; PubMed=1162582;
RA Hamada T., Ui-Tei K., Imaki J., Miyata Y.;
RT "Molecular Cloning of SCDGF-B, a Novel Growth Factor Homologous to
RT SCDGF/PDGF-C/fallotin.",
RL Biochem. Biophys. Res. Commun. 280:733-737(2001).
CC -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AB033830; BAB19969.1; -.
DR InterPro; IPR000859; CUB domain.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; PDGF; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF; 2; 1.
SQ SEQUENCE 345 AA; 38734 MW; F296DA6E9B765D10 CRC64;

Query Match 97.5%; Score 1801; DB 11; Length 345;
Best Local Similarity 96.8%; Pred. No. 6.1e-162;
Matches 334; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 MLLGLLLLTALAGQRTGTRAESNLSSKQLQSSDKQNGVQDPRHVRVTTISGNGSIHS 60
Db 1 MLLGLLLLTALAGQRTGTRAESNLSSKQLQSSDKQNGVQDPRHVRVTTISGNGSIHS 60

QY 61 PKFPHYPRNMVLRVLRVAVDENVRVQLTFDERRFGLDEPDDICKYDFVEVEEPSDGSVL 120
Db 61 PKFPHYPRNTVLVWLRVAVDENVRVQLTFDERRFGLDEPDDICKYDFVEVEEPSDGSVL 120

QY 121 GRWCSGTVPGKQTSKGNHIRIRFVSDEVFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Db 121 GRWCSGTVPGKQTSKGNHIRIRFVSDEVFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180

QY 181 LSLLDLNNAVTAFSTLEELIRYLEPRDQVLDLSLYKPTWQLLGKAFYKKSQVNLNL 240
Db 181 LSLLDLNNAVTAFSTLEELIRYLEPRDQVLDLSLYKPTWQLLGKAFYKKSQVNLNL 240

QY 241 LKEEVKLYSCTPRNFSVIRELKRKTDTFRWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
Db 241 LKEEVKLYSCTPRNFSVIRELKRKTDTFRWPGCLLVKRCGNCACCLHNCNECQCVPRK 300

RESULT 5
Q9UL22 PRELIMINARY; PRT; 345 AA.
ID Q9UL22
```

```
AC Q9UL22;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Secretory growth factor-like protein FALLOTEIN (SPINAL CORD-derived
DE growth factor) (Platelet-derived growth factor C).
GN HSCDGF OR PDGFC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Tsai Y.J., Lee R.K.K., Lin S.P.;
RT "Fallotein, a novel growth factor like gene identified in human
RT uterus.",
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20317014; PubMed=10858496;
RA Hamada T., Ui-Tei K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SCDGF, is a unique
RT member of the PDGF/VEGF family.",
RL FEBS Lett. 475:97-102(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21347863; PubMed=11297552;
RA Gilbertson D.G., Duff M.E., West J.W., Kelly J.D., Sheppard P.O.,
RA Hofstrand P.D., Gao Z., Shoemaker K., Bukowski T.R., Moore M.,
RA Feldhaus A.L., Humes J.M., Palmer T.E., Hart C.E.;
RT "Platelet-derived Growth Factor C (PDGF-C), a Novel Growth Factor That
RT Binds to PDGF alpha and beta Receptor.",
RL J. Biol. Chem. 276:27406-27414(2001).
CC -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AF091434; AAF00049.1; -.
DR EMBL; AB033831; BAB03266.1; -.
DR EMBL; AF260738; AAK51637.1; -.
DR InterPro; IPR000859; CUB domain.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF; 2; 1.
SQ SEQUENCE 345 AA; 39029 MW; CDE9E51F40633E78 CRC64;

Query Match 90.2%; Score 1667; DB 4; Length 345;
Best Local Similarity 87.0%; Pred. No. 2.9e-149;
Matches 300; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLLTALAGQRTGTRAESNLSSKQLQSSDKQNGVQDPRHVRVTTISGNGSIHS 60
Db 1 MSLFGLLLLTALAGQRTGTRAESNLSSKQFSSNKQNGVQDPOHERITVTSGSIHS 60

QY 61 PKFPHYPRNMVLRVLRVAVDENVRVQLTFDERRFGLDEPDDICKYDFVEVEEPSDGSVL 120
Db 61 PRFPHYPRNTVLVWLRVAVDENVRVQLTFDERRFGLDEPDDICKYDFVEVEEPSDGTIL 120

QY 121 GRWCSGTVPGKQTSKGNHIRIRFVSDEVFPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180
Db 121 GRWCSGTVPGKQTSKGNHIRIRFVSDEVFPSEPGFCIHYNIVMQFTTEAVSPSVLPSS 180

QY 181 LSLLDLNNAVTAFSTLEELIRYLEPRDQVLDLSLYKPTWQLLGKAFYKKSQVNLNL 240
Db 181 LPDLNLNNAITAFSTLEELIRYLEPERWQDLEDLYRPTWQLLGKAFVGRKSRVVDNL 240

QY 241 LKEEVKLYSCTPRNFSVIRELKRKTDTFRWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
Db 241 LKEEVRLYSCPTPRNFSVIRELKRKTDTFRWPGCLLVKRCGNCACCLHNCNECQCVPRK 300
```

QY 301 VTKYHEVLQRPKGTGKGLHLSLTDVALEHHEECDCVCRGNAGG 345  
 ID Q9NRA1 PRELIMINARY; PRT; 345 AA.  
 DB 301 VTKYHEVLQRPKGTGKGLHLSLTDVALEHHEECDCVCRGSGTG 345

## RESULT 6

QY 301 VTKYHEVLQRPKGTGKGLHLSLTDVALEHHEECDCVCRGNAGG 345  
 ID Q9NRA1 PRELIMINARY; PRT; 345 AA.  
 DB 301 VTKYHEVLQRPKGTGKGLHLSLTDVALEHHEECDCVCRGSGTG 345

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RA MEDLINE=20268201; PubMed=10806482;  
 RA Li X., Ponten A., Aase K., Karlsson L., Abramsson A., Uutela M.,  
 RA Backstrom G., Hellstrom M., Bostrom H., Li H., Soriano P.,  
 RA Bethsholtz C., Heidin C.-H., Alitalo K., Oestman A., Eriksson U.,  
 RT "PDGF-C is a new protease-activated ligand for the PDGF alpha-  
 receptor.";  
 RL Nat. Cell Biol. 2:302-309(2000).  
 CC -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
 DR EMBL; AF244813; AAF80597.1; --.  
 DR Genew; HGNC:8801; PDGFC.  
 DR InterPro; IPR000859; CUB\_domain.  
 DR Pfam; PF00431; CUB; 1.  
 DR Pfam; PF00341; PDGF; 1.  
 DR SMART; SM00042; CUB; 1.  
 DR SMART; SM00141; PDGF; 1.  
 DR PROSITE; PS01180; CUB; 1.  
 DR PROSITE; PS50278; PDGF 2; 1.  
 SQ SEQUENCE 345 AA; 39043 MW; 590889CEA55CC5EA CRC64;

Query Match 90.0%; Score 1664; DB 4; Length 345;  
 Best Local Similarity 86.7%; Pred. No. 5.7e-149;  
 Matches 299; Conservative 28; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLLGLLLTSALAGORTGTRAEISLSSKQLSSDKQNGVDPHRRVVTISGNGSIHS 60  
 DB 1 MSLFGLLLVTSALAGORRGTQAEISLSSKQFSSNKEQNGVDPQHERIITVSTNGSIHS 60  
 QY 61 PKFPHYPRNMLVWRLVAVDENVRIQLTFDERFGLDEDDICKYDFVEVEEPPSDGVL 120  
 DB 61 PFPHYPRNTVLWRLVAVDENVWIQLTFDERFGLDEDDICKYDFVEVEEPPSDGTL 120  
 QY 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIMPOVTTTSPSVLPSS 180  
 DB 121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIMVQFTAVSPSVLPSS 180  
 QY 181 LSLDLLNNAVTAFTLEELIRYLEPDRWQVLDLSYKPTWQLLGKAFLYGKSKVNNL 240  
 DB 181 LPLDLLNNAITAFSTLEDLIRYLEPERWQLEDLYRPTWQLLGKAFVGRKSRVVDLNL 240  
 QY 241 LKEEVKLYSCTPRNFSVSIRELKRDTTFWPGCLLVKRCGNCACCLHNCNCCQVPRK 300  
 DB 241 LTEEVRLYSCTPRNFSVSIRELKRDTTFWPGCLLVKRCGNCACCLHNCNCCQVPSK 300

QY 301 VTKYHEVLQRPKGTGKGLHLSLTDVALEHHEECDCVCRGNAGG 345  
 DB 301 VTKYHEVLQRPKGTGKGLHLSLTDVALEHHEECDCVCRGSGTG 345

## RESULT 7

QY 301 VTKYHEVLQRPKGTGKGLHLSLTDVALEHHEECDCVCRGNAGG 345  
 ID Q91946 PRELIMINARY; PRT; 345 AA.  
 AC Q91946

DT 01-OCT-2000 (TReMBLrel. 15, Created)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
 DT 01-NAR-2003 (TReMBLrel. 23, Last annotation update)  
 DE Spinal cord-derived growth factor.  
 GN SCDGF.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=white leghorn; TISSUE=Spinal cord;  
 RX MEDLINE=20317014; PubMed=10858496;  
 RA Hamada T., Ui-Tei K., Miyata Y.;  
 RT "A novel gene derived from developing spinal cords, SCDGF, is a unique  
 member of the PDGF/VEGF family.";  
 RL FEBS Lett. 475:97-102(2000).  
 CC -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
 DR EMBL; AB033829; BAB03265.1; --.  
 DR InterPro; IPR000859; CUB\_domain.  
 DR Pfam; PF00431; CUB; 1.  
 DR Pfam; PF00341; PDGF; 1.  
 DR SMART; SM00042; CUB; 1.  
 DR SMART; SM00141; PDGF; 1.  
 DR PROSITE; PS01180; CUB; 1.  
 DR PROSITE; PS50278; PDGF 2; 1.  
 SQ SEQUENCE 345 AA; 38940 MW; 97ACEA992BF5128C CRC64;

Query Match 84.0%; Score 1552; DB 13; Length 345;  
 Best Local Similarity 80.3%; Pred. No. 2.3e-138;  
 Matches 277; Conservative 37; Mismatches 31; Indels 0; Gaps 0;

QY 1 MLLGLLLTSALAGORTGTRAEISLSSKQLSSDKQNGVDPHRRVVTISGNGSIHS 60  
 DB 1 MLLGLLLTSALAGRRHGAASDLSSKFPFGAKEQNGVDPQHEKIITVTSNGSIHS 60  
 QY 61 PKFPHYPRNMLVWRLVAVDENVRIQLTFDERFGLDEDDICKYDFVEVEEPPSDGVL 120  
 DB 61 PFPHYPRNTVLWRLVAVDENVWIQLTFDERFGLDEDDICKYDFVEVEEPPSDGTVL 120  
 QY 121 GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIMPOVTTTSPSVLPSS 180  
 DB 121 GRWCGSSVPSQISKGNQIRIRFVSDEYFPSPGFCIHYTLVPHHTAPSPSSLPPSA 180  
 QY 181 LSLDLLNNAVTAFTLEELIRYLEPDRWQVLDLSYKPTWQLLGKAFLYGKSKVNNL 240  
 DB 181 LPLDVNNNAVAGFSTVEELIRYLEPDRWQLEDLYRPTWQLLGKAYIHGRKSRVVDLNL 240  
 QY 241 LKEEVKLYSCTPRNFSVSIRELKRDTTFWPGCLLVKRCGNCACCLHNCNCCQVPRK 300  
 DB 241 LKEEVRLYSCTPRNFSVSIRELKRDTTFWPLCLLVKRCGNCACCHQNCNCCQIPIYK 300  
 QY 301 VTKYHEVLQRPKGTGKGLHLSLTDVALEHHEECDCVCRGNAGG 345  
 DB 301 VTKYHEVLQRPKRGVRLHLSLTDVPLEHHEECDCVCKGNSEG 345

## RESULT 8

QY 301 VTKYHEVLQRPKGTGKGLHLSLTDVALEHHEECDCVCRGNAGG 345  
 ID Q8K429 PRELIMINARY; PRT; 258 AA.  
 AC Q8K429;  
 DT 01-OCT-2002 (TReMBLrel. 22, Created)  
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
 DT 01-NAR-2003 (TReMBLrel. 23, Last annotation update)  
 DE Platelet-derived growth factor C (Fragment).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.

```

RC STRAIN-Sprague-Dawley; TISSUE=Skin;
RA Brown S.A., Coberly D.M., Rohrich R.R., Chao J.J.;
RT "Platelet Derived Growth Factor C (PDGF-C) Expression in Wound
RT Healing";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AF058348; AAM47265.1; -.
DR InterPro; IPR000859; CUB domain.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS02278; PDGF_2; 1.
FT NON TER 1
FT SEQUENCE 258 AA; 29255 MW; 88625B989FCC3F8B CRC64;

Query Match 74.4%; Score 1375; DB 11; Length 258;
Best Local Similarity 96.9%; Pred. No. 8.6e-122;
Matches 250; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 42 QDPHERVVTISGNSIHSPKPHPTPRNMVLVAVDENVRQLTDFERFGLDPEP 101
DB 1 QDPHERVVTISGNSIHSPKPHPTPRNTVLVAVDENVRQLTDFERFGLDPEP 60
QY 102 DICKYDFVEVEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDYFPPSPGFCIHYS 161
DB 61 DLCKYDFVEVEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDYFPPSPGFCIHYS 120
QY 162 IIMPOVTTSPVLPPSSLSLDLNNVAVTSTLEELIRYLEPDRWQVDLSLYKPTWQ 221
DB 121 IIMPOVTTSPVLPPSSLSLDLNNVAVTSTVEELIRFLEPDRWQVDLSLYKPTW 180
QY 222 LLGKAFYKSKSVNLLKKEVKLYSCTPRNFVSIREELKRTDTIIFWPGCLLVKRCG 281
DB 181 LLGKAFYKSKSVNLLKKEVKLYSCTPRNFVSIREELKRTDTIIFWPGCLLVKRCG 240
QY 282 GNCACCLHNCQCQVPR 299
DB 241 GNCACCLHNCQCQVPR 258

RESULT 9
Q9EQT1 PRELIMINARY; PRT; 370 AA.
AC Q9EQT1
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Spinal-cord derived growth factor-B.
GN RSCDGF-B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21092670; PubMed=11162582;
RA Hamada T., Ui-Tei K., Imaki J., Miyata Y.;
RT "Molecular Cloning of SCDGF-B, a Novel Growth Factor Homologous to
RT SCDGF/PDGF-C/fallotain.";
RL Biochem. Biophys. Res. Commun. 280:733-737(2001).
CC -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AB052170; BAB18920.1; -.
DR InterPro; IPR000859; CUB domain.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS02278; PDGF_2; 1.
FT SEQUENCE 370 AA; 42809 MW; 7BB8A251F679BF73 CRC64;

Query Match 40.8%; Score 754; DB 11; Length 370;
Best Local Similarity 46.2%; Pred. No. 8.5e-63;
Matches 151; Conservative 62; Mismatches 86; Indels 28; Gaps 10;

QY 37 EQNGVQD-PRHERVVTISGNSIHSPKPHPTPRNMVLVAVDENVRQLTDFERFG 95
DB 42 ESNHLTDLYRDRDENIRVTGTHVQSPRPFNSYPRNLLTWRLHS-QEKTRIQAFDHFQ 100
QY 96 LEDPEDDICKYDFVEVEPSDGS--VLGRWCGSGTVPGKQTSKGNHIRIRFVSDYFPPSE 153
DB 101 LEEAENDICRYDFVEVEDVSESTVVRGWCGHKEIPPRITSTNQIKTKTFQDDDFVAK 160
QY 154 PGCFIHYSII---MPQ-----VTET-----TSPSVLPSPSSLDLNNVAVTST 195
DB 161 PGFKIYVSFVEDFQPEAASEINWESVTSFSGVSYHSPSVM-DSTLTADALDKAIAEFT 219
QY 196 LBEILRYLEPDRWQVDLSLYKPTWQLLGKAFYKSKSVNLLKKEVKLYSCTPRNF 255
DB 220 VEDLLKYFPASQDDLENLYMDTPRYGRSY-HERKSK-VLDRLNDVDYKYSCTPRNH 277
QY 256 SVSIREELKRTDTIIFWPGCLLVKRCGNCACCLHNCQCQVPRKVKYHEVLQLRP-- 313
DB 278 SVNLREELKLTNAVFPFRCCLLVQRCGNCGCGTLLNWKSTCCSSGKTVKTHEVLKPEGH 337
QY 314 -KTGVKGLHSLDVALEHHEECDCVC 339
DB 338 FKRRGKAKNALVDIQLDHERCDCIC 364

RESULT 10
Q9GZP0 PRELIMINARY; PRT; 370 AA.
AC Q9GZP0;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE SPINAL CORD-derived growth factor-B (MSTP036) (IRIS-expressed growth
DE factor long form) (Platelet-derived growth factor D).
GN HSCDGF-B OR IEGF OR PDGPD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hamada T., Ui-Tei K., Imaki J., Miyata Y.;
RT "Molecular Cloning of SCDGF-B, a Novel Growth Factor Homologous to
RT SCDGF/PDGF-C/fallotain.";
RL Biochem. Biophys. Res. Commun. 0:0-0(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RA Liu B., Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Liu S.,
RA Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J.,
RA Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q.,
RA Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Iris;
RA Wistow G.;
RL "Iris-expressed Growth Factor (IEGF).";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX PubMed=1131881;
RA Bergsten E., Uetala M., Li X., Pietras K., Ostman A., Heldin C.H.,
RA Alitalo K., Eriksson U.;
RT "PDGF-D is a specific, protease-activated ligand for the PDGF beta-
RT receptor.";
RL Nat. Cell Biol. 3:512-516(2001).
RN [5]
RP SEQUENCE FROM N.A.

```

RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Testis;
RA	Strausberg K.;
RL	Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AY027518; AAK20082.1; -
DR	EMBL; BC030645; AAH30645.1; -
DR	InterPro; IPR000859; CUB domain.
DR	InterPro; IPR00072; PD growth factor.
DR	InterPro; IPR000531; TonB_boxC.
DR	Pfam; PF00431; CUB; 1.
DR	PROSITE; PS01180; CUB; 1.
DR	PROSITE; PS00278; PDGF 2; 1.
DR	PROSITE; PS00430; TONB DEPENDENT REC 1; 1.
DR	SEQUENCE 364 AA; 42166 MW; 245C53E8DDEA9EAC CRC64;
DR	SEQUENCE
QY	Query Match 40.6%; Score 750.5; DB 4; Length 364;
QY	Best Local Similarity 45.6%; Pred.No.1.8e-62;
QY	Matches 145; Conservative 58; Mismatches 88; Indels 27; Gaps 8
QY	45 RHEVVVTISGNGSIHGPKFPHTYPNNVLVWRIVAVDENVRIQLTDFERFGLGEDPEDDIC 104
Db	45 RRDETTOVGKGVGVQPRFNPSYRNLLTWRLHS-QENTRIQLVFNDQFGLEEAENDIC 103
QY	105 KYDFVEVERPDSGVIL--GWCSGSVPVKGQTSGKNHIRIRFVSDETPPSPGPCIHYSI 162
Db	104 RYDFVEVEDISETSIIRGRWCGHKVEPPRIKSRNTQIKITFKSDDYFVAKPGFKIYYSL 163
QY	163 I---MPQVIETT-----SPSVLPSPSSLSLDLNNNAVTAFTSLEEILRYLE 204
Db	164 LEDFQFAAASETNWESVTSISGSVNSPSTDP-TLIADALDKKIAEFDTVDLLKYFN 222
QY	205 PDRQWDLDSLKYPTMQLLGKAFLYGKKSKVYNLLLKKEVKLYSCTPRNFVSVIREELK 264
Db	223 PESMQEDLENMYLDTPIRYGRSY-HDRKSK-VOLDRLNDDAKRYSCTPRNYSVNIREELK 280
QY	265 RTDTIFWPGLLVKRCGGNCACCLHNCCQCVPKRVTKKYKHEVLQLRP---KTGVKGLH 321
Db	281 LANWFPPRCLLVQRCGNCGCVTVNRWSCNCGTKVKKYKHEVLQRFEPGHKRRGRANT 340
QY	322 KS LTDVALHEHEECDCVC 339
Db	341 MALVLDIQLDHERCDIC 358
RESULT 12	
Q92517	PRELIMINARY; PRT; 370 AA.
ID	Q92517 Q9DJU18;
AC	01-DSC-2001 (TREMBrel. 19, Created)
DT	01-DSC-2001 (TREMBrel. 19, Last sequence update)
DT	01-MAR-2003 (TREMBrel. 23, Last annotation update)
DE	Platelet-derived growth factor D (18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1110003109 product:platelet-derived growth factor D).
DE	DN PDGFD.
GN	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxId=10090;
OX	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=BALE/c;
RX	MEDLINE=21231380; PubMed=11331882;
RA	Larocheille W.J., Jeffers M., McDonald W.F., Chillakuru R.A.,
RA	Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C.,
RA	Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shimkets J.,
RA	Shimkets R.A., Rothberg J.M., Lichenstein H.S.;
RT	"PDGP D, A Novel Protease-Activated Growth Factor.";
RL	Nat. Cell Biol. 3:517-521(2001).
RL	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6J; TISSUE=Body;



